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Evaluation of sesame (*Sesamum Indicum* L.) genotypes on growth and yield performance using cluster analysis and GYT biplot graph tools

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SESAME is recognized as a global oilseed crop due to its high nutritional value and potential medicinal benefits. This study evaluated 16 sesame genotypes over two seasons (2022 and 2023) to assess genetic variability, yield performance, and related parameters using multivariate analysis of seven quantitative traits. Analysis of variance revealed statistically significant differences among genotypes for all studied traits. Notably, genotypes Intro 289-1 and Hybrid 489-26 outperformed others in average yield, showing strong potential for release. The yield–trait combination (GYT) biplot, which accounted for 74.70% of the total variation, ranked Hybrid 489-26 as the top-performing high-quality genotype, followed by Intro 289-1. Cluster analysis grouped the accessions into six clusters. The second cluster showed high mean values for seed yield and number of branches per plant, making these genotypes valuable for future crossing. Crossing genotypes from different clusters may generate promising segregants for improvement programs. Significant genetic variability, as indicated by genetic parameters and correlations, provides a strong foundation for enhancing sesame genotypes. A breeding program based on hybridization among divergent clusters is recommended and can be effectively designed using these findings to develop superior sesame cultivars.

Keywords: Sesame accessions, Cluster analysis, Genetic distance, GYT biplot.

Introduction

Sesame was referred to as the "Queen of Oilseeds" due to its superior nutritional qualities, long shelf life, and antioxidant capabilities. Sesame oil is used in the manufacture of cosmetics and is also the basis of many preparations (Mukhthambica *et al.*, 2023). Although sesame is useful for food, medicine, and petroleum, its yield potential is not extremely high because sesame is grown in sub marginal areas and high quality, high yields are not achieved due to a lack of appropriate breeding programs (Manjeet *et al.*, 2020).

A bottleneck production issue that explains the lower yield and limited cropping system in the country is the absence of superior genotypes. This makes assessing genotypes that are both adapted to the environmental condition and have a high potential for yield essential (Legesse and Sharew, 2024).

Genotypic selectivity for valuable oil seeds, such as the sesame crop, is significant because of the limited edible oil production in the country. Sesame has a high nutritional value for humans and is one of Egypt's and the world's most important oil crops. Given its ancient presence on Egypt's agricultural map, it was necessary to increase its production to accommodate the rapid growth of the population (Abdelsattar *et al.*, 2020 and Mahdy et al., 2023).

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The total amount of edible oil produced and consumed is substantial with a self-sufficiency rate of about 10% and reliance on imports of 90%. To reduce the production and gap in edible oil, Egypt has to develop a national strategy to increase the area planted to sesame and an effective breeding program to efficiently produce high-yielding varieties (Bedawy and Mohammed, 2018).

Any crop improvement effort that involves characterizing the agro-morphological traits of germplasm must have diversity in order to be successful. It is an intriguing tool for researching genetic diversity because of its affordability and ease of use, but it is subject to strong environmental influences (Tabatabaei *et al.,* 2011; and Badra *et al.,* 2025). It permits the intensity of variation calculated between genotypes to be the primary determinant for the effective conservation and subsequent use of genetic resources (Patel *et al.,* 2024).

The use of multivariate analysis tools to investigate genetic differences and the degree of trait relationships is growing in significance. Consequently, a number of authors have reported the use of cluster analysis (Derbew, 2020; Dido et al., 2020; Yan and Frégeau-Reid (2018). Researchers advise utilizing cluster analysis's significant benefit, which is the ability to group genotypes based on many of intricate traits (Adilova *et al.,* 2020) to select the best genotypes for hybridization programs develop new crop varieties, and understand plant genetic diversity. Therefore, a new method based on multi-trait genotype selection proposed by Yan and Frégeau-Reid (2018) calculates genotypes through yield*trait (GYT) biplot. Methods and attributes can be other than Yield; these can be agronomic properties, seed quality, processing quality, and nutritional quality properties. The GYT biplot uses size levels to rank genotypes. when yield is combined with other traits of interest. Radar charts provide a good visualization of the production genotype, making it easier to see the overall production of each genotype.

This study aimed to (1) identify superior sesame genotypes based on multiple agronomic traits and (2) explore the interrelationships among these traits to support targeted improvement. It focused on currently cultivated, newly developed genotypes that represent the active genetic base in ongoing breeding programs. The novelty of this work lies in its integrative use of genetic parameters, correlation analysis, cluster analysis, and genotype-by-trait (GYT) biplot to establish a comprehensive and precise selection framework. This approach is particularly valuable for sesame, a self-pollinated crop with slow genetic progress, where efficient identification of promising genotypes is essential. Unlike traditional methods that rely solely on seed yield, this study combines multi-trait analysis and clustering to enhance selection accuracy, making it a strategic tool for accelerating sesame improvement.

Materials and Methods:

Plant material

The current investigation was carried out in the summers of 2022 and 2023 at the Agricultural Research Center in Egypt's Giza Agricultural Research Station. New sixteen commercial genotypes representing a wide range of variations were selected. Table 1 displays the origins of the sesame genotypes used in this investigation. They received it from the Field Crop Research Institute's Department of Oil Crop Research at the Agricultural Research Center in Egypt.

