

An Integrated IDOCRIW-MCDM Framework for the Evaluation and Selection of Indian Mustard (*Brassica juncea*) Genotypes

Nidahamteinsar Papang¹, Priya Sharma^{2,3} and Bishal Gurung¹

¹North Eastern Hill University, Shillong

²University of Delhi, Delhi

³Fortune Institute of International Business, New Delhi

Received 23 May 2026; Revised 06 June 2026; Accepted 09 June 2026

SUMMARY

Identifying the best-performing genotypes of Indian mustard (*Brassica juncea*) across multiple agronomic criteria is rarely straightforward, as no single genotype tends to excel across the board. This study developed a systematic approach to this challenge, drawing on two independent datasets of genotypes information recorded under well-defined evaluation conditions. Rather than relying on intuition, this study builds a structured decision framework using three well-established Multi-Criteria Decision-Making (MCDM) methods: the Technique for Order Preference by Similarity to Ideal Solution (TOPSIS), ViseKriterijumsaOptimizacija I KompromisnoResenje (VIKOR), and Complex Proportional Assessment (COPRAS). Since neither dataset provides predefined criterion weights, the Integrated Determination of Objective Criteria Weights (IDOCRIW) method is applied to derive them objectively from the data itself. For the first dataset, TOPSIS and COPRAS arrive at identical rankings ($\rho = 1.000$), while VIKOR diverges sharply ($\rho = -1.000$), reflecting its compromise-based logic. Results obtained that genotype A₅ (IC212031) consistently emerges as the top performer. For the second dataset, VIKOR and COPRAS both placed A₁₇ (NRC YS 5-2) at the top and A₂₅ (Anuradha) at the bottom, an agreement at both extremes that highlights the reliability and robustness of the proposed framework.

Keywords: Multi-criteria decision making (MCDM); TOPSIS; VIKOR; COPRAS; Genotypes; IDOCRIW.

1. INTRODUCTION

The term *genotype* was introduced by Wilhelm Johannsen in the early twentieth century, during the formative period of Mendelian genetics [1]. In genetics, a genotype is broadly understood as a theoretical construct representing the complete genetic makeup of an organism the specific combination of genes carried by an individual that, while not directly observable, fundamentally shapes its criteria and characteristics [2]. Genotypes constitute the fundamental units of variation in breeding and experimental research, and their systematic evaluation is essential for identifying candidates that exhibit desirable and well-balanced performance across multiple criteria.

Indian mustard (*Brassica juncea*) is a prominent industrial and commercial oilseed crop extensively

cultivated across India [3]. Among the seven edible oilseed crops grown in the country, rapeseed mustard contributes approximately 28.6% of total oilseed production, ranking second only to groundnut, which accounts for 27.8% of India's oilseed economy. Mustard-growing regions span a wide range of agro-climatic conditions, and the cultivation of different rapeseed mustard species across various parts of the country reflects considerable genetic and environmental diversity [4]. The present study focuses on the evaluation and selection of multiple genotype alternatives of Indian mustard across several key criteria derived from experimental trials. The primary objective is to identify genetically divergent parental lines and to quantify the relative contribution of individual criteria to overall genetic divergence, thereby providing valuable insights for crop improvement and breeding programs.

Corresponding author: Priya Sharma

E-mail address: priyasharma.du.aor.17@gmail.com

Given the multi-dimensional nature of genotype performance, MCDM framework offers a structured and systematic approach for comparing and ranking alternatives when decisions involve multiple, often conflicting, criteria [5]. MCDM is particularly well-suited to complex decision problems where simple evaluation rules fall short. By employing technically rigorous and transparent methodologies, it enables decision-makers to arrive at scientifically justified conclusions [6]. In plant breeding, where selection decisions must simultaneously balance several desirable criteria, MCDM methods provide a practical means of identifying superior genotypes based on overall performance rather than any single criterion alone. Indeed, the growing adoption of MCDM in plant breeding stems from its ability to evaluate numerous alternatives across multiple criteria while accounting for trade-offs, recognising that genotypes rarely excel in every desirable characteristic, and that strengths in certain criteria may reasonably compensate for weaknesses in others.

Recent advances in plant breeding have further demonstrated the value of MCDM techniques as effective tools for genotype evaluation and selection. For example, PROMETHEE II was applied to rank 156 Brazilian table grape genotypes based on multiple agronomic and fruit-quality characteristics [7]. MCDM methods have also been used to identify soybean genotypes with superior stability under drought and salinity stress conditions [8]. In lentil research, the integration of TOPSIS with entropy weighting was successfully applied to evaluate and rank cultivars across several agronomic criteria [9]. TOPSIS has also been employed to identify ideal bread wheat genotypes combining high yield with desirable agronomic criteria [10]. Kumar *et al.* [11] went further by integrating TOPSIS with several stability parameters to construct a composite stability index, enabling the identification of genotypes that performed consistently well across diverse environments. Collectively, these studies underscore the utility of MCDM as a decision-support tool that enhances the transparency, objectivity, and reliability of genotype selection, ultimately supporting the development of high-performing, stable, and sustainable crop varieties.

In the context of MCDM, the accuracy of any final ranking depends substantially on the appropriate determination of criteria weights and the effective evaluation of alternatives. Criteria weights represent the relative importance assigned to each criterion with respect to the decision objective; however, such information is rarely available in raw experimental data. Existing weighting approaches in the literature are generally classified into three categories: subjective, objective, and hybrid methods, each carrying distinct advantages and limitations. Subjective methods, such as the Stepwise Weight Assessment Ratio Analysis (SWARA) [12] and the Best Worst Method (BWM) [13] rely on expert judgment and effectively capture decision-maker preferences, though they may introduce bias or inconsistency. Objective methods, by contrast, derive weights directly from the data using mathematical and statistical measures, including, such as the Standard Deviation, Coefficient of Variation, Entropy, CRITIC, MEREC, and SECA methods ([14],[15],[16]). However, these methods generally rely on a single mathematical concept, including data dispersion, inter-criteria correlation, or criterion removal effects which may not adequately represent the multidimensional relationships inherent in complex decision-making problems.

