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Multi-trait Genotype -Ideotype Distance Index (MGIDI) approach for identifying superior genotypes in sesame (*Sesamum indicum*. L)

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Abstract

Sesame (*Sesamum indicum* L.) is a globally significant oilseed crop, valued for its high oil content (45–57 %) and antioxidant properties. Despite its importance, the productivity of sesame remained low mainly due to unavailability of suitable cultivars to diverse agroclimatic conditions resulting in low yields. To address these constraints, the Multi-Trait Genotype-Ideotype Distance Index (MGIDI), a modern multi-trait selection tool, was applied to identify superior genotypes based on multiple traits simultaneously rather than focussing on one trait at a time. In the present study, 56 sesame genotypes were evaluated for eleven yield-related traits and oil content. Significant genetic variability was observed and principal component analysis (PCA) indicated that the first four components explained 65 % of the total phenotypic variation. Selection gain estimates revealed high potential for genetic improvement in seed yield, plant height and number of capsules per plant. Based on MGIDI scores, eight superior genotypes were identified, namely Rajeswari, YLM-17, YLM-193, YLM-188, SI-32655, YLM-195, YLM-189 and YLM-11 exhibiting favourable trait combinations which may be used as promising candidates for future sesame crop improvement programmes depending on the objective.

Keywords: Factor Analysis, Sesame, Smith-Hazel index, PCA, Multi-collinearity, MGIDI.

INTRODUCTION

Sesame (*Sesamum indicum* L.) is one of the most ancient important oil seed crops belonging to the family Pedaliaceae. It is recognised as “Queen of oilseed crops” due to its great nutritional quality and quantity of oil (40-63 %). It is rich in unsaturated fatty acids and proteins. Lignans present in the sesame seeds have strong antioxidant activity and its oil have significant pharmacological benefits and health benefits. Despite its importance, the productivity of sesame has remained low due to poor management practices, unavailability of suitable cultivars to diverse agroclimatic conditions.

Hence, development of high yielding cultivars is the major objective in sesame breeding (Begna *et al*., 2022). In plant breeding, the simultaneous improvement of multiple agronomic traits is a major objective, yet it presents considerable statistical and biological challenges. Traditional selection methods often focus on single traits such as seed yield/ oil content neglecting the multi-dimensional nature of crop improvement. Multi-trait selection indices, such as the Smith-Hazel index (Smith, 1936; Hazel, 1943), though widely used, are often constrained by limitations including multicollinearity among traits and the requirement for subjective economic weights. Such multicollinearity often leads to ill-conditioned matrices and biased index coefficients, ultimately compromising the accuracy of predicted genetic gains (Smith, 1936). These limitations can reduce the reliability and biological relevance of selection decisions. Hence, there is a growing need for robust multi-trait selection strategies that can efficiently identify superior genotypes combining multiple desirable attributes.

To address these challenges, Olivoto and Nardino (2021) proposed the Multi-Trait Genotype-Ideotype Distance Index (MGIDI), a robust, flexible, and user-friendly index that integrates factor analysis and ideotype-based selection principles. Unlike classical indices, MGIDI does not rely on economic weights; instead, it computes the Euclidean distance between

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each genotype and an ideotype (a hypothetical genotype with optimal trait values) in a multivariate trait space. Genotypes with lower MGIDI values are considered closer to the ideotype and, therefore, more desirable for selection. This method is based on the concept of an ideotype which represents hypothetical genotype possessing the most desirable trait values. The MGIDI value measures the distance between each genotype and this ideotype with lower values indicating genotypes closer to the ideal combination of traits.

The MGIDI approach enhances selection efficiency by reducing trait dimensionality *via*., factor analysis, addressing multicollinearity, and facilitating a biologically meaningful ranking of genotypes. It has been successfully applied in multiple crops, including maize, wheat, rice, and sesame, demonstrating its potential to improve selection accuracy in multi-trait breeding programs (Debnath *et al.,* 2024).