Table 1. Origin of the sesame genotypes used in the study.

No.	Genotypes	Origin	Branching type
1	Intro 164	India	Branched
2	B 21	Egypt	Branched
3	Intro 463	USA	Branched
4	Hybrid 484-10		Branched
5	Hybrid 484-16		Branched
6	Intro 527	India	Branched
7	B4-2	Egypt	Branched
8	Intro 203	India	Branched
9	Hybrid 489-26	Local 25 × NA129	Branched
10	Intro 673		Branched
11	Intro 602	Greece	Branched
12	Intro 200	Tanzania	Branched
13	Intro 289-1	USA	Branched
14	Intro 648	Japan	Branched
15	Local 131	Egypt	Branched
16	Intro 641	USA	Non-Branched

Experimental design

On the first of June in both summer seasons of 2022 and 2023, the sixteen sesame genotypes were randomly planted and distributed in a Randomized Complete Block Design in three replicates. Plots of five rows, each measuring 4 m in length and 60 cm in width, were used to sow each genotype. In hills, the seeds were spaced 20 cm apart. For exactly one plant per hill, thinning was carried out after 30 days following sowing. Over the duration of the growing season, the suggested cultural practices were followed. After harvest, oil extraction was estimated using the method outlined by Horwitz *et al.* (1965) using Soxhlet apparatus.

Measured traits

The following traits were also measured: plant height (PH, cm), height of first capsule (FCL, cm) on the main stem, fruiting zone length (FA, cm), number of branches/plant (NBP), number of capsules/plant (NCP), 1000-seed weight (SW, g), seed yield/plant (SY/P, g), seed yield/feddan (SY/fed, kg), and seed oil content (Oil%) using using Soxhlet apparatus as mentioned above. Total quantity of seeds obtained from random maturity plant in every plot.
Statistical procedures

Analysis of variance

Collected data were subjected to analysis of variance (ANOVA) as specified by Steel *et al.*, 1997 using "Genstat" statistical program. We conducted a combined analysis of variance over two seasons after confirming the homogeneity of all the traits under study using *the Levene* test (1960). To find significant differences between genotype means, the least significant difference (LSD) test was employed.

Genetic Parameters and Correlation Coefficients

Genotypic and phenotypic coefficients of variation (GCV% and PCV%) were estimated following Singh & Chaudhury (1985). Broad-sense heritability (h^2b%) was calculated as described by Allard (1960), while genetic advance and its percentage of the mean (GA% of mean) were determined according to Assefa et al. (1999). Correlation coefficients among traits were computed based on Steel & Torrie (1980).

Cluster Analysis

Using Minitab v-16 software, genotype was clustered to evaluate the genetic distance between 16 sesame accessions. Based on the method "Word," a dendrogram was created using the distance matrix from genotype. A dendrogram representing the cluster analysis results was displayed. Additionally, a Euclidean distance measure was used to run the cluster analysis model on the genotypes. It is the most widely used measure for comparing between items. It is just a measurement of the distance in a straight line between the two items.

Genotype by Yield * Trait (GYT) Biplot

Enhancing crop yield and quality is the common objective of both breeding and agronomic management research. Agronomic management studies and crop variety trial data analysis have frequently focused on a single attribute, often yield, whereas genotype and/or management decisions must take into account a number of traits (Yang *et al.*, 2023). Excellent varieties must be identified based on several characteristics based on experiments in multiple settings.

The genotype by yield*trait (GYT) biplot is a new method of genotype selection based on multiple traits, was proposed by Yan and Frégeau-Reid (2019). With that approach, a trait can be any breeding aim other than yield; it could be an attribute related to agronomy, seed quality, processing quality, or nutritional quality. The GYT biplot displays each genotype's trait profile while ranking them according to how well they combine yield with other desired features (Boureima and Yaou, 2019).

Consequently, the GYT biplot technique was applied to determine whether the combination had an impact on the results or whether their ranking changed when the value of a trait of any genotype was low and seed yield was high, or vice versa.
The yield*trait combination value for the number of capsules per plant (NCP) was calculated by multiplying the yield value (SYP) by the trait value for each genotype, for example, SYP*NCP. A value that is greater in the GYT table is always preferred to maximize the production; hence, the values for the yield-trait combinations were calculated by dividing the yield value by the trait value for each genotype, such as plant height (PH/SYP), Consequently, in the GYT table, a lower number is always preferred. (Boureima and Yaou, 2019).
The GYT were analyzed using the adjusted mean values of the traits. By standardizing these mean values to mean zero and unity variance, biases resulting from disparities in trait scales were reduced. The following is how the genotype by yield*trait (GYT) data (Table 2) was acquired.

Selection score

Seven characters and sixteen genotypes were employed in the construction of the selection indices, which were calculated using discriminant function analysis. Multivariate data can be visualized in two dimensions using the radar map, a multi-statistical map (Zhang, 2017). The condition of several sesame indices, including tolerance, antixenosis, and antibiosis, can be graphically and clearly projected.

Table 2. Standardized genotype by yield*trait (GYT) data for the genotypes over the two seasons for all studied traits.