Among the objective weighting techniques, the IDOCRIW method, proposed by Zavadskas and Podvezko [17], integrates both the entropy method and the Criterion Impact Loss (CILOS) approach, capturing data heterogeneity and impact-loss effects in a complementary manner. While the entropy method assigns weights based on the degree of variation within each criterion, CILOS evaluates the effect loss associated with each criterion when it is prioritised. Owing to this complementary structure, IDOCRIW has been successfully applied across a range of decision-making contexts, including waste-to-energy technology ranking [18] and electric vehicle battery recycling [19]. Therefore, given the absence of predefined criteria weights, IDOCRIW is employed to systematically derive the weights, which are subsequently incorporated into the proposed MCDM framework. In this study, three established MCDM techniques: TOPSIS, VIKOR, and COPRAS are applied to rank Indian mustard genotypes based on aggregated evaluation criteria, with the term *alternative* used throughout as the primary unit of evaluation.

1.1 Organization of the study

The structure of the paper is organized as follows: **Section 2** outlines the methodology employed in this study. **Section 3** represents the demonstration of the proposed methodology via a numerical illustration followed by a detailed discussion of these results in **Section 4**. Finally, **Section 5** concludes the paper by highlighting key insights, practical implications and remarks.

2. METHODOLOGY

This section gives the stepwise methodology of the study to help understand the process in detail. Suppose a DM evaluates ‘ n ’ alternatives A_i ($i=1,2,\dots,n$) based on a multiple criteria set C_j ($j=1,2,\dots,p$)

$$X_{n \times p} = \begin{bmatrix} x_{11} & x_{12} & x_{13} & \cdots & x_{1p} \\ x_{21} & x_{22} & x_{23} & \cdots & x_{2p} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ x_{n1} & x_{n2} & x_{n3} & \cdots & x_{np} \end{bmatrix} \quad (1)$$

Since the original data sets do not explicitly define the relative importance of the evaluation criteria, therefore this study employed the IDOCRIW method which systematically derive the criteria weights, that are subsequently incorporated into the decision framework to rank the potential genotype alternatives.

2.1 The Integrated Determination of Objective Criteria Weights (IDOCRIW)

The IDOCRIW method, proposed by Zavadskas and Podvezko [17], was adopted in this study due to its ability to provide a comprehensive and reliable estimation of objective criterion weights. Traditional objective weighting techniques, such as the Standard Deviation, Coefficient of Variation, Entropy, CRITIC, MEREC, and SECA methods ([14], [15], [16]), generally rely on a single mathematical concept, including data dispersion, inter-criteria correlation, or criterion removal effects. Although these approaches effectively capture specific aspects of criterion importance, they may not adequately represent the multidimensional relationships inherent in complex decision-making problems.

In contrast, IDOCRIW combines two complementary objective weighting approaches: the Entropy method and the CILOS (Criterion Impact

Loss) method. The Entropy method evaluates the informational content and variability of criteria within the decision matrix, assigning higher weights to criteria that contribute greater discriminatory power among alternatives. The CILOS method, on the other hand, assesses the relative loss of criterion significance by measuring the impact associated with prioritizing a particular criterion. By integrating these two perspectives, IDOCRIW simultaneously accounts for both the variability of criterion values and the interactions among criteria. It provides a more balanced and robust weighting framework than methods based on a single weighting principle. This characteristic makes it particularly suitable for genotype evaluation studies, where multiple agronomic criteria collectively influence overall performance and stability. By reflecting both the information content of the data and the relative impact of individual criteria, IDOCRIW enhances the objectivity, reliability, and interpretability of the resulting genotype rankings.

The input information of the IDOCRIW method is expressed by a decision matrix:

$$X_{n \times p} = [x_{ij}]_{n \times p}$$

where x_{ij} denotes the performance value of the i^{th} alternative with respect to the j^{th} criterion.

Step 1: Normalization of the decision matrix

The normalized decision matrix is obtained as:

$$\tilde{x}_{ij} = \frac{x_{ij}}{\sum_{i=1}^n x_{ij}}, \quad i = 1, 2, \dots, n; \quad j = 1, 2, \dots, p \quad (2)$$

Step 2: Degree of entropy

The degree of entropy for each criterion is calculated using:

$$E_j = -\frac{1}{\ln m} \sum_{i=1}^n \tilde{x}_{ij} \ln \tilde{x}_{ij}, \quad j = 1, 2, \dots, p, \quad 0 \leq E_j \leq 1 \quad (3)$$

Step 3: Entropy weight

The deviation degree of entropy is computed as:

$$d_j = 1 - E_j, \quad j = 1, 2, \dots, p \quad (4)$$

The entropy weight of each criterion is then obtained by:

$$Ew_j = \frac{d_j}{\sum_{j=1}^p d_j} \quad (5)$$

Step 4: Construction of the square matrix

To handle non-beneficial criteria, the decision matrix is transformed as:

$$\hat{x}_{ij} = \frac{\min_i x_{ij}}{x_{ij}}, \quad i = 1, 2, \dots, n; \quad j = 1, 2, \dots, p \quad (6)$$

After normalization, the maximum value for each criterion is identified as:

$$a_j = \max_i \hat{x}_{ij}, \quad j = 1, 2, \dots, p \quad (7)$$

A square matrix is then formed using the rows corresponding to these maximum values.

Step 5: Relative impact loss matrix

The relative impact loss matrix is calculated as:

$$r_{ij} = \frac{a_j - \hat{x}_{ij}}{a_j}, \quad i, j = 1, 2, \dots, p, \quad r_{jj} = 0 \quad (8)$$

where r_{ij} represents the relative impact loss of the j^{th} criterion.