MATERIALS AND METHODS

The present investigation was carried out using 56 sesame genotypes including two checks evaluated in alpha lattice design for twelve yield, yield contributing attributes and oil content at Agricultural College Farm, Bapatla, Andhra Pradesh during *rabi*, 2024-25. Each genotype was grown in two rows of 4.0 m length with a spacing of 30 cm between rows and 10 cm between plants, within the row. The data was recorded on five competitive plants taken from each replication for 12 characters *viz.,* plant height (cm), number of primary branches per plant, number of capsules per plant, capsule length (cm), capsule width (cm), basal length of the stem to the first capsule bearing (cm), 1000 seed weight (g), harvest index (%) and oil content (%). Days to 50% flowering, days to maturity and seed yield per plot (g) were recorded on plot basis. To calculate MGIDI values, the innovative method put forward by Olivoto and Nardino (2020) was utilized.

The multi-trait genotype–ideotype distance index (MGIDI) was calculated following the methodology of Olivoto and Nardino (2021), which involves four steps: rescaling the traits, conducting factor analysis, designing the ideotype (which exhibits a rescaled value of 100 for all evaluated traits), and computing the MGIDI index (Dormann *et al*., 2013). Statistical analysis for the Multi-Trait Genotype–Ideotype Distance Index (MGIDI) was performed using the 'Metan' R Package version 1.18.0, which was developed by Olivoto and Lúcio (2020). All computations were executed in R version 4.3.1.

RESULTS AND DISCUSSION

In crop improvement programs, it is crucial to effectively utilize available germplasm and identify superior genotypes that exhibit distinct and desirable traits for systematic evaluation and characterization. The MGIDI approach enhances selection efficiency by reducing trait dimensionality *via*., factor analysis, addressing multicollinearity, and facilitating a biologically meaningful ranking of genotypes. As a result, the genotype scores produced are more robust, allowing for efficient multi-trait selection (Benakanahalli *et al*., 2021).

Mean performance and estimates of variability

The data from 56 sesame genotypes was evaluated for 12 quantitative traits to estimate the extent of variability. The univariate analysis of variance revealed that all genotypes differed significantly for all traits included in the study (**Table 1**). This finding indicated the presence of substantial genetic variability among the genotypes, suggesting ample scope for effective selection. Babu *et al.* (2024) in their study identified six superior blackgram genotypes using MGIDI at 5 % selection intensity. They concluded that the MGIDI index is effective in identifying genotypes as parents (genitors) in hybridization programmes aimed at developing superior varieties. Similar approach has also been employed to estimate variability in elephant grass by Rocha *et al.* (2018).

Table 1. Analysis of variance for 12 yield, yield attributes and oil content in sesame

S. No.	Source of variation	d.f.	DFF	DM	PH	NPB	NCP	CL	CW	BSFCB	TSW	HI	OC	SYP
							Mean sum of squares							
1	Replication	1	0.143	35.438	15.825	0.438	1.424	0.000	0.000	9.782	0.002	11.895	7.252	966.437
2	Treatments	55	21.062**	44.496**	223.834**	1.135**	973.216**	0.026**	0.005**	85.749**	0.316**	37.942**	39.885**	4088.80**
3	Blocks	6	6.002	4.937	35.508	0.154	31.262	0.007	0.001	23.645	0.002	5.317	2.672	272.562
4	Error	49	3.058	12.172	17.187	0.172	26.752	0.006	0.001	17.434	0.003	5.098	3.446	350.483
5	Total	111	30.265	97.043	292.354	1.899	1032.654	0.039	0.007	136.610	0.323	60.252	53.255	5678.291

** Significance at 1% level

DFF- Days to 50 % flowering, DM- Days to maturity, PH - Plant height, NPB- Number of primary branches per plant, NCP- Number of capsules per plant, CL - Capsule length, CW - Capsule width, BSFCB - Basal length of the stem to the first capsule bearing, TSW – 1000 seed weight, HI - Harvest index, OC - Oil content, SYP -Seed yield per plot.