Genotypes	SYP/ PH	SYP* FCL	SYP* FA	SYP* NBP	SYP* NCP	SYP* 1000 SW	SYP* Oil%
Intro 164	-1.96	0.47	-0.38	-0.59	-1.06	-0.51	-1.26
B 21	0.41	1.18	-0.70	1.35	0.07	0.79	0.42
Intro 463	0.33	-0.57	0.02	-0.59	-0.21	-0.62	0.31
Hybrid 484-10	-0.19	-1.18	0.49	-0.51	-0.35	0.05	-0.02
Hybrid 484-16	0.88	1.19	-1.22	0.89	0.49	-0.91	0.19
Intro 527	-0.70	-1.06	1.03	0.20	0.00	-0.39	0.08
B4-2	-0.95	0.08	-0.70	-0.45	0.21	-1.00	-0.50
Intro 203	-1.44	0.20	-1.75	-0.41	-1.31	-1.02	-1.50
Hybrid 489-26	1.21	1.62	0.78	2.22	1.12	2.63	1.38
Intro 673	0.47	0.39	2.61	0.23	0.65	0.65	2.22
Intro 602	-0.20	0.60	-0.63	0.61	1.35	-0.39	-0.31
Intro 200	0.02	-0.64	0.02	-0.33	-0.76	-0.87	-0.06
Intro 289-1	1.61	0.90	0.11	0.88	2.09	-0.14	1.05
Intro 648	-0.79	-1.92	-0.16	-1.26	-0.44	-0.30	-1.53
Local 131	0.02	-0.30	0.10	-0.54	-0.10	0.63	0.02
Intro 641	1.29	-0.96	0.38	-1.71	-1.75	1.40	-0.49

Results and Discussion

Mean performance

Results obtained of the average performance of 16 sesame genotypes was displayed in Table 3. for the studied traits that were significantly affected by genetic makeup. Individual error variances satisfied homogeneity for all studied traits, allowing combined analysis across both seasons. It summarized the average performance of the studied sesame genotypes in terms of oilseeds, seed yield, and other studied morphological characteristics.

Significant differences were found between the sesame genotypes for each trait that was analyzed. In this connection, it is also noticed that the estimate values and coefficient variation were in the statistically acceptable limits for each studied trait, excluding the number of branches per plant, which showed that these characteristics varied significantly. These results are in agreement with Aremu *et al.* (2011).

The genotype (Intro 164) produced the highest plants height (260 cm), followed by genotype (Intro 673) recording (248.3 cm), and genotype (Intro 527) was 228.3 cm. However, genotype Intro 641 had the shortest plants being 184.2 cm. The maximum values of first capsule length (FCL) were produced by genotypes (Intro 203 and Intro 164) while the minimum values were obtained by genotype (Intro 648).

The current investigation showed that genotype (Hybrid 489-26) has the highest number of branches per plant, the heaviest weight of seed/plant, thousand seed weight, and seed yield per fed, while Intro 673 has superior performance for fruiting area (FA), oil percentage (Oil%), seed weight per plant, and plant height. Finally, the highest seed yield/fed (738.53 g) was recorded by genotypes (Intro 289-1) followed by Hybrid 489-26 (732.80 g), then B 21 (627.13 g).

The above results indicated the possibility of designing adequate breeding programs for sesame. The results that were obtained were consistent with those of Abdelsatar *et al.*, 2020 and Shammoro *et al.*, 2020 who reported the presence of significant variation between sesame genotypes. Tesfaye *et al.* (2021) found that the number of primary branches per plant, number of pods per plant, seed production, and thousand seed weight differed significantly between genotypes.

Table 3. Mean performance for 16 sesame genotypes of nine traits combined over the two seasons of 2022 and 2023.

#	Genotype	Genotype Means for all characters								
		PH, cm	**FCL, cm**	**FA**	**NBP**	**SYP, g**	**NCP**	**1000 SW, g**	**Oil %**	**SY/fed, kg**
1	**Intro 164**	260.0	121.7	138.3	5.7	35.8	166	3.48	48.8	557.13
2	**B 21**	208.3	113.3	95.8	10.2	46.5	183	3.37	52.1	627.13
3	**Intro 463**	197.5	69.2	128.3	4.7	43.5	182	2.80	54.7	501.20
4	**Hybrid 484-10**	205.8	53.3	152.5	5.2	41.5	182	3.33	54.1	535.53
5	**Hybrid 484-16**	192.5	114.2	78.3	8.8	46.3	205	2.48	50.3	568.20
6	**Intro 527**	228.3	56.7	171.7	7.5	41.8	200	3.05	54.7	389.57
7	**B4-2**	218.3	101.2	117.2	5.8	38.0	233	2.97	54.0	453.27
8	**Intro 203**	208.3	122.8	85.5	7.0	32.6	165	3.44	50.6	452.80
9	**Hybrid 489-26**	224.2	103.3	120.0	10.5	56.5	193	3.57	49.7	732.80
10	**Intro 673**	248.3	75.8	172.5	5.7	56.0	176	2.73	56.2	596.70
11	**Intro 602**	212.3	105.8	106.5	8.7	42.7	268	2.98	49.8	552.20
12	**Intro 200**	201.7	69.2	132.5	5.7	42.2	158	2.75	52.8	536.47
13	**Intro 289-1**	199.2	92.5	107.7	7.7	53.1	247	2.52	50.4	738.53
14	**Intro 648**	190.8	36.7	154.2	3.2	34.3	215	3.78	47.7	484.60
15	**Local 131**	207.5	77.5	131.7	4.8	43.4	188	3.52	52.1	565.13
16	**Intro 641**	184.2	53.3	130.8	1.0	47.0	93	3.65	43.8	535.53
Mean		**211.7**	**85.4**	**126.5**	**6.4**	**43.8**	**191**	**3.15**	**51.4**	**551.68**
LSD 0.05		**14.90**	**15.24**	**19.34**	**1.53**	**29.33**	**5.88**	**3.595**	**46.86**	**0.342**
CV		**6.1**	**15.5**	**13.2**	**20.7**	**13.3**	**9.9**	**7.1**	**7.4**	**9.4**