Step 6: Weight system matrix

Based on the relative impact loss values, the weight system matrix is constructed as:

$$F = \begin{bmatrix} \sum_{i=1}^n r_{i1} & r_{12} & \cdots & r_{1n} \\ r_{21} & \sum_{i=1}^n r_{i2} & \cdots & r_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ r_{n1} & r_{n2} & \cdots & \sum_{i=1}^n r_{in} \end{bmatrix} \quad (9)$$

Step 7: Criterion impact loss weight

The criterion impact loss (CILOS) weights are obtained by solving:

$$Fq^T = 0 \quad (10)$$

where $q = [q_1, q_2, \dots, q_p]$ is the vector of criterion impact loss weights.

Step 8: Aggregate weight

The final aggregate weight of each criterion is computed by combining entropy and CILOS weights:

$$w_j = \frac{q_j Ew_j}{\sum_{j=1}^p q_j Ew_j}; \quad j = 1, 2, \dots, p \quad (11)$$

A higher aggregate weight indicates greater importance of the corresponding criterion in the decision-making process.

2.2 Clustering analysis (For large number of alternative)

In this study, the clustering algorithm employed to group a large number of alternatives is discussed in detail. Clustering is an unsupervised learning technique that identifies inherent groupings within a dataset. In the context of the MCDM problem, alternatives are grouped based on their similarity with respect to aggregated criteria. To enhance clustering performance, the K-means++ algorithm is utilized, which improves upon the traditional K-means by addressing its sensitivity to initial centroid selection and its tendency to converge to suboptimal solutions. K-means++ selects initial centroids iteratively, with the choice of each new centroid influenced by its distance from previously chosen centroids. This probabilistic initialization reduces the likelihood of poor local minima and yields more stable and accurate clustering results.

To evaluate the quality of the clustering, the silhouette method [20] is applied. The Python functions

KMeans and *silhouette_score* from the *sklearn* library is used to perform clustering and assess its quality. K-means++ is employed to overcome the sensitivity of traditional K-means to centroid initialization, ensuring more reliable clustering outcomes. The silhouette analysis evaluates the cohesion and separation of clusters, helping determine the optimal number of clusters. The silhouette coefficient measures how well a data point fits within its assigned cluster, considering both intra-cluster cohesion and inter-cluster separation. The coefficient ranges from -1 to 1 , where higher positive values indicate that a point is well-matched to its cluster, while negative values suggest a possible misclassification. For a dataset partitioned into C clusters, with a data point h in cluster C_h ,

$$S(h) = \begin{cases} \frac{y(h) - x(h)}{\max(x(h), y(h))}, & \text{if } |C_h| > 1 \\ 0, & \text{if } |C_h| = 1 \end{cases} \quad (12)$$

where $x(h)$ denotes the average distance of h to all other points in the same cluster, and $y(h)$ represents

the mean distance from h to all points in the nearest neighbouring cluster C_h' ($C_h' \neq C_h$).

2.3 TOPSIS (Technique for Order Performance by Similarity to Ideal Solution)

The TOPSIS investigated by Hwang *et al.* [21] is widely used method due to its straightforward computational procedure, strong mathematical foundation, and intuitive logic. The core idea of TOPSIS is to rank alternatives based on their relative distance from two reference points: the positive ideal solution and the negative ideal solution. In decision-making, the most desirable alternative is expected to be as close as possible to the ideal solution while being as far as possible from the non-ideal (negative ideal) solution. Consequently, the alternative that is closest to the positive ideal solution is also the one farthest from the negative ideal solution and is therefore considered the best option.

The TOPSIS method can be applied to evaluate decision-making units (DMUs). Let n denote the number of alternatives (rows) and p denote the number of evaluation criteria (columns). The performance value of the i^{th} alternative with respect to the j^{th} criterion is represented by d_{ij} . The TOPSIS procedure consists of the following steps:

Step 1: Normalization of the decision matrix

The decision matrix

$$X_{n \times p} = [x_{ij}]_{n \times p}$$

is normalized to remove scale differences. The normalized decision matrix

$$Y_{n \times p} = [y_{ij}]_{n \times p}$$

is calculated as:

$$y_{ij} = \frac{x_{ij}}{\sqrt{\sum_{i=1}^n x_{ij}^2}}, i = 1, 2, \dots, n; j = 1, 2, \dots, p \quad (13)$$

Step 2: Weighted normalized decision matrix

The weighted normalized decision matrix

$$V_{n \times p} = [v_{ij}]_{n \times p}$$

is obtained by multiplying each normalized value by the corresponding criterion weight w_j :

$$v_{ij} = w_j y_{ij}, i = 1, 2, \dots, n; j = 1, 2, \dots, p \quad (14)$$

Step 3: Positive and negative ideal solutions

The positive ideal solution S^+ and the negative ideal solution S^- are defined as:

$$S^+ = \{v_1^+, v_2^+, \dots, v_p^+\} = \{\max_i v_{ij}, j \in B; \min_i v_{ij}, j \in C\} \quad (15)$$

$$S^- = \{v_1^-, v_2^-, \dots, v_p^-\} = \{\min_i v_{ij}, j \in B; \max_i v_{ij}, j \in C\} \quad (16)$$

where B and C represent the sets of benefit-type and cost-type criteria, respectively.