Selection differential, heritability and expected selection gain

Estimates of heritability, genetic associations, and expected selection gain are fundamental for designing an effective breeding strategy (Barth *et al.*, 2020). The potential response to selection can be anticipated by interpreting heritability estimates in combination with the corresponding genetic gains. The MGIDI index provides both the selection differential and the selection gain for each trait, enabling identification of genotypes with desirable values (**Table 2**). Generally, for traits where lower values are preferred, the percentage selection differential should be negative, depending on the direction of selection and the ideotype defined for improvement. In the present study, negative selection differential values were recorded for days to 50 % flowering and days to maturity which is desirable. But basal length of the stem to the first capsule bearing and capsule width SD values were also negative. This is because the selected genotypes in the present study had lower values than the population mean, which is desirable for these traits. Reduction in basal length ensures compact plant architecture and earliness, while moderate capsule width reduces shattering tendency and supports better capsule filling in sesame.

The remaining traits in the present study had positive selection differential with higher desired values. Olivoto *et al.* (2021) reported analogous selection differentials in strawberry, achieving a 91% efficacy rate, with the desired directional response observed in 20 out of 22 evaluated traits.

All evaluated traits demonstrated substantial broad-sense heritability exceeding 60 per cent, underscoring the strong genetic control underlying these characteristics. Notably, traits such as the number of capsules per plant and seed yield per plot exhibited elevated heritability accompanied by high expected genetic gain, indicative of a predominant additive genetic architecture amenable to effective selection (**Table 2**). Conversely, plant height presented high heritability but only moderate expected gain, suggesting a complex genetic basis involving both additive and non-additive gene interactions. The remaining traits showed high heritability yet limited genetic gain, implying a significant influence of non-additive genetic effects, potentially dominance or epistasis. Insights into these gene action mechanisms are critical for devising optimal breeding strategies tailored to enhance the genetic improvement of target traits. These findings corroborate the complex inheritance patterns previously reported by Barth *et al*. (2020) for yield-associated traits in strawberry, reflecting the multifaceted genetic architecture characteristic of this species.

Factor loadings (FA) and factor delineation

Among the 12 principal components which were obtained from genetic correlation matrix, four components showed eigen values greater than one with cumulative variance of 65.08 % (**Table 3**). After varimax rotation, communality ranged from 0.35 (1000 seed weight) to 0.86 (harvest index) with an average communality of 0.650. The first factor was found to have high genetic correlation for plant height, number of capsules per plant, 1000 seed weight and seed yield per plot, which indicated that major yield contributing factors in the present study were grouped under this factor. Days to 50% flowering, number of primary branches per plant, capsule width, basal length of the stem to the first capsule bearing and oil content were grouped into second factor. For third factor, high correlations were recorded for days to maturity and capsule length, where,

Table 2. Selection differential, heritability and selection gain percentages for 12 traits in sesame

S.No.	Trait	Overall genotypes mean	Selected genotypes mean	SD (%)	h^2 (%)	SG (%)
1	Days to 50% flowering	41.82	41.28	-1.27	83.95	-1.06
2	Days to maturity	82.95	80.66	-2.76	74.41	-2.05
3	Plant height (cm)	87.66	97.26	10.95	91.42	10.01
4	Number of primary branches/ plants	3.24	3.24	0.14	85.03	0.11
5	Number of capsules per plant	63.86	77.99	22.11	97.20	21.41
6	Capsule length (cm)	2.91	2.97	2.00	77.65	1.55
7	Capsule width (cm)	0.7	0.7	-0.22	86.45	-0.19
8	Basal length of the stem to the first capsule bearing (cm)	32.87	31.16	-5.20	78.87	-4.05
9	1000 seed weight (g)	2.76	3.01	9.10	98.95	9.00
10	Oil content (%)	46.29	47.39	2.39	91.57	2.19
11	Harvest index (%)	24.62	26.82	8.92	86.50	7.72
12	Seed yield per plot (g)	169.36	207.17	22.32	91.63	20.45

Table 3. Eigen values, factor loadings of different factors and communalities in sesame