***Abbreviation:** plant high (PH), first capsule length (FCL), fruiting area (FA), branches number per plant (NBP), seed yield per plant (SYP), capsules number per plant (NCP), 1000 seed weight (1000 Sw), oil percentage (Oil %) and seed yield per feddan (SY/fed).

Genetic parameter and correlation coefficient

As there have been few efforts to improve the genetics and breeding of sesame, the effects of these efforts have been slow to appear. Breeders need more genetic information and effective selection criteria; just these are insufficient. Effectiveness selection techniques that are related to the production of sesame seeds would be applied. For a plant breeder, an abundance of information on genotypic and phenotypic diversity would be available. This is reported by Boureima *et al.* (2016) and Gimbichu *et al.* (2023).

A degree of genetic variability among population members is one of the prerequisites for genetic improvements. This broad range of variance offered a favorable chance to increase yield (Abdelsatar *et al.,* 2020). Table 4 showed estimates of broad sense heritability (h2), genetic advance (GA), and genotypic (GCV) and phenotypic (PCV) coefficients of variation represented as a percentage of the grand mean (at 5% election intensity) for the seven attributes. Significant differences in phenotype, genotype, and genotype-environment interaction were found for every characteristic under study.

The results in Table 4 showed that all studied traits showed high heritability average from 67 to 85%, except in oil% was the lowest value about 18%.

For each trait under study that shows some environmental influence, the phenotypic coefficients of variation (PCV%) were greater than the genotypic coefficients of variation (GCV), so that among the genotypes under investigation, selection would be successful in improving these traits. The examined attributes were categorized as high GCV% and PCV% for FCL, FA, NBP, and NCP, and moderate for SYP, 1000 SW, and seed yield/fed. With the exception of PH and oil percentage, which showed low GCV and moderate PCV.

Genetic advance was estimated at 5%, with selection intensity (K) equal to 2.06 as a constant. The seed yield per feddan recorded the highest GA (174.23), followed by NCP (67.65), FCL (50.15), FA (47.59), PH (33.33), to be moderate with SYP (13.10), then became weak in NBP (4.37), Oil% (2.11) and 1000 SW (0.68). the GA% mean was high (over 20% up to 69%) in all tested traits except in PH was moderate (15.74) and Oil% was weak (4.10). This is reported by (Kumari et al., 2023)

At 5% selection intensity, the high heritability and genetic advance percentage values were taken with

PH, FCL, FA, NCP, seed yield /feddan that demonstrated how important additive gene effects are and how early generations will benefit from selection for these traits. For plant height mean selection, the modest genetic advancement values combined with the high heritability values would cause a delay in subsequent generations (Badu-Apraku *et al.,* 2018).

As shown in Table 5, the genetic correlation showed fluent in significant through non, high, and highly positive in all studied traits except the 1000 SW and FA, which were negatively correlated with most other traits. The genetic correlation was recorded as highly positive and significant in the number of branches/plant, except with 1000 SW, which has a highly negative and significant correlation. The 1000 SW character has a negative relationship with all other traits except the plant height and fruit area traits, which have a weakly positive correlation. Regarding the seed yield/feddan that appeared highly positive related to FCL, NCP, and SYP. And also, it recorded highly and/or negatively correlated with FA and oil extraction%. The FA showed a highly negative correlation with NBP and FCL **(Aye *et al.,* 2024; and *Ghule et al.,* 2024)**

Table 4. Genetic parameters of Seed yield and its related characters computed from 16 sesame genotypes evaluated over two seasons.

Characters	**P H**	**FCL**	**FA**	**NBP**	**SYP**	**NCP**	**1000 SW**	**Oil %**	**Seed yield /fed**
H^2b	67.82	81.62	72.96	75.90	83.85	71.65	67.28	18.37	85.27
GCV	9.28	31.55	21.38	38.22	15.86	20.34	12.72	4.64	16.60
PCV	11.27	34.92	25.03	43.87	17.32	24.03	15.51	10.83	17.98
GA	33.33	50.15	47.59	4.37	13.10	67.65	0.68	2.11	174.23
GA% means	15.74	58.72	37.63	68.59	29.91	35.46	21.49	4.10	31.58

Table 5. Genetic correlation of Seed yield and its related characters computed from 16 sesame genotypes evaluated over two seasons.

