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RESEARCH ARTICLE

Identification of promising mutants for enhanced yield and component traits in Indian mustard (*Brassica juncea* L.) through multi-trait selection index for improved genetic gain

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Abstract

Brassica juncea is a major oilseed crop of substantial economic and nutritional significance, extensively utilised in food systems, edible oil extraction and diversified agricultural production. Improving its productivity remains a primary breeding objective, particularly through the development of an ideotype that integrates high yield potential with resilience and broad adaptability. The present investigation combined agronomic evaluation with genetic analysis to promote sustainable mustard improvement. Conventional multi-trait selection procedures, such as the Smith-Hazel selection index, are often constrained by multicollinearity among traits and reliance on subjective economic weights. Therefore, the multi-trait genotype-ideotype distance index (MGIDI) was adopted as a more flexible and statistically robust alternative. The experiment was conducted at the Agricultural Research Farm, BHU, Varanasi, during the rabi seasons of 2019–20 and 2020–21 using a randomised block design with three replications, where sixteen agronomic and yield-related traits were recorded. Combined analysis of variance revealed significant genetic variability among the mutants, while genotype × environment interaction was largely non-significant except for seeds per siliqua. Principal component analysis was performed to reduce the data complexity, classifying traits into five principal factors explaining 79.6 % of total variation. Application of MGIDI resulted in a cumulative genetic gain of 85.3 %, with notable improvement in secondary branches and siliqua per plant. Four mutants, TM-130, TPM-1, TM-53 and Kranti were identified as superior genotypes for future breeding, underscoring MGIDI's effectiveness in multi-trait mustard improvement programmes.

Keywords: factor analysis; genetic gain; Indian mustard; MGIDI; mutants; principal components

Introduction

Indian mustard (*Brassica juncea*) plays an indispensable role in enhancing food security, providing a sustainable source of nutrition, income and environmental benefits. Its seeds, which contain 30-40 % oil, are a rich source of unsaturated fatty acids, essential for cardiovascular health. While primarily cultivated as an oilseed crop, its young leaves serve as a nutritious vegetable offering significant amounts of vitamin A (865 µg RAE), vitamin C (70 mg/100 g), calcium and iron (1). The plant's resilience to abiotic stresses such as drought and frost makes it highly suitable for semi-arid regions, ensuring stable yields even under shifting climatic conditions (2). With a short growing season, the compatibility of Indian mustard with crop rotation systems and biofumigation properties that suppress soil-borne pathogens, it significantly contributes to sustainable farming practices (3). India represents 90 % of the area under brassica oilseeds, holding fifth position globally by contributing 7.4 % of the worlds' oilseed output, which makes it the second most important vegetable oilseed crop in the country (4).

Beyond agriculture, mustard cultivation supports rural livelihoods by generating income for smallholder farmers. Its by-products, such as seed cake, serve as valuable livestock feed, enhancing its economic importance. Indian mustard constitutes 75-80 % of India's total rapeseed-mustard production and contributes 24.2 % of the nation's edible oil supply. As global demand for vegetable oils rises, Indian mustard helps reduce reliance on imports, strengthening national food sovereignty. The crop's ability to thrive on marginal lands and rehabilitate degraded soils underscores its role in addressing global food security challenges (2). Mustard oil, with its high content of mono and polyunsaturated fatty acids, is a healthier cooking option (2). Additionally, the crop's biofumigation properties are vital in pest and disease management; its potential for phytoremediation, absorbing heavy metals from contaminated soils, enhances its role in environmental restoration

(5). With increasing demand for sustainable agricultural practices, Indian mustards' resilience to climate variability and multifunctional utility make it a crop of crucial importance for future food security and environmental management.

A primary objective in any crop improvement program is to enhance yield potential by analysing factors influencing seed yield. Yield is a complex trait reliant on various morphological characteristics, often influenced by environmental conditions. Direct selection for yield and yield-related traits is often challenging because these traits usually show low heritability, which restricts the scope for rapid genetic improvement. Therefore, studying genotype × environment interactions through multi-environment trials becomes important to identify genotypes that can perform consistently across different growing conditions. In this process, genetic gain plays a key role in shaping the progress and long-term success of plant breeding programmes. Selection based on a few traits may neglect potential improvements in other critical characteristics. To address this, breeders aim to combine diverse desirable traits into a single genotype for optimal performance. The concept of an ideotype-a genotype with specific attributes optimized for high performance guides crop improvement efforts (6). Designing ideotypes requires balancing multiple traits, often aided by selection indices, though assigning realistic economic weights to traits poses a challenge.