S.No.	Trait	FA1	FA2	FA3	FA4	Communality	Uniqueness
1	Days to 50% flowering	-0.14	**0.76**	0.05	0.15	0.62	0.38
2	Days to maturity	-0.34	-0.01	**0.66**	-0.04	0.55	0.45
3	Plant height	**-0.72**	0.32	-0.18	-0.16	0.68	0.32
4	Number of primary branches per plant	-0.40	**0.69**	0.06	-0.20	0.69	0.31
5	Number of capsules per plant	**-0.88**	0.20	0.12	0.01	0.83	0.17
6	Capsule length	-0.30	-0.09	**-0.61**	0.16	0.50	0.50
7	Capsule width	-0.12	**-0.80**	0.01	-0.08	0.66	0.34
8	Basal length of the stem to the first capsule bearing	-0.17	**0.65**	-0.52	-0.20	0.77	0.23
9	1000 seed weight	**-0.51**	-0.26	0.02	0.15	0.35	0.65
10	Harvest index	0.01	0.11	-0.10	**0.92**	0.86	0.14
11	Oil content	-0.03	**-0.58**	-0.43	-0.31	0.62	0.38
12	Seed yield per plot	**-0.82**	0.08	-0.04	-0.05	0.69	0.31
	Eigen value	3.36	2.03	1.33	1.08	-	-
	Variance (%)	28.04	16.93	11.08	9.01	-	-
	Cumulative variance (%)	28.04	44.98	56.06	**65.08**	-	-

Note:Values in bold indicate that the trait in that row is grouped into the factor in the corresponding column.

as harvest index was accounted for fourth factor (**Table 3**). Comparable studies in wheat conducted by Olivoto and Nordino (2020) using the MGIDI method reduced 14 original traits to five latent variables (factors), which together explained approximately 87 % of the total variability in the data. Likewise, Olivoto *et al*. (2021) identified five significant factors with eigenvalues greater than one, accounting for 90.48 % of the total variation among the evaluated traits in strawberry. In another study on rice mutants, Mamun *et al.* (2022) reduced 16 traits to six factors, explaining nearly 73 % of the total variance. This dimensional reduction facilitates breeders' perception and decision-making processes. Because factor analysis generates orthogonal axes among final components, genotype scores can be obtained without multicollinearity.

The Multi-Trait Genotype-Ideotype Distance Index (MGIDI) was computed for each genotype in the present study by leveraging genotype scores derived from factor analysis to quantify the Euclidean distance between observed genotypes and a predefined ideotype. The MGIDI visualization facilitates intuitive selection, wherein genotypes exhibiting lower MGIDI values demonstrate superior multi-trait performance, exhibiting greater proximity to the ideotype, thereby being preferentially selected. According to the MGIDI rankings, the eight top-performing genotypes identified were Rajeswari, YLM-17, YLM-193, YLM-188, SI-32655, YLM-195, YLM-189, and YLM-11, with their individual trait performances summarized in **Table 4**. The MGIDI values and ranking of all genotypes are presented in **Table 5 & Fig.1**.

Strengths and weaknesses of selected genotypes

The proportional contribution of each of the four factor loadings (FAs) to the MGIDI value for the eight selected genotypes is illustrated in **Fig. 2.** The dashed line represents the theoretical scenario where all factors contribute equally. Factors positioned outside this dashed line signify positive strengths of the respective genotypes. Factors contributing more to a genotype's elevated MGIDI value are plotted closer to the centre, indicating that the traits grouped under these factors contribute less favourably toward the genotype's closeness to the ideotype. Conversely, factors with lower contributions to the MGIDI value are located near the plot's edge, and the corresponding traits within these factors exhibit higher contributions, aligning closer to the desired ideotype trait values.

Genotypes associated with Factor 1 (FA1), such as Rajeswari and YLM-195, demonstrated particular strengths for traits such as plant height, number of capsules per plant, 1000 seed weight and seed yield per plot. On the other hand, genotypes like SI-32655 and Rajeswari grouped under FA2, showcased strength in traits like days to 50 per cent flowering, number of primary branches per plant, basal length of the stem to the first capsule bearing and oil content. Furthermore, FA3 has recorded strength to the genotypes YLM-189, YLM-17 and SI-32655 which include traits like days to maturity and capsule length. Finaly, Factor 4 (FA4) with genotypes like YLM-188 and YLM-17 demonstrated strength in trait harvest index. Knowledge of the strengths and weaknesses of genotypes can provide useful guidance for choosing parents in future breeding programs based on the desired objectives.