Step 4: Distance from ideal solutions

The Euclidean distances of each alternative from the positive and negative ideal solutions are calculated as:

$$D_i^+ = \sqrt{\sum_{j=1}^p (v_{ij} - v_j^+)^2}, i = 1, 2, \dots, n \quad (17)$$

$$D_i^- = \sqrt{\sum_{j=1}^p (v_{ij} - v_j^-)^2}, i = 1, 2, \dots, n \quad (18)$$

Step 5: Relative closeness to the ideal solution

The relative closeness of each alternative to the ideal solution is computed as:

$$C_i = \frac{D_i^-}{D_i^+ + D_i^-}, i = 1, 2, \dots, n \quad (19)$$

Step 6: Ranking of alternatives

Alternatives are ranked according to their relative closeness values C_i . A larger value of C_i indicates a better alternative, and the alternative with the highest C_i is considered the best.

2.4 COPRAS (Complex Proportional Assessment)

The COPRAS method, introduced by Zavadskas and Kaklauskas [22], is used to evaluate the superiority of one alternative over another and allows for systematic comparison of multiple alternatives. The method considers both the performance values of alternatives and the relative importance (weights) of the evaluation criteria, enabling a comprehensive assessment of alternative solutions. It is based on the principle that the significance and utility of an alternative are directly proportional to its performance under beneficial criteria and inversely proportional to its performance under non-beneficial criteria. By simultaneously considering

ideal and worst-case conditions, the method provides a rational framework for determining the relative priority and utility degree of each alternative. Therefore, in this study, the COPRAS method is employed to evaluate and rank genotypes based on multiple agronomic criteria. The procedural steps involved in the COPRAS analysis are described below. Let n denote the number of alternatives (rows) and p denote the number of criteria (columns).

Step 7: The decision matrix given in Eq. 1 is normalized to obtain dimensionless matrix:

$$Y_{n \times p} = [y_{ij}]_{n \times p}$$

where y_{ij} is the normalized value of the i^{th} alternative under the j^{th} criterion, and it is calculated as:

$$y_{ij} = \frac{x_{ij}}{\sum_{i=1}^n x_{ij}}, \quad i = 1, 2, \dots, n; \quad j = 1, 2, \dots, p \quad (20)$$

Step 8: Weighted normalize decision matrix

The normalized values from Eq. 2 are then multiplied by the corresponding criterion weights obtained from Eq. 11: $V_{n \times p} = [v_{ij}]_{n \times p}$

is obtained as:

$$v_{ij} = w_j y_{ij}, \quad i = 1, 2, \dots, n; \quad j = 1, 2, \dots, p \quad (21)$$

Step 9: Calculation of sums for beneficial and non-beneficial criteria

$$S_i^+ = \sum_{j \in B} v_{ij} \quad (22)$$

$$S_i^- = \sum_{j \in C} v_{ij} \quad (23)$$

where B and C denote beneficial and non-beneficial criteria, respectively.

Step 10: *Determination* of relative significance using Eq. 24. The relative significance Z_i of each alternative is calculated as:

$$Z_i = S_i^+ + \frac{S_{\min}^-}{\sum_{i=1}^n \frac{S_{\min}^-}{S_i^-}}, \quad i = 1, 2, \dots, n \quad (24)$$

Step 11: Calculation of quantitative utility and ranking of alternatives

The utility degree of each alternative is computed as:

$$U_i = \frac{Z_i}{Z_{\max}} \times 100, \quad i = 1, 2, \dots, n \quad (25)$$

where $z_{\max}$ is the maximum relative significance value. The alternative with the highest utility degree U_i is considered the most desirable and receives the highest rank.

2.5 VIKOR (Vise Kriterijumsa Optimizacija I Kompromisno Resenje)

The VIKOR method developed by Opricovic *et al.* [23] focuses on ranking and selecting alternatives in the presence of conflicting criteria. The method identifies a compromise solution by simultaneously considering maximum group utility and minimum individual regret. It is particularly useful when DMs seek a solution closest to the ideal alternative.

Step 13: From the decision matrix $X_{n \times p} = [x_{ij}]_{n \times p}$, determine best and worst criterion values using Eq. 26

$$f_j^+ = \max_i f_{ij}, \quad f_j^- = \min_i f_{ij}, \quad j = 1, 2, \dots, p \quad (26)$$

Step 14: Compute utility and regret measures

The group utility measure S_i and individual regret measure R_i are calculated as:

$$S_i = \sum_{j=1}^p w_j \frac{f_j^+ - f_{ij}}{f_j^+ - f_j^-}, \quad i = 1, 2, \dots, n \quad (27)$$

$$R_i = \max_j \left[w_j \frac{f_j^+ - f_{ij}}{f_j^+ - f_j^-} \right], \quad i = 1, 2, \dots, n \quad (28)$$

where w_j is the weight of the j^{th} criterion.

Step 15: The compromise ranking index Q_i is computed as:

$$Q_i = v \cdot \frac{S_i - S^+}{S^- - S^+} + (1 - v) \cdot \frac{R_i - R^+}{R^- - R^+}, \quad i = 1, 2, \dots, n \quad (29)$$

and (v) represents the weight assigned to the strategy of maximum group utility, generally taken as $(v=0.5)$.

Where, $S^+ = \min_i (S_i)$, $S^- = \max_i (S_i)$ and $R^+ = \min_i (R_i)$, $R^- = \max_i (R_i)$

Step 4: The alternatives are evaluated and arranged in ascending order of Q_i . A lower Q_i value indicates a more desirable alternative. The alternative with the minimum Q_i value is considered the best compromise solution, provided that it satisfies the acceptable advantage and acceptable stability conditions defined by the VIKOR method.

3. ILLUSTRATION

This section is organised into three interconnected subsections. The first section introduces the alternatives examined in this study, giving the reader a clear sense of what is being compared and why these options are of interest. The second explains the criteria used for evaluation and the weights assigned to each, shedding light on how the assessment framework was constructed and what guided the prioritisation of certain factors over others. The third and final subsection brings everything together by presenting and discussing the results, offering a deeper understanding of what the findings mean in practice and how they contribute to the broader objectives of this study.