The Smith-Hazel selection index has long been applied in plant breeding to facilitate simultaneous improvement of multiple traits (7). However, it is limited by several challenges, including multicollinearity among traits, reliance on subjective economic weights, computational complexity, restricted flexibility and the potential neglect of important traits (8). To overcome these limitations, the Multi-Trait Genotype–Ideotype Distance Index (MGIDI) was developed as a more robust and versatile alternative. MGIDI allows the simultaneous assessment of multiple traits, enabling the identification of genotypes that are closest to the ideal ideotype and thereby enhancing the efficiency and effectiveness of breeding programs. Unlike conventional selection approaches, MGIDI combines information from all traits into a single index while effectively accounting for the correlations among them. By doing so, it overcomes issues such as poorly conditioned matrices and biased index coefficients that often affect other selection indices. The MGIDI approach simplifies complex multivariate data, enhances selection efficiency and supports more balanced genetic improvement across traits. Its application is especially valuable in multi-environment trials, where it aids in identifying stable and widely adaptable genotypes, a key requirement under increasing climate variability.

Despite challenges such as data quality, trait weighting and computational complexity, MGIDI significantly enhances plant breeding efforts by promoting efficient resource use and targeted selection of superior genotypes. MGIDI aligns breeding programs with global food security and sustainability goals. Its application has demonstrated substantial genetic gains, marking a transformative advancement in multivariate selection methods (9). This promising tool sets the stage for revolutionizing breeding strategies to address complex trait interactions and economic considerations.

Materials and methods

Plant dematerial and experimental sign

The field experiment was conducted at the Agricultural Research Farm, IAS, BHU, Varanasi, Uttar Pradesh, India (25.26° N latitude, 82.99° E longitude) during the rabi seasons of 2019 and 2020. The study included 20 Indian mustard mutants developed at the Bhabha Atomic Research Centre (BARC) along with the national check variety, Kranti (Table 1). All genotypes were cultivated in the same field over the two consecutive years. The experiment followed a randomised block design with three replications. Each genotype was grown in five rows per replication, with rows measuring 5 m in length. Spacing of 30 cm between rows and 10 cm between plants within a row was maintained consistently. The crop was raised using recommended agronomic and management practices to ensure uniform growth and development across all genotypes.

Recording of observations

A total of sixteen traits were evaluated in this study, including plant height (PH), days to 50 % flowering (DF), days to maturity (DM), number of primary branches (NPB), number of secondary branches (NSB), length of the main raceme (LMR), number of siliqua on the main raceme (NSMR), total number of siliqua per plant (NSPP), siliqua length (SL), seeds per siliqua (SPS), seed yield per plant (SYPP), biological yield per plant (BYPP), harvest index (HI), test weight (TW), seed yield per hectare (SYPH) and chlorophyll content (CC). For most traits, five competitive plants from each genotype in every replication were randomly tagged for measurement. In contrast, days to 50 % flowering and days to maturity were recorded on a plot basis for both growing seasons. Harvest index was calculated as the ratio of seed yield per plant to the corresponding biological yield per plant.

Statistical analysis

A combined ANOVA was conducted to assess varietal differences across 16 traits. Bartlett's test was employed to evaluate the homogeneity of error variances across the two growing seasons, determining whether data from individual environments (E) could be combined for analysing the G E interaction. Homogeneity was assessed using the F-test, also known as the "variance ratio" test. The analysis partitioned the variation to examine genotype differences and the G E interaction. The MGIDI was computed using the R package metan (version 1.18.0) (10). All analyses were performed in R software version 4.3.1. The construction of the MGIDI index followed a

Table 1. List of genotypes taken under investigation

S. No	Name of entry/ genotype	Source
1	TPM-1	Bhabha Atomic Research Centre (BARC), Trombay, Mumbai
2	TM-52	
3	TM-53	
4	TM-106	
5	TM-108	
6	TM-108-1	
7	TM-117	
8	TM-130	
9	TM-134	
10	TM-143	
11	TM-172-1	
12	TM-3	
13	TM-179	
14	TM-204	
15	TM-217	
16	TM-263-3	
17	TM-258	
18	TM-273	
19	TM-276	
20	TM-277	
21	KRANTI	I. Ag. Sc BHU, Varanasi.