Table 4. Mean performance of the selected eight genotypes based on MGIDI values in sesame

S. No.	Selected genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of capsules per plant	Capsule length (cm)	Capsule width (cm)	Basal length of the stem to the first Capsule bearing (cm)	1000 seed weight (g)	Harvest Index (%)	Oil content (%)	Seed yield per plot (g)
1	Rajeswari	41.0	90.0	112.3	3.0	99.3	3.0	0.8	27.1	3.76	23.18	54.5	203.5
2	YLM-17	43.5	77.0	111.0	2.0	90.2	3.0	0.7	32.6	2.26	32.11	47.0	187.5
3	YLM-193	42.0	82.0	89.5	3.3	64.7	3.0	0.8	36.8	2.87	26.51	48.5	166.5
4	YLM-188	42.5	77.0	91.8	4.2	94.0	2.9	0.7	30.5	3.28	30.63	38.5	233.0
5	SI-32655	35.0	69.0	83.0	2.3	54.3	2.8	0.7	20.8	2.88	29.61	53.5	182.5
6	YLM-195	47.5	78.5	107.0	3.6	94.8	2.8	0.7	29.7	2.86	28.15	41.0	274.5
7	YLM-189	41.0	81.5	99.8	3.5	59.8	3.1	0.7	41.9	2.99	23.09	52.5	218.5
8	YLM-11	37.0	84.0	90.9	4.1	70.1	2.9	0.7	34.8	3.26	24.07	44.5	219.0

Table 5. The multi-trait genotype- ideotype distance index for sesame genotypes

Genotype	MGIDI	Rank	Genotype	MGIDI	Rank
RAJESWARI	3.25	1	YLM-161	5.37	29
YLM-17	3.91	2	YLM-168	5.48	30
YLM-193	4.37	3	YLM-180	5.52	31
YLM-188	4.39	4	YLM-185	5.60	32
SI-32655	4.49	5	YLM-177	5.67	33
YLM-195	4.52	6	DS-18-46	5.79	34
YLM-189	4.52	7	YLM-181	5.80	35
YLM-11	4.55	8	YG-VZM-25	5.95	36
YLM-175	4.56	9	YLM-179	6.03	37
YG-VSP-26	4.66	10	PCU-40	6.08	38
YLM-176	4.71	11	YLM-187	6.14	39
YLM-166	4.77	12	YLM-194	6.15	40
GKVKS-2	4.77	13	YLM-197	6.19	41
YLM-186	4.87	14	YLM-142	6.20	42
YLM-174	4.90	15	GOURI	6.28	43
TPTS-24	4.95	16	YLM-199	6.28	44
YLM-198	4.98	17	YLM-192	6.28	45
TPT5S-21	5.01	18	YG-VSP-22	6.35	46
YLM-173	5.16	19	IC-205317	6.35	47
YLM-196	5.18	20	YG-VSP-25	6.41	48
TPTS-18	5.19	21	YLM-183	6.45	49
PCU-39	5.19	22	YLM-182	6.50	50
YLM-190	5.23	23	YLM-184	6.67	51
YLM-66	5.27	24	YLM-146	6.86	52
YLM-165	5.29	25	GT-10	6.88	53
YLM-172	5.30	26	YLM-162	6.89	54
YLM-191	5.33	27	SI-982	7.13	55
IC-326984	5.35	28	YLM-171	7.56	56