3.1 Study region

This study utilized two independent data sets of genotypes of Indian mustard (*Brassica juncea*) evaluations to provide a comprehensive representation of genotype characteristics. Each data set consists of systematically recorded genotypic information collected under well-defined conditions and organized according to standardized evaluation criteria. For the first data set, genotype evaluation was carried out using twenty-two predefined criteria reported in the genotype collection. The evaluation criteria used in this study are listed in Table 1. These criteria provide a structured basis for assessing genotype performance across multiple dimensions, while the corresponding genotypic alternatives are presented in Table 2. The second dataset consists of forty-five alternatives of genotypes selected for quality-based evaluation Table 20. Genotype performance was assessed using four quality evaluation criteria Table 19. These datasets were analysed and evaluated using a MCDM approach along with IDOCRIW criteria weights determination approach for identifying genotypes with superior overall performance for effective genotype selection.

3.2 Analysis of the First Dataset for Genotype Selection

The first dataset comprises six genotype alternatives of Indian mustard (*Brassica juncea*), i.e., ($A_1 A_6$): NATP124, PJaiKisan, RL1359, Maya, IC212031, and HB9902, as shown in Table 2. A total of twenty-two evaluation criteria ($C_1 C_{22}$) were considered, encompassing a range of physiological, phenological, and yield-related criteria for comprehensive genotype assessment.

3.3 Analysis of the second Dataset for Genotype Selection

The second dataset consists of forty-five alternatives of genotypes ($A_1 A_{45}$) selected for quality-based evaluation Table 20. Genotype performance was assessed using four quality evaluation criteria Table 19.

3.4 Clustering of a large number of alternatives

To efficiently handle a large number of alternatives, clustering is performed after aggregating the alternatives according to their relevance in the decision-making process. The clustering process is carried out using the KMeans algorithm from the *sklearn* Python library. Incorporating the K-means++ initialization strategy to improve centroid selection. To assess the quality and validity of the obtained clusters, silhouette analysis is employed using the *silhouette_score* function. This evaluation ensures that the resulting clusters exhibit strong intra-cluster similarity and adequate inter-cluster separation. The final clusters represent groups of alternatives with similar decision-making characteristics are given below:

$$CL_1 = \{A_{10}, A_{11}, A_{12}, A_{13}, A_{14}, A_{15}, A_{17}, A_{18}, A_{22}, A_{23}, A_{24}, A_{25}, A_{26}, A_{27}, A_{29}, A_{30}, A_{31}, A_{34}, A_{36}, A_{39}\}$$

$$CL_2 = \{A_{28}\}$$

$$CL_3 = \{A_1, A_2, A_3, A_4, A_6, A_7, A_{16}, A_{19}, A_{20}, A_{21}, A_{32}, A_{33}, A_{35}, A_{40}, A_{41}, A_{42}, A_{45}\}$$

$$CL_4 = \{A_5, A_8, A_9, A_{37}, A_{38}, A_{43}, A_{44}\}$$

Here, Cluster 1 (CL_1) is considered for subsequent genotype evaluation, as it represents the most suitable group of alternatives.

Table 1. List of the genotype evaluation criteria

C _j	Criteria	C _j	Criteria	C _j	Criteria	C _j	Criteria
C ₁	NcontentSeed	C ₇	NuptakeSiliquaHusk	C ₁₃	DateOfBud	C ₁₉	SPAD
C ₂	NcontentStover	C ₈	NuptakeRoot	C ₁₄	DateOfFlowering	C ₂₀	Nitrate
C ₃	NcontentSiliquaHusk	C ₉	TotalNuptake	C ₁₅	Flowering	C ₂₁	NR
C ₄	NcontentRoot	C ₁₀	NHI	C ₁₆	Senescence	C ₂₂	NiR
C ₅	NuptakeSeed	C ₁₁	NutE	C ₁₇	SeedWeight		
C ₆	NuptakeStover	C ₁₂	AvailableN	C ₁₈	OilContent		

Table 2. List of the suitable genotype alternatives

A _i	Genotypes	A _i	Genotypes
A ₁	NATP124	A ₄	Maya
A ₂	PJaiKisan	A ₅	IC212031
A ₃	RL1359	A ₆	HB9902

Table 3. Original decision matrix

A _i / C _j	C ₁	C ₂	C ₃	C ₄	C ₅	C ₆	C ₇	C ₈	C ₉	C ₁₀	C ₁₁
<u>A₁</u>	3.12	0.42	0.59	0.42	42.00	12.70	6.30	5.40	66.40	0.63	20.30
<u>A₂</u>	3.03	0.41	0.55	0.38	35.40	10.80	5.10	3.70	55.00	0.64	21.20
<u>A₃</u>	2.94	0.40	0.56	0.38	32.90	9.10	4.70	3.80	50.40	0.64	22.00
<u>A₄</u>	2.99	0.42	0.56	0.41	30.40	9.30	4.60	3.10	47.60	0.64	21.40
<u>A₅</u>	3.36	0.50	0.69	0.46	49.20	14.90	7.70	6.20	77.90	0.62	18.50
<u>A₆</u>	3.12	0.41	0.54	0.42	38.70	12.80	5.60	4.90	62.00	0.62	20.20
A _i /C _j	C ₁₂	C ₁₃	C ₁₄	C ₁₅	C ₁₆	C ₁₇	C ₁₈	C ₁₉	C ₂₀	C ₂₁	C ₂₂
<u>A₁</u>	185.30	39.75	44.98	58.42	80.13	4.45	39.13	45.43	4.44	0.03	0.36
<u>A₂</u>	181.20	39.03	43.30	57.20	80.70	5.37	39.27	44.89	4.84	0.02	0.23
<u>A₃</u>	176.40	41.08	45.60	60.55	86.13	4.12	38.71	45.40	4.92	0.02	0.31
<u>A₄</u>	182.40	39.40	45.28	59.95	83.92	4.45	38.97	44.25	5.09	0.03	0.30
<u>A₅</u>	183.60	39.17	44.02	60.28	83.72	4.00	39.87	46.96	4.81	0.03	0.45
<u>A₆</u>	185.10	43.17	49.17	65.60	85.33	4.90	39.51	48.07	5.57	0.02	0.38