series of steps. The first step in computing the MGIDI index was to rescale the matrix X so that all the values have a 0-100 range (9, 10). Rescaling traits (Normalisation). The rescaled value for the j^{th} trait of the i^{th} genotype (rX_{ij}) was obtained as described in Eqn. 1.

$$r\mathbf{X}_{ij} = \frac{\eta_{nj} - \varphi_{nj}}{\eta_{oj} - \varphi_{oj}} \times (\theta_{ij} - \eta_{oj}) + \eta_{nj} \quad \text{(Eqn.1)}$$

Where, η_{nj} and ϕ_{nj} are the new maximum and minimum values for the trait j after rescaling, respectively; η^{oj} and ϕ_{oj} are the original maximum and minimum values for the trait j, respectively and θ_{ij} is the original value for the j^{th} trait of the i^{th} genotype. In the second step, exploratory factor analysis was carried out to group correlated traits into common factors, followed by the estimation of factor scores for each genotype. The factor analysis was performed based on Eqn. 2.

$$X = \mu + Lf + \varepsilon \quad \text{(Eqn. 2)}$$

In this model, X denotes a p × 1 vector of observations, μ is a p × 1 vector of standardized means, L represents a p × f matrix of factor loadings, f is a p × 1 vector of common factors and ε is a p × 1 vector of residuals, where p corresponds to the number of traits and f to the number of retained factors. Eigenvalues and eigenvectors were derived from the correlation matrix of the two-way data matrix (rX). Only factors with eigenvalues exceeding one were retained for estimating the initial loadings. Varimax rotation was then applied to simplify and clarify the factor structure, resulting in the final factor loadings. Genotype scores were subsequently calculated as in Eqn. 3.

$$F = Z(A^{T}R^{-1})^{T} \quad \text{(Eqn. 3)}$$

Where F is a g × f matrix with the factorial scores; Z is a g × p matrix with the standardised means (rX); A is a p × f matrix of canonical loadings and R is a p × p correlation matrix between the traits. g, f and p represent the number of genotypes, factors retained and analysed traits, respectively.

Ideotype planning and computation of the MGIDI index

Define an ideotype by specifying target values for traits based on known or desired characteristics. This step involves determining the ideal combination of trait values for a genotype. The final step is to compute MGIDI index (9) as follows (Eqn. 4):

$$MGIDI_i = \sqrt{\sum_{j=1}^{f}(F_{ij} - F_j)^2} \quad \text{(Eqn. 4)}$$

In this equation, $MGIDI_i$ represents the multi-trait genotype-ideotype distance index for the i^{th} genotype, F_{ij} denotes the score of the i^{th} genotype for the jth factor (i = 1, 2,…., g; j = 1, 2,…., f), where g and f are the total number of genotypes and retained factors, respectively and F_j is the ideotype score for the j^{th} factor. Genotypes with lower MGIDI values are considered closer to the ideotype, reflecting a more desirable combination of the measured traits. The contribution of each factor to the MGIDI of a genotype (ω_{ij}) was determined using Eqn. 5.

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=1}^{f}\sqrt{D_{ij}^2}} \quad \text{(Eqn. 5)}$$

Where, D_{is} is the distance between the ith genotype and the ideotype for the j^{th} factor. For a given genotype, factors with low contributions suggest that such a genotype is close to the ideotype for the traits within that factor. The selection gain in percentage, SG (%), was calculated for each trait considering a selection intensity of 15 % based on the following equation (Eqn. 6).

$$SG(\%) = \frac{(\bar{X}_s - \bar{X}_o) \times h^2}{\bar{X}_o} \times 100 \quad \text{(Eqn. 6)}$$

Where Xs is the mean of the selected genotypes, Xo is the mean of the original population and h^2 is the broad-sense heritability.

Results and Discussion

Variance components and likelihood ratio test

Bartlett's test confirmed the homogeneity of error variances across seasons, as all Fmax values were below three and non-significant. Consequently, an unweighted combined analysis of variance (ANOVA) was conducted to evaluate genotypic differences for the studied traits. The results indicated significant variation among genotypes for all traits (Table 2). Seasonal effects, represented by year, were significant for most traits, except biological yield per plant and chlorophyll content. The genotype × year interaction was non-significant for all traits except seeds per siliqua, suggesting stable genotype performance across seasons for the majority of traits, while seeds per siliqua exhibited variable responses. Mean values and ranges for each trait are provided in Table 3.