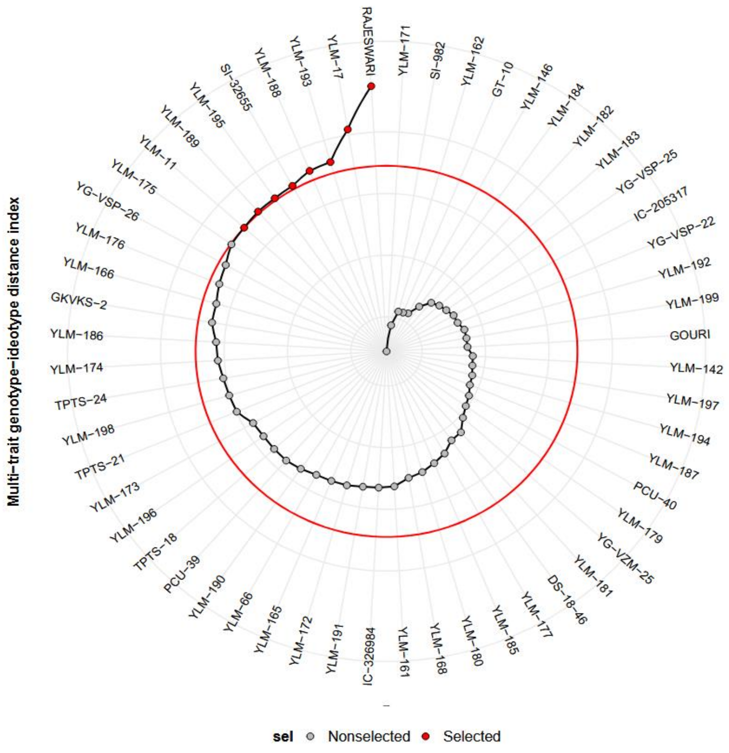

Fig. 1. Genotype ranking based on the MGIDI

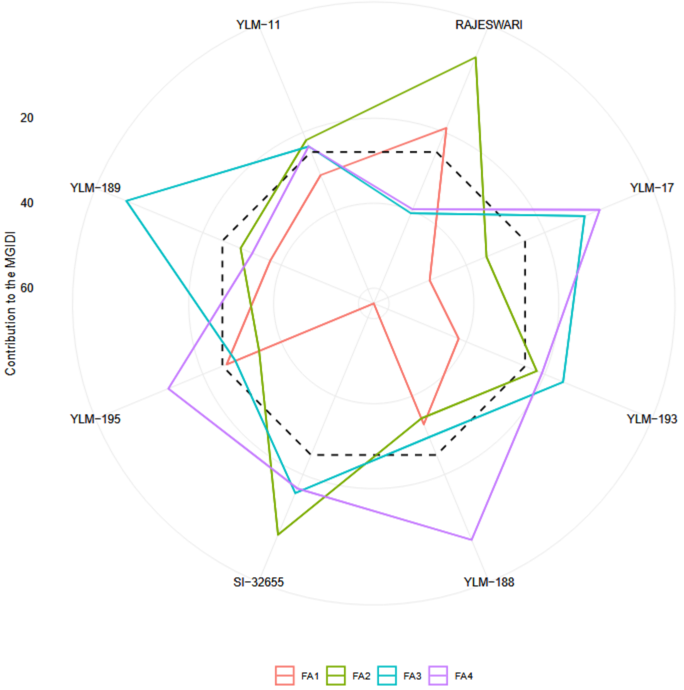

Fig. 2. The proportionate contribution of each factor to the MGIDI for selected genotypes

The present study demonstrated the efficiency of the Multi- trait genotype- Ideotype Distance Index (MGIDI) in identifying superior sesame genotypes based on combination of yield and yield related traits and oil content. In the study, the index effectively integrated multiple traits simultaneously, minimizing the challenges of multicollinearity and providing a balanced selection approach. Genotypes with the lowest MGIDI values were found low to defined ideotype, indicating their overall superiority. Negative selection differentials observed for traits such as basal length of the stem to the first capsule bearing and capsule width reflected desirable reduction contributing to improved plant architecture and yield stability. These findings highlighted that MGIDI is a robust and reliable tool for simultaneous selection of multiple traits, enabling breeders to make more informed and efficient decisions. The application of this approach can accelerate sesame genetic improvement and support the development of ideotype- based breeding strategies aimed at higher yield and productivity under diverse environments.

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