	PH	**FCL**	**FA**	**NBP**	**SYP**	**NCP**	**1000 SW**	**Oil %**
FCL	0.356^{**}							
FA	0.368^{**}	-0.738^{**}						
NBP	0.260^{*}	0.693^{**}	-0.503^{**}					
SYP	0.074^{NS}	0.007^{NS}	0.046^{NS}	0.340^{**}				
NCP	0.068^{NS}	0.251^{*}	-0.198^{NS}	0.551^{**}	0.018^{NS}			
1000 SW	0.010^{NS}	-0.182^{NS}	0.187^{NS}	-0.305^{**}	-0.368^{**}	-0.425^{**}		
Oil %	0.474^{**}	-0.046^{NS}	0.392^{**}	0.359^{**}	0.159^{NS}	0.379^{**}	-0.715^{**}	
Seed Yield/fed	0.043^{NS}	0.312^{**}	-0.277^{**}	0.420^{**}	0.776^{**}	0.147^{NS}	-0.123^{NS}	-0.222^{*}

Cluster Analysis

In the data mining process, clustering is one of the most useful methods for finding groupings and discovering new, intriguing patterns in the underlying data. An effective method for detecting the structural associations between tested genotypes and giving them a hierarchical classification is cluster analysis. Based on similarities or differences, clustering algorithms divide data objects into subsets (clusters). A good cluster's patterns are more similar to one another than they are to patterns from other clusters.

In the current study, the accession mean values for eight quantitative variables (seed yield and related characters) were used to evaluate the similarity levels of the 16 sesame genotypes. These genotypes were divided into two major groups, each of which had six sub-clusters. The genotypes in each group had similar phenotypic performance.

Table 6 tabulated these genotypes' clustering pattern, and Figure 1 diagrammatically illustrates the relationships between the 16 sesame genotypes based on seed yield and each of its components. This result showed that while accession from the same cluster shared many characteristics, they differed in one or more attributes from accession belonging to other groups. This result is similar to Shammoro *et al*. (2020) and Tesfaye *et al*. (2021).

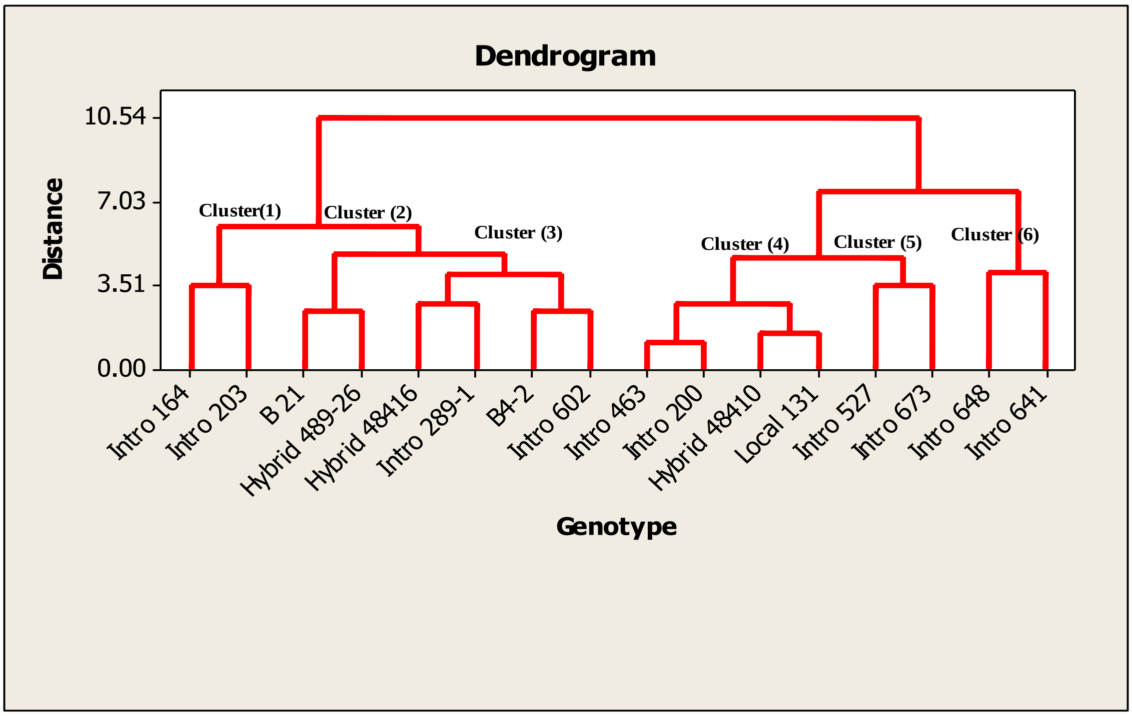

Fig. 1. Linkage dendrogram demonstrating 16 sesame genotypes' affection based on seed yield and associated traits.