Likelihood ratio tests were performed for the analysed traits using the BLUP approach, considering genotype as a random effect and replication as a fixed effect, which revealed a significant effect due to GEI for all the evaluated traits. Most traits displayed high heritability (h_{bs} > 0.60), except for chlorophyll content. Genotypic selection accuracy (AS) values ranged from 0.82 for chlorophyll content (CC) to 0.99 for days to flowering (DF), days to maturity (DM), length of main raceme (LMR) and test weight (TW). Traits such as number of secondary branches (NSB), length of main raceme (LMR), test weight (TW) and seed yield per hectare (SYPH) showed the highest genotypic coefficients of variation (CVg). Researchers in cotton and green gram have also identified and explained similar components in their respective studies (11).

Principal component analysis and factor delineation

Principal Component Analysis (PCA) was performed using mutant genotypes to evaluate 16 yield-related traits. PCA reduces numerous correlated variables into a few principal components that capture most of the variation in the dataset, thereby reducing dimensionality. It also helps identify the traits that contribute most to variability among genotypes or samples. The analysis identified five principal components (PCs) with eigenvalues greater than 1, collectively accounting for approximately 79.6 % of the total variation (Table 4). PC1, with an eigenvalue of 6.1, explained 38.1 % of the variability, followed by PC2 (eigenvalue 2.18, 13.6 %), PC3

Table 2. Combined/pooled ANOVA of two season for 16 characters in Indian mustard (*Brassica juncea* L.)

Source of variation	Replication within year	Year	Year × Genotypes	Overall sum	Genotypes	Pooled error	C.D. 5%
df	2	1	2	5	20	100	
DF	185.98	1334.19**	10.83	345.56*	1956.89**	137.76	13.44
DM	5.5	17.43**	0.22	5.78	203.60**	11.91	3.95
PH	18.41	12.72*	2.88	11.06	254.75**	45.89	7.76
NPB	0.26	4.45**	0.26	1.09**	1.34**	0.23	0.55
NSB	1.45	111.12**	1.25	23.30**	36.32**	1.92	1.59
LMR	71.05*	401.28**	25.58	118.91**	433.57**	15.28	4.48
NSMR	0.49	46.30**	1.72	10.15	153.18**	14.85	4.41
NSPP	1114.56	10719.17**	434.86	2763.60**	13021.09**	752.09	31.41
SL	0.1	7.68**	0.15	1.63**	0.61**	0.14	0.42
SPS	2.45	27.79*	5.20*	8.62**	4.47**	1.32	1.31
SYPP	3.03	15.77**	2.08	5.19**	14.64**	1.25	1.28
BYPP	2.04	145.75	47.42	48.94	238.41**	40.32	7.27
HI	4.31	11.74**	0.31	4.2	35.40**	5.9	2.78
TW	0.15	2.51**	0.2	0.64**	4.20**	0.19	0.5
SYPH	65228.61	322388.8**	46707.7	109252.28**	309101.29**	27539.72	190.09
CC	22.6	2.51	4.77	11.45	71.63**	10.17	3.65

***** and ****** Significant at 5 % and 1 % level of significance, respectively. PH: Plant height (cm); DF: Days to 50 % flowering; DM: Days to maturity; NPB: Number of primary branches; NSB: Number of secondary branches; LMR: Length of main raceme (cm); NSMR: number of siliqua on main raceme; NSPP: Number of siliqua per plant; SL: Siliqua length (cm); SPS: Seeds per siliqua; SYPP: Seed yield per plant (g); BYPP: Biological yield per plant (g); HI: Harvest index; TW: Test weight (g); CC: Chlorophyll content; SYPH: Seed yield per hectare (kg/ha).

Table 3. Likelihood ratio test and variance components for 16 traits evaluated in mutants of Indian mustard pooled over rabi 2019 and rabi 2020