Table 4. Normalization

A _i / C _j	C ₁	C ₂	C ₃	C ₄	C ₅	C ₆	C ₇	C ₈	C ₉	C ₁₀	C ₁₁
A ₁	0.17	0.16	0.17	0.17	0.18	0.18	0.19	0.20	0.18	0.17	0.16
A ₂	0.16	0.16	0.16	0.15	0.15	0.16	0.15	0.14	0.15	0.17	0.17
A ₃	0.16	0.16	0.16	0.15	0.14	0.13	0.14	0.14	0.14	0.17	0.18
A ₄	0.16	0.16	0.16	0.17	0.13	0.13	0.14	0.11	0.13	0.17	0.17
A ₅	0.18	0.20	0.20	0.19	0.22	0.21	0.23	0.23	0.22	0.16	0.15
A ₆	0.17	0.16	0.15	0.17	0.17	0.18	0.16	0.18	0.17	0.16	0.16
A _i /C _j	C ₁₂	C ₁₃	C ₁₄	C ₁₅	C ₁₆	C ₁₇	C ₁₈	C ₁₉	C ₂₀	C ₂₁	C ₂₂
A ₁	0.17	0.16	0.17	0.16	0.16	0.16	0.17	0.17	0.15	0.17	0.18
A ₂	0.17	0.16	0.16	0.16	0.16	0.20	0.17	0.16	0.16	0.17	0.11
A ₃	0.16	0.17	0.17	0.17	0.17	0.15	0.16	0.17	0.17	0.16	0.15
A ₄	0.17	0.16	0.17	0.17	0.17	0.16	0.17	0.16	0.17	0.18	0.15
A ₅	0.17	0.16	0.16	0.17	0.17	0.15	0.17	0.17	0.16	0.19	0.22
A ₆	0.17	0.18	0.18	0.18	0.17	0.18	0.17	0.17	0.19	0.14	0.19

Table 5. Compute entropy weight

A_i / C_j	C_1	C_2	C_3	C_4	C_5	C_6	C_7	C_8	C_9	C_{10}	C_{11}
A_1	-0.30	-0.30	-0.30	-0.30	-0.31	-0.31	-0.31	-0.32	-0.30	-0.30	-0.30
A_2	-0.30	-0.29	-0.29	-0.29	-0.29	-0.29	-0.28	-0.27	-0.30	-0.30	-0.30
A_3	-0.29	-0.29	-0.29	-0.29	-0.28	-0.27	-0.27	-0.28	-0.30	-0.30	-0.31
A_4	-0.29	-0.30	-0.29	-0.30	-0.27	-0.27	-0.27	-0.25	-0.30	-0.30	-0.30
A_5	-0.31	-0.32	-0.32	-0.31	-0.33	-0.33	-0.34	-0.34	-0.30	-0.30	-0.28
A_6	-0.30	-0.29	-0.29	-0.30	-0.30	-0.31	-0.30	-0.31	-0.30	-0.30	-0.30
S_j	-1.79	-1.79	-1.79	-1.79	-1.78	-1.78	-1.77	-1.76	-1.78	-1.79	-1.79
E	1.00	1.00	1.00	1.00	0.99	0.99	0.99	0.98	0.99	1.00	1.00
D_j	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.02	0.01	0.00	0.00
W_j	0.01	0.02	0.03	0.02	0.10	0.12	0.13	0.21	0.11	0.00	0.01
A_i / C_j	C_{12}	C_{13}	C_{14}	C_{15}	C_{16}	C_{17}	C_{18}	C_{19}	C_{20}	C_{21}	C_{22}
A_1	-0.30	-0.30	-0.30	-0.29	-0.29	-0.30	-0.30	-0.30	-0.28	-0.30	-0.31
A_2	-0.30	-0.30	-0.29	-0.29	-0.29	-0.32	-0.30	-0.30	-0.30	-0.30	-0.25
A_3	-0.29	-0.30	-0.30	-0.30	-0.30	-0.29	-0.30	-0.30	-0.30	-0.29	-0.29
A_4	-0.30	-0.30	-0.30	-0.30	-0.30	-0.30	-0.30	-0.29	-0.30	-0.31	-0.28
A_5	-0.30	-0.30	-0.30	-0.30	-0.30	-0.28	-0.30	-0.30	-0.30	-0.32	-0.33
A_6	-0.30	-0.31	-0.31	-0.31	-0.30	-0.31	-0.30	-0.31	-0.31	-0.27	-0.31
S_j	-1.79	-1.79	-1.79	-1.79	-1.79	-1.79	-1.79	-1.79	-1.79	-1.79	-1.77
E	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.99
D_j	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
W_j	0.00	0.01	0.01	0.01	0.00	0.04	0.00	0.00	0.02	0.04	0.15

4. DISCUSSION

This study focuses on the evaluation and selection of multiple genotype alternatives of Indian mustard (*Brassica juncea*) across several key criteria derived from experimental trials. The primary objective is to identify genetically divergent parental lines and to quantify the relative contribution of individual criteria to overall genetic divergence. Criteria weights are determined using the IDOCRIW approach, which combines entropy-based weights with CILOS-derived impact weights. The final criteria weights are obtained by integrating these two components. The entropy degree of each criterion is computed using **Eq. 3**, yielding $E_j = (0.999, 0.998, 0.998, 0.998, 0.993, 0.992, 0.991, 0.984, 0.992, 0.999, 0.991, 0.999, 0.999,$