Results in Figure 1 showed that 16 sesame genotypes were grouped into two main clusters, divided into six sub clusters. It's noted that each of the 1st, 2nd, 5th, and 6th sub-clusters consisted of only two genotypes. Meanwhile, the 3rd and 4th sub-clusters included the maximum number of items, four genotypes for each one, for a total of 8 out of 16 genotypes. Tadesse *et al.*, 2023; and Tabatabaei, 2011 obtained similar results. The genotypes of the first and sixth sub clusters showed the greatest genetic diversity. Thus, lineages from those clusters 1 and 6 can hybridize to produce excellent recombinants. Nonetheless, the genotypes of sub-clusters 2 and 3 had the smallest genetic distance, followed by sub clusters 4 and 5.

Table 6. Summary of cluster analysis showed the included genotypes, and cluster means of the 16 sesame genotypes using the studied yield characters.

	Clusters					
	cluster I			cluster II		
Subcluster	**1**	**2**	**3**	**4**	**5**	**6**
Genotypes	**G1,G8**	**G2,G9**	**G5,G7,G11,G13**	**G3,G4,G12,G15**	**G6,G10**	**G14,G16**
PH, cm	234.17	216.25	205.58	203.13	238.33	187.50
FCL	122.25	108.33	103.42	67.29	66.25	45.00
FA	111.92	107.92	102.42	136.25	172.08	142.50
NBP	6.33	10.33	7.75	5.08	6.58	2.08
SYP, g	34.18	51.48	45.00	42.63	48.88	40.64
NCP	165.58	188.25	238.17	177.21	187.92	153.83
1000 SW	3.46	3.47	2.74	3.10	2.89	3.71
Oil %	49.73	50.88	51.13	53.43	55.42	45.71
SY/fed, kg	504.97	679.97	578.05	534.58	493.13	510.07

According to table 6, the genotypes with the tallest mean values for the first capsule length were grouped together in the first sub cluster, whereas the genotypes with the heaviest seed yield/plants and seed yield/fed were grouped together in the second sub cluster. The genotype with the greatest number of capsules comprised the third one. In sub cluster 4, none of the characters had the highest mean value. The fifth sub cluster consisted of the genotypes that had the tallest plant height, number of capsules, fruiting area, and oil percentage. Genotypes with the heaviest seed index (weight of 1000 seeds) were included in the sixth sub-cluster. In the second subcluster, the majority of characters had high mean values. Therefore, choosing the genotypes in subcluster two based on these traits may result in an acceptable yield. The result is consistent with that of Mukhthambica *et al*., 2023.

Therefore, the hybridization program may have more heterotic effects if genotypes are chosen and given in distinct clusters with greater genetic distance, preferably from diverse geographic origins. Similar, diverse clustering patterns in sesame were reported by Swathy *et al.* (2018); Bhattacharjee *et al.* (2019) and Ramya (2020).

Given earlier findings that showed significant genetic variation among the genotypes studied, there was an equitable probability that hybridization between genotypes derived from different clusters would provide adequate opportunity for sesame genotypic improvement.

Genotype by yield * trait (GYT)

A genotype's superiority should be assessed based on how well it combines yield with other target features rather than how well it produces individual traits. Yield is the most important attribute, and the other target traits are only significant when paired with high yield. The polygon view of genotypes and yield-trait combinations is shown in Figure 2.

All other genotypes are encompassed within the polygon, which was created by joining the markers of the genotypes that are most distant from the biplot origin. For every polygon side, a line perpendicular to the polygon side and beginning at the biplot origin was drawn. The yield-trait combinations were separated into six sectors by these lines, four of which are trait-free. Sectors devoid of attributes show that the genotypes that fall into these sectors comprise genotypes with poor performance. For example, all examined traits showed low values for the following genotypes: intro 164, intro 463, hybrid 484-10, B4-2, intro 602, intro 200, and local 131.

For the yield-trait combinations positioned within the relevant sector, the genotype positioned on a vertex performs the best (Banerjee, 2009; Yan and Frégeau-Reid, 2018). For the yield-trait combinations positioned within the relevant sector, the genotype positioned on a vertex performs the best. Given that the genotype (Hybrid 489-26) had the largest NCP values, genotype no. 9 (Hybrid 489-26) was the most effective and superior genotype when it came to integrating seed yield with the majority of its traits. concerning the superiority index. Among the examined genotypes, the hybrid 489-26 genotype was ranked first, confirming the earlier findings from the GY*T biplot graph. Due to their shared sector, genotypes B 21 and Intro 289-1 also exhibited comparable behavior when it came to mixing seed yield with the previously described features. It is seen that these genotypes' points and the combination of seed yield attributes were grouped into a single sector, and the acute angles between them demonstrated their linear correlations with each other.

When a genotype is placed on a vertex, the expected 1000SW/PH and SYP*Oil% is 10. This above equation measured how seed yield and other related trait contents were combined in a genotype. Within the standardized data, 76.21% of the variation was explained by the GY*T biplot of the mean performance of seed yield and its components. PC1 and PC2, the first and second principal components, respectively, accounted for 53.01% and 23.21% of the explanation. Dique *et al.* (2023); Sadak *et al.* (2022); and Yan and Kang (2002) stated that for the biplot model to have a decent fit, the first two PCs should represent more than 60% of the total variation.