Parameters	Mean	Range	$\sigma^2 g$	σ^2_r	$\sigma^2 p$	h^2_{bs}	h^2_{mg}	AS	CV_g	CV_r	CV_g/CV_r	LRT_{ge}	P value
DF	51.29	44.0-60.50	33.51	1.27	34.78	0.96	0.99	0.99	11.29	2.19	5.15	111.07	5.71×10^{-26}
DM	135.51	122.0-144.83	41.83	1.89	43.71	0.96	0.99	0.99	4.77	1.01	4.71	104.34	1.70×10^{-24}
PH	171.88	133.58-199.73	312	42.41	354.41	0.88	0.96	0.98	10.28	3.79	2.71	64.62	9.10×10^{-16}
NPB	4.97	4.19-6.0	0.19	0.1	0.29	0.65	0.85	0.92	8.77	6.49	1.35	24.94	5.90×10^{-07}
NSB	12.05	8.34-17.05	5.8	0.77	6.57	0.88	0.96	0.98	19.99	7.27	2.75	65.55	5.67×10^{-16}
LMR	54.22	37.0-68.18	70.44	5.47	75.91	0.93	0.97	0.99	15.48	4.31	3.59	84.2	4.46×10^{-20}
NSMR	43.84	32.40-51.0	22.75	8.33	31.08	0.73	0.89	0.94	10.88	6.58	1.65	34.64	3.97×10^{-09}
NSPP	323.8	244.78-417-58	2005.81	493.14	2498.95	0.8	0.92	0.96	13.83	6.86	2.02	45.76	1.33×10^{-11}
SL	4.55	3.83-5.22	0.09	0.05	0.14	0.64	0.84	0.92	6.48	4.85	1.34	24.46	7.59×10^{-07}
SPS	12.54	10.93-14.42	0.61	0.4	1.01	0.61	0.82	0.91	6.24	5.03	1.24	21.45	3.62×10^{-06}
SYPP	12.1	8.40-15.08	2.27	0.53	2.79	0.81	0.93	0.96	12.44	5.99	2.08	47.49	5.51×10^{-12}
BYPP	56.16	42.54-73.17	32.63	21.31	53.95	0.6	0.82	0.91	10.17	8.22	1.24	21.29	3.95×10^{-06}
HI	21.77	17.79-29.52	4.76	3.12	7.88	0.6	0.82	0.91	10.01	8.1	1.24	21.23	4.07×10^{-06}
TW	4.76	3.02-6.10	0.69	0.04	0.73	0.94	0.98	0.99	17.43	4.29	4.07	93.35	4.38×10^{-22}
SYPH	1394.71	883.07-1834.42	47662.33	11562.72	59225.06	0.8	0.93	0.96	15.65	7.71	2.03	46.16	1.09×10^{-11}
CC	42.24	35.97-49.87	8.05	11.66	19.71	0.41	0.67	0.82	6.72	8.08	0.83	9.07	0.0026

Please see Table 2 for trait abbreviations.

Table 4. Eigenvalues, % variance and cumulative eigenvalues of mutants

Principal components (PC)	Eigenvalues	Variance (%)	Cumulative variance (%)
PC1	6.10	38.1	38.1
PC2	2.18	13.6	51.8
PC3	1.99	12.4	64.2
PC4	1.47	9.20	73.4
PC5	1.00	6.23	79.6
PC6	0.83	5.21	84.8
PC7	0.72	4.51	89.4
PC8	0.56	3.52	92.9
PC9	0.36	2.25	95.1
PC10	0.32	1.98	97.1
PC11	0.21	1.33	98.4
PC12	0.11	0.69	99.1
PC13	0.08	0.51	99.6
PC14	0.05	0.34	100
PC15	0	0.01	100
PC16	0	0	100

(eigenvalue 1.99, 12.4 %), PC4 (eigenvalue 1.47, 9.2 %) and PC5 (eigenvalue 1.00, 6.23 %). Beyond these, subsequent PCs contributed progressively less to the total variation. The first principal component, representing a linear combination of the original variables, captured the largest proportion of variance, making it critical for determining the direction of maximum variability. The significant variability explained by PC1, with a contribution of 38.1 %, highlights its importance in selecting desirable lines for further breeding. Several studies have utilised principal components to reduce data dimensionality and explain genetic diversity effectively (12–14).

Factor analysis in MGIDI groups correlated traits into independent latent factors, reducing multicollinearity and simplifying multi-trait data, which improves the accuracy of genotype–ideotype distance calculation for selection. Factor analysis of sixteen traits identified four principal factors that collectively explained 79.6 % of the total variation, highlighting clear groupings of correlated traits and providing insights into their interrelationships. Factor 1 was mainly associated with yield-related traits, including HI, SYPP and SYPH, underscoring its role in productivity assessment. Factor 2 encompassed developmental and structural traits, such as DF, DM, PH and SPS, reflecting its relevance to plant growth and reproductive timing. Factor 3 captured branching and biomass-related traits, including NPB, NSB and BYPP, emphasising its contribution to vegetative growth and plant robustness. Factor 4 included traits related to the main raceme and seed characteristics, such as the LMR, NSMR, NSPP, SL, TW and CC, highlighting its importance for reproductive structures and photosynthetic efficiency. The average communality and uniqueness values accounted for 73.5 % and 26.5 % of the total genetic variability, respectively (Table 5). These results illustrate the effectiveness of factor analysis in simplifying complex datasets, identifying key traits and supporting the development of a robust multi-trait selection index for targeted breeding. Reseaerch have also demonstrated the value of factor analysis in understanding trait groupings and reported communality and uniqueness values comparable to those observed here (15, 16).