$0.99, 0.999, 0.999, 0.997, 0.99, 0.991, 0.998, 0.997, 0.988)$ Based on **Eq. 4**, the corresponding deviation values are obtained as $d_j = (0.001, 0.001, 0.002, 0.001, 0.008, 0.008, 0.009, 0.015, 0.008, 5.64305, 0.0008, 7.673, 0.001, 0.001, 0.001, 0.0001, 0.002, 2.504, 0.0002, 0.001, 0.002, 0.01)$. Finally, the entropy weights are compute using **Eq. 5** $Ew_j = (0.007, 0.022, 0.027, 0.016, 0.095, 0.116, 0.126, 0.206, 0.106, 0.001, 0.011, 0.001, 0.005, 0.006, 0.007, 0.003, 0.038, 0.000, 0.003, 0.017, 0.038, 0.150)$. Subsequently, the CILOS weights are determined. A square matrix is constructed by selecting, for each criterion, the row from the normalized matrix corresponding to its maximum value. For example, the maximum value in the first column (0.320) occurs for the fourth alternative; therefore, the fourth row is

selected. This procedure is repeated for all criteria, allowing duplicate rows when maxima originate from the same alternative. The resulting square matrix is presented in **Table 6**, the relative impact loss matrix is then computed using **Eq. 8 (Table 7)**, followed by the derivation of the weight system matrix based on **Eq. 9 (Table 8)**. Solving the system of linear equations given in **Eq. 10** yields the CILOS weight vector $q_j = (0.045, 0.033, 0.037, 0.032, 0.012, 0.012, 0.014, 0.008, 0.012, 0.149, 0.031, 0.062, 0.083, 0.050, 0.045, 0.066, 0.032, 0.154, 0.073, 0.027, 0.017, 0.007)$. Finally, the entropy and CILOS weights are aggregated using **Eq. 11** and the final is criteria weights obtained as $w_j = (0.021, 0.048, 0.066, 0.034, 0.075, 0.091, 0.116, 0.109, 0.085, 0.007, 0.023, 0.004, 0.026, 0.020, 0.020, 0.011, 0.080, 0.003, 0.014, 0.031, 0.043, 0.071)$. These values are adopted as the final criteria weights for the subsequent evaluation and ranking of alternatives.

The second data set followed a similar structure and was used to support genotype assessment under forty-five alternatives of genotypes (A_1 – A_{45}) selected for quality-based evaluation **Table 20**. Genotype performance was assessed using four quality evaluation criteria given in **Table 19**. The entropy degree of each criterion is computed using the same equation as mentioned above **Eq. 3**, yielding $E_j = (0.271, 0.263, 0.272, 0.194)$ and the corresponding deviation values are obtained using **Eq. 4**, yielding $d_j = (1.993, 1.934, 1.996, 1.428)$. Based on the **Eq. 5** the entropy weight is obtained as $Ew_j = (0.2711, 0.2631, 0.2715, 0.1943)$. The same thing CILOS weights is determined producing a square matrix present in **Table 22**. The relative impact loss matrix is then computed using **Eq. 8 (Table 23)**, followed by the derivation of the weight system matrix based on **Eq. 9 (Table 24)**. Solving the system of linear equations given in **Eq. 10** yields the CILOS weight vector $q_j = (0.197, 0.198, 0.199, 0.197)$. Finally, the entropy and CILOS weights are aggregated using **Eq. 11** to obtain the IDOCRIW weight vector $w_j = (0.271, 0.263, 0.271, 0.194)$. Together, the two data sets enabled a structured and data driven evaluation of genotype performance across multiple criteria.

The final rankings of the genotype alternatives were obtained using the TOPSIS, VIKOR, and COPRAS methods, and the comparative results for the two datasets are presented in **Table 17** and **Table 29**, respectively. For the first dataset, the overall ranking indicates strong agreement between the TOPSIS and COPRAS methods. This is confirmed by Spearman's rank correlation analysis, which shows perfect concordance between the two approaches ($\rho = 1.000$), implying that both methods rank the genotypes in exactly the same order. In contrast, VIKOR exhibits a perfect negative correlation with TOPSIS and COPRAS ($\rho = -1.000$), reflecting a complete reversal in ranking. This divergence can be criteria to VIKOR's compromise-based decision logic, which emphasizes a balance between group utility and individual regret rather than strict closeness to an ideal solution. Based on the first dataset, the ranking of alternatives indicates that A_5 (IC212031) attains the highest preference, followed by A_1 , A_6 , A_2 , A_3 , and A_4 , respectively. The strong consistency observed between TOPSIS and COPRAS suggests that this genotype demonstrates superior and stable performance, thereby identifying it as the most suitable among the evaluated alternatives. In contrast, for the second dataset, which comprises a large number of alternatives, the K-means++ clustering algorithm is applied which strengthened through the integration of silhouette analysis. This enhancement allows for the formation of more meaningful and well-separated clusters by simultaneously capturing intra-cluster cohesion and inter-cluster dissimilarity. The resulting clusters are then consolidated into cluster-based alternatives (CBAs) and evaluated using an extended decision-making framework. The ranking outcomes demonstrate partial convergence across methods. In particular, both VIKOR and COPRAS consistently identify the best- and worst-performing genotype alternatives at identical positions; specifically, both methods rank A_{17} (NRC YS 5-2) as the top-performing alternative and A_{25} (Anuradha) as the lowest-ranked alternative. Such agreement at the extremes of the ranking spectrum underscores the robustness of these two in reliably distinguishing superior and inferior genotypes.