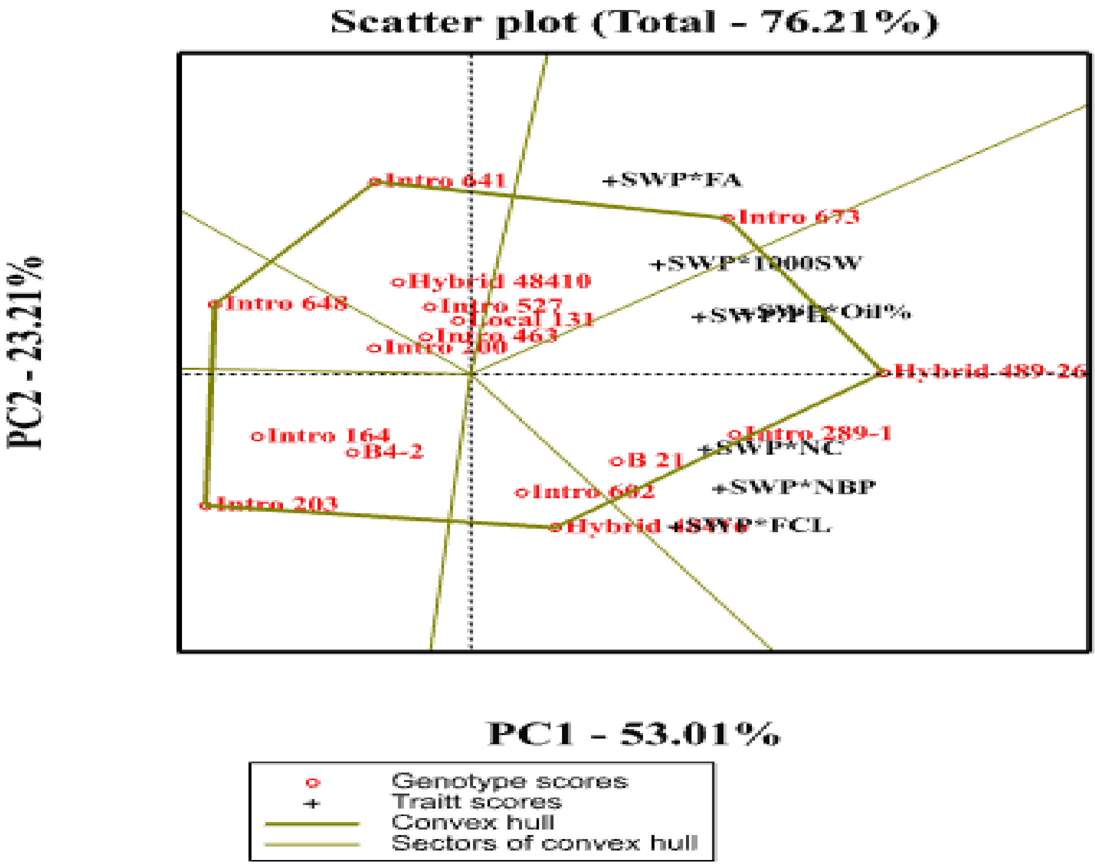

Fig. 2. The "which-won-where" view of the genotype by yield*trait (GYT) biplot to highlight genotypes with outstanding profiles.

Abbreviation: first capsule length (FCL), fruiting area (FA), branches number per plant (NBP), seed yield per plant (SYP), capsules number per plant (NCP) and oil percentage (Oil %) and seed yield per feddan (SY/fed).

A novel technique called the yield*trait genotype (GY*T) biplot was put out by Yan and Frégeau Reid (2018) To take up a problem of multiple trait genotype evaluation. The following assumptions form the basis of it: 1) The most important attribute is yield; all other desired characteristics are only relevant when combined with high yield. 2) When evaluating a genotype's superiority, its weight—which is determined by the combination of yield and other goal features rather than by individual traits—should be used. This method allows the trait to be any breeding objective other than yield, such as agronomic traits, seed quality, nutritional or processing quality traits, disease resistance, biotic tolerance, or abiotic adaptation. This approach is simple, effective, objective, and intuitive when compared to other approaches. (Boureima and Yaou, 2019). In a breeding program, breeders can disable a feature in an attempt to improve another trait. For this, a yield genotype*trait (GYT) biplot evaluation of all features is used, which yields more precise findings.

Selection score

An effective way to measure selection potential is using selection indices as well as providing a good chance for more efficient selection. For more accurate calculations and explanation of the results, a correlated response between a primary and a secondary trait When the secondary characteristic is selected for more genetic gain than the primary trait is selected for directly, it can be used to boost the expression of the primary trait (Abbas *et al.*, 2021; Badu-Apraku *et al.*, 2018; and Hallauer *et al.*, 2010). Selection indices were constructed using the discriminate function of Fisher (Fisher, 1936).