MGIDI and selection gains

The MGIDI analysis highlighted four superior mutants- TM-130, TPM-1, TM-53 and Kranti-as the top-performing genotypes under a 15 % selection intensity (Fig. 1). These mutants consistently outperformed others across multiple traits, indicating their potential for simultaneous multi-trait improvement in mustard breeding programs. Analysis of the MGIDI index showed positive genetic gains

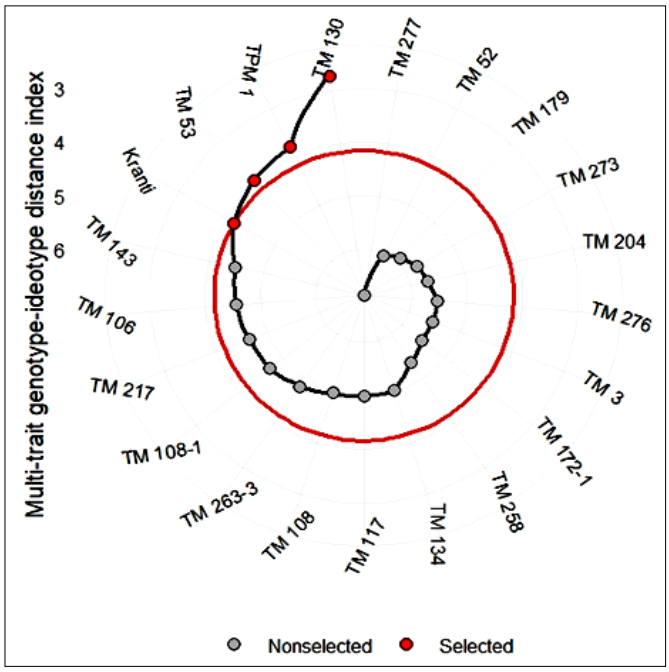

Fig. 1. Ranking of mutants showing selected genotype using the MGIDI. The selected accessions are shown as red dots, while the unselected accessions are shown as black dots. The red circle represents the cut point according to the selection pressure.

Table 5. Factor loadings obtained using varimax rotation and communalities resulting from the factor analysis.

VAR	FA1	FA2	FA3	FA4	Communality	Uniquenesses
Days to 50 % flowering	-0.230	0.850	-0.130	0.210	0.830	0.170
Days to maturity	-0.050	0.830	-0.210	0.070	0.750	0.250
Plant height (cm)	0.040	-0.710	0.010	-0.440	0.700	0.300
Number of primary branches	0.010	0.110	-0.760	0.170	0.620	0.380
Number of secondary branches	-0.190	0.050	-0.770	0.180	0.660	0.340
Length of main raceme (cm)	0.040	-0.350	-0.080	-0.830	0.820	0.180
Number of siliqua on the main raceme	0.100	-0.430	-0.220	-0.740	0.790	0.210
Number of siliqua per plant	0.090	0.000	-0.700	-0.480	0.730	0.270
Siliqua length (cm)	0.020	0.470	0.040	-0.560	0.540	0.460
Seeds per siliqua	0.440	0.470	0.120	0.140	0.450	0.550
Seed yield per plant (g)	0.690	-0.160	0.180	-0.630	0.930	0.070
Biological yield per plant (g)	-0.060	-0.150	0.330	-0.800	0.780	0.220
Harvest index	0.920	-0.030	-0.130	0.080	0.880	0.120
Test weight (g)	0.390	-0.180	0.360	-0.580	0.650	0.350
Seed yield per hectare (g)	0.690	-0.170	0.190	-0.630	0.930	0.070
Chlorophyll content	0.520	-0.220	0.270	-0.550	0.700	0.300
					0.735	0.265

Please see Table 2 for trait abbreviations.

for most traits, except biological yield and test weight. Negative gains were observed for days to 50 % flowering, days to maturity and plant height, which is desirable in mustard breeding as early maturity helps to avoid many stresses, including aphids, terminal heat and drought stress and short to moderate plant stature is generally preferred as they confer lodging resistance. The highest gains were observed for the number of secondary branches and siliqua per plant, demonstrating the effectiveness of MGIDI in capturing favourable combinations of traits (Table 6). Overall, these findings confirm that MGIDI is a robust and efficient tool for identifying promising breeding lines and facilitating targeted genetic improvement in mustard.

The versatility of the MGIDI model is highlighted by its widespread and successful application in evaluating ideal yield and yield-related traits across a range of crops. Studies have demonstrated its effectiveness in crops such as maize, wheat, eggplant, guar, rice, soybean, bajra, cotton and sorghum (12, 15-23). For instance, in rice, positive gains were reported by Pallavi and his coworkers for all twenty-one traits studied, with spikelet fertility showing the highest gain (25.6 %). These studies underscore the adaptability of the MGIDI model across diverse crop species and environmental conditions, emphasising its reliability in managing the complexities of multivariate selection. By enabling the simultaneous selection of multiple desirable traits, MGIDI provides an efficient and practical approach for improving crop performance. Furthermore, MGIDI has been identified as a highly efficient selection index for identifying genotypes with optimal traits, further validating its utility (10). Collectively, these findings demonstrate the model's critical role in advancing crop improvement strategies, making it an indispensable tool for modern plant breeding programs aiming to achieve genetic gains across diverse traits.

Strengths and weaknesses of genotypes based on MGIDI factors provides detailed representation of the strengths and weaknesses exhibited by various genotypes, categorised according to the contribution of each factor to the MGIDI (Fig. 2). This analysis highlights the unique trait advantages associated with specific factors, offering insights into their suitability for targeted breeding programs. Mutants linked to Factor 1 (FA1), such as TM-130 and TM-258, exhibit significant strengths in traits directly related to productivity, including harvest index, seed yield per plant, seed yield per hectare and chlorophyll content. These traits underscore the potential of these mutants for enhancing overall yield and photosynthetic efficiency (Fig. 2, Table 5). Conversely, mutants such as TPM-1, TM-143 and TM-172-1, associated with Factor 2 (FA2), display strengths in traits like days to 50 % flowering, days to maturity, siliqua length and seeds per siliqua. These traits are crucial for improving reproductive performance and fine-tuning phenological characteristics. Additionally, mutants TM-3 and TM-53, linked to Factor 3 (FA3), show notable strengths in traits such as the number of primary and secondary branches, which contribute to enhanced vegetative growth and branching architecture. Lastly, Factor 4 (FA4) is represented by the mutant TM-179, which demonstrates strengths in traits like plant height, the length of the main raceme and the number of siliqua on the main raceme. These attributes are vital for improving plant structure and maximising siliqua production on key reproductive axes. This comprehensive

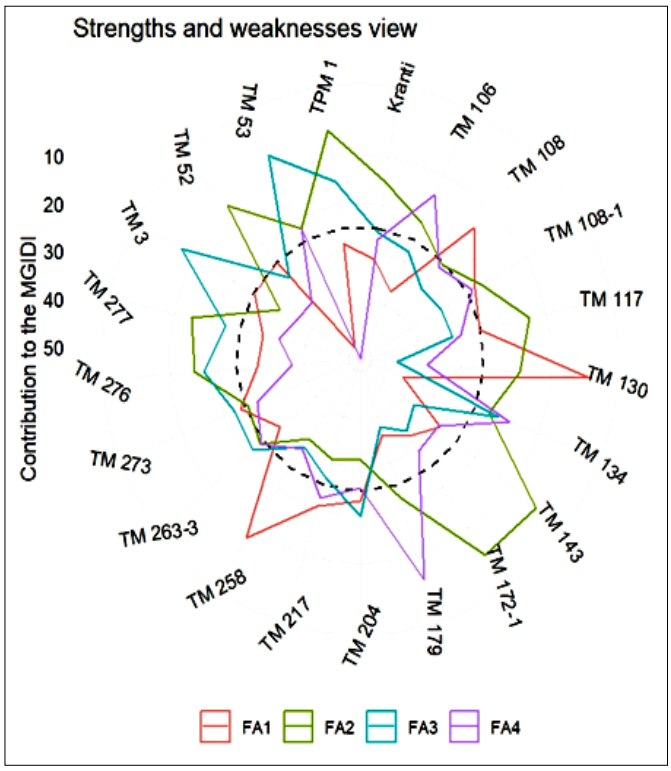

Fig. 2. The strengths and weaknesses of the selected genotypes are shown as the proportion of each factor on the computed MGIDI. The smaller the proportion explained by a factor (closer to the external edge), the closer the traits within that factor are to the ideotype. The black broken circle at the centre shows the theoretical value if all the factors contributed equally.