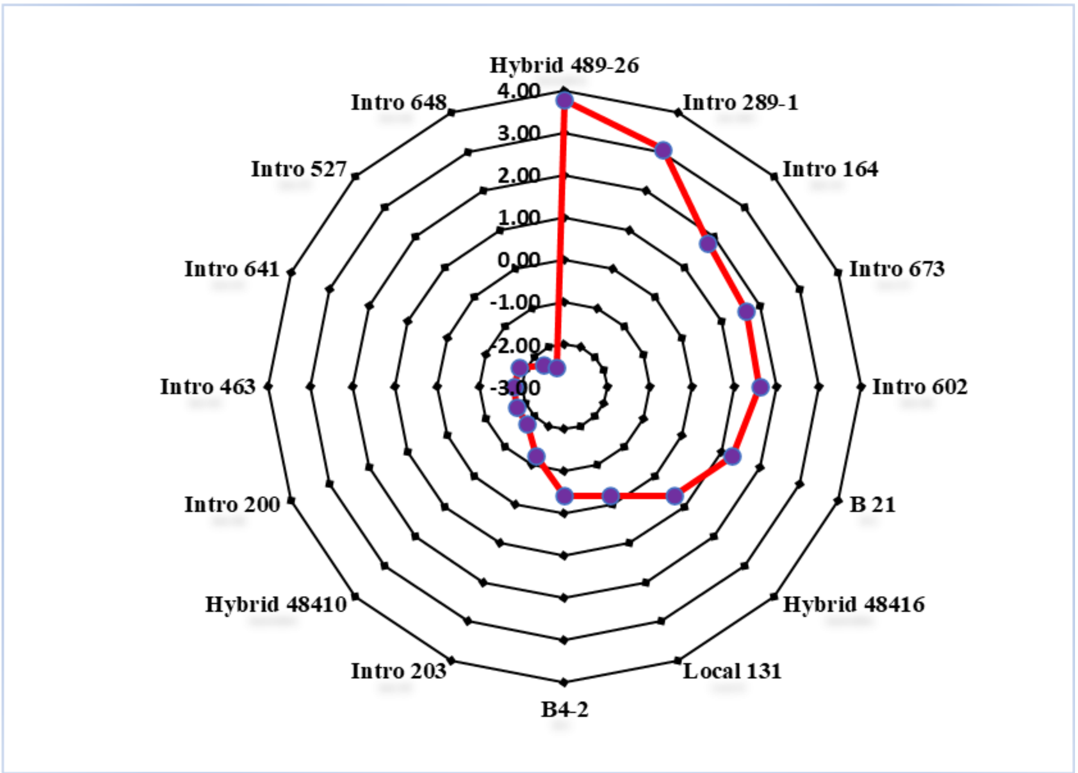

Fig. 3. Radar chart of the discriminant score of the 16 genotypes across the two seasons (2022 and 2023).

Radar charts are plots made up of a series of radii, or equiangular spokes, each of which represents a variable. The magnitude of the variable for the data point in relation to the maximum magnitude of the variable across all data points determines the data length of a spoke. Each spoke's data values are linked together by a line. This gives the plot a star-like look and is where one of its well-known names originated from. Each of the eight elements in our beer example creates a separate axis that is positioned symmetrically around a point. the point (anchor) on the column (axis) represents the value of each aspect. Each spoke's data values are connected by a line. The personalities were effectively visualized by the radar chart. Plant breeders may find this technique useful for screening and assessing various cultivars (Najafabadi *et al.*, 2021; Li *et al.*, 2021; and Gad *et al.*, 2019).

Radar charts were used in our work to illustrate and display the score discrimination analysis. To determine the selection of superior genotypes, the sixteen genotypes were produced and analyzed, ranked from highest to lowest area selection indices for seed yield per plant and other attributes.

The best genotype can be defined as the one with the highest yield and its components. The selection score data was examined using discriminant functions. Fig. 3 revealed that, among the examined genotypes, the hybrid 489-26 genotype was ranked the top, confirming the previous results from the GY*T biplot graph and mean performance. And the genotype Intro 289-1 was ranked the second-score genotype. The rest genotypes were ranked as follows: Intro164, Intro 673, Intro 602, B21, Hybrid 484-16, Local 131, B4-2, Intro 203, Hybrid 484-10, Intro 200, Intro 463, Intro 641, Intro 527, and Intro 648, respectively.

Conclusion

Sesame is an essential oilseed crop worldwide. Developing superior sesame genotypes requires an understanding of the underlying genetic factors that affect seed and oil yields. This enables the identification and selection of high-performing genotypes for breeding programs, industrial applications, and direct cultivation. In this study, 16 advanced sesame breeding lines were evaluated, revealing a wide range of genetic variability, which offers a promising opportunity for effective selection within improvement programs. Unlike previous work focusing solely on seed yield, this study emphasizes the importance of integrating key yield components into the selection process using a discriminant function approach. This strategy allows breeders to maximize genetic gain using fewer but more informative traits, which reduces time and effort. Therefore, assigning appropriate weights to yield-contributing traits ensures more accurate and efficient selection. The novelty lies in the strategic application of discriminant function analysis in sesame breeding, offering a more targeted and potentially superior alternative to traditional selection based on seed yield alone.

Consent for publication:

All authors declare their consent for publication.

Author contribution:

This work was carried out in collaboration among all authors. The manuscript was edited and revised by all authors.

Conflicts of Interest:

The authors declare that they have no competing financial interests or personal relationships.

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