Table 6. Selection differential and selection gains of 16 traits in selected mutants using the MGIDI approach

Trait	Xo	Xs	SD	SD %	h^2	SG	SG %	Sense
SYPP	12.10	12.8	0.725	5.99	0.928	0.673	5.56	Increase
HI	21.80	23.8	1.98	9.1	0.821	1.63	7.47	Increase
SYPH	1390.0	1500.0	105	7.55	0.925	97.4	6.99	Increase
DF	51.30	46.3	-4.95	-9.66	0.988	-4.89	-9.54	Decrease
DM	136.0	129.0	-6.69	-4.93	0.985	-6.59	-4.86	Decrease
PH	172.0	162.0	-9.5	-5.52	0.957	-9.08	-5.28	Increase
SPS	12.5	12.8	0.298	2.38	0.822	0.245	1.96	Increase
NPB	4.97	5.36	0.39	7.86	0.846	0.33	6.64	Increase
NSB	12.0	14.3	2.3	19.1	0.958	2.2	18.3	Increase
NSPP	324.0	387.0	62.8	19.4	0.924	58	17.9	Increase
LMR	54.2	54.6	0.409	0.754	0.975	0.398	0.735	Increase
NSMR	43.8	45.3	1.47	3.36	0.891	1.31	2.99	Increase
SL	4.55	4.73	0.182	4.01	0.843	0.153	3.38	Increase
BYPP	56.2	54.6	-1.6	-2.86	0.821	-1.32	-2.35	Increase
TW	4.76	4.54	-0.22	-4.62	0.98	-0.215	-4.53	Increase
CC	42.2	42.6	0.343	0.812	0.675	0.232	0.548	Increase

Please see Table 2 for trait abbreviations.

breakdown of strengths and weaknesses, as visualised in Fig. 2, emphasises the value of MGIDI in identifying genotypes with optimal trait combinations. By highlighting specific trait advantages, the analysis facilitates the selection of genotypes tailored to meet specific breeding objectives, thereby enhancing the efficiency of crop improvement strategies.

The insights gained from evaluating the strengths and weaknesses of genotypes can provide crucial guidance for selecting parental lines in future breeding programs. The importance of identifying ideal rice mutants using MGIDI has been highlighted, noting their significant potential to improve quantitative traits (24). Other studies have also highlighted the potential of selected rice genotypes using MGIDI, underscoring their strategic selection as an asset for breeding programs (25). In a similar vein, the genotypes identified in this study emerge as promising candidates for future mustard breeding programs, playing a key role in enhancing the overall quality of the crop. By strategically utilising the identified factors and traits, this approach contributes to the development of resilient, high-performing mustard varieties with improved traits, ensuring progress in breeding efforts aimed at optimising crop yield and quality.

Conclusion

The MGIDI demonstrated exceptional efficiency in identifying superior mutants, revealing significant improvements across multiple traits. The genotypes TM-130, TPM-1, TM-53 and Kranti, selected through MGIDI, highlight their potential for commercial release or as valuable breeding materials for mustard improvement programs. A comprehensive evaluation of the strengths and limitations of these genotypes provided valuable insights, highlighting the importance of identifying ideal mustard genotypes with superior quantitative traits. The genotypes identified through this approach represent promising candidates for use in future breeding programmes, thereby reinforcing the effectiveness of MGIDI as a powerful tool for improving mustard varieties with enhanced productivity. The integration of MGIDI into breeding strategies offers a promising and innovative approach to advancing crop improvement, contributing to the development of resilient, high-performing varieties that support sustainable agricultural practices, ensuring greater productivity and long-term agricultural success.

Authors' contributions

KR conceived the study design, conducted the field experiments and performed data curation. GKP performed the statistical analysis and interpreted the results. SP contributed to methodology development and visualisation. AVK wrote the original draft and reviewed the literature. OBS curated data and assisted in formal analysis. DJJ contributed to software validation and resources. MMH assisted in the investigation and project administration. KS supervised the study, provided resources and reviewed and edited the final manuscript. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

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