Table 6. Final square matrix

A/C _j	C ₁	C ₂	C ₃	C ₄	C ₅	C ₆	C ₇	C ₈	C ₉	C ₁₀	C ₁₁	C ₁₂	C ₁₃	C ₁₄	C ₁₅	C ₁₆	C ₁₇	C ₁₈	C ₁₉	C ₂₀	C ₂₁	C ₂₂
C ₁	1.0	1.0	1.0	1.0	0.9	1.0	1.0	0.8	0.9	1.0	0.8	1.0	1.0	1.0	0.9	0.9	1.0	1.0	1.0	0.9	0.9	0.8
C ₂	1.0	1.0	1.0	1.0	0.9	1.0	1.0	0.8	0.9	1.0	0.8	1.0	1.0	1.0	0.9	0.9	1.0	1.0	1.0	0.9	0.9	0.8
C ₃	0.9	1.0	0.9	0.9	0.7	0.7	0.7	0.6	0.7	1.0	0.9	1.0	1.0	1.0	1.0	1.0	0.9	1.0	1.0	1.0	0.8	0.6
C ₄	1.0	1.0	1.0	1.0	0.9	0.8	0.9	0.8	0.9	1.0	0.9	1.0	1.0	1.0	1.0	1.0	0.8	1.0	1.0	0.9	0.8	1.0
C ₅	1.0	1.0	1.0	0.9	1.0	1.0	1.0	1.0	1.0	1.0	0.9	1.0	1.0	1.0	1.0	1.0	0.9	1.0	1.0	0.9	0.8	0.8
C ₆	1.0	1.0	1.0	1.0	0.9	1.0	1.0	0.8	0.9	1.0	0.8	1.0	1.0	1.0	0.9	0.9	1.0	1.0	1.0	0.9	0.9	0.8
C ₇	1.0	1.0	1.0	0.9	1.0	1.0	1.0	1.0	1.0	1.0	0.9	1.0	1.0	1.0	1.0	1.0	0.9	1.0	1.0	0.9	0.8	0.8
C ₈	1.0	1.0	1.0	0.9	1.0	1.0	1.0	1.0	1.0	1.0	0.9	1.0	1.0	1.0	1.0	1.0	0.9	1.0	1.0	0.9	0.8	0.8
C ₉	1.0	1.0	1.0	0.9	1.0	1.0	1.0	1.0	1.0	1.0	0.9	1.0	1.0	1.0	1.0	1.0	0.9	1.0	1.0	0.9	0.8	0.8
C ₁₀	0.9	0.8	0.8	0.8	0.6	0.6	0.6	0.5	0.6	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	0.9	0.9	0.7	0.5
C ₁₁	0.9	0.8	0.8	0.8	0.6	0.6	0.6	0.5	0.6	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	0.9	0.9	0.7	0.5
C ₁₂	1.0	1.0	1.0	1.0	0.9	1.0	1.0	0.8	0.9	1.0	0.8	1.0	1.0	1.0	0.9	0.9	1.0	1.0	1.0	0.9	0.9	0.8
C ₁₃	1.0	1.0	1.0	1.0	0.9	0.8	0.9	0.8	0.9	1.0	0.9	1.0	1.0	1.0	1.0	1.0	0.8	1.0	1.0	0.9	0.8	1.0
C ₁₄	1.0	1.0	1.0	1.0	0.9	0.8	0.9	0.8	0.9	1.0	0.9	1.0	1.0	1.0	1.0	1.0	0.8	1.0	1.0	0.9	0.8	1.0
C ₁₅	1.0	1.0	1.0	1.0	0.9	0.8	0.9	0.8	0.9	1.0	0.9	1.0	1.0	1.0	1.0	1.0	0.8	1.0	1.0	0.9	0.8	1.0
C ₁₆	0.9	1.0	0.9	0.9	0.7	0.7	0.7	0.6	0.7	1.0	0.9	1.0	1.0	1.0	1.0	1.0	0.9	1.0	1.0	1.0	0.8	0.6
C ₁₇	0.9	0.8	0.8	0.8	0.6	0.6	0.6	0.5	0.6	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	0.9	0.9	0.7	0.5
C ₁₈	1.0	1.0	1.0	1.0	0.9	1.0	1.0	0.8	0.9	1.0	0.8	1.0	1.0	1.0	0.9	0.9	1.0	1.0	1.0	0.9	0.9	0.8
C ₁₉	1.0	1.0	1.0	0.9	1.0	1.0	1.0	1.0	1.0	1.0	0.9	1.0	1.0	1.0	1.0	1.0	0.9	1.0	1.0	0.9	0.8	0.8
C ₂₀	0.9	1.0	0.9	0.9	0.7	0.7	0.7	0.6	0.7	1.0	0.9	1.0	1.0	1.0	1.0	1.0	0.9	1.0	1.0	1.0	0.8	0.6
C ₂₁	0.9	1.0	1.0	0.9	0.8	0.7	0.8	0.6	0.8	1.0	0.9	1.0	0.9	0.9	0.9	0.9	0.8	1.0	0.9	0.8	1.0	0.6
C ₂₂	1.0	1.0	1.0	1.0	0.9	0.8	0.9	0.8	0.9	1.0	0.9	1.0	1.0	1.0	1.0	1.0	0.8	1.0	1.0	0.9	0.8	1.0

Table 7. Relative impact loss matrix

A/C _j	C ₁	C ₂	C ₃	C ₄	C ₅	C ₆	C ₇	C ₈	C ₉	C ₁₀	C ₁₁	C ₁₂	C ₁₃	C ₁₄	C ₁₅	C ₁₆	C ₁₇	C ₁₈	C ₁₉	C ₂₀	C ₂₁	C ₂₂
C ₁	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.2	0.1	0.0	0.2	0.0	0.1	0.1	0.1	0.1	0.0	0.0	0.0	0.1	0.2	0.3
C ₂	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.2	0.1	0.0	0.2	0.0	0.1	0.1	0.1	0.1	0.0	0.0	0.0	0.1	0.2	0.3
C ₃	0.1	0.1	0.0	0.1	0.3	0.3	0.3	0.4	0.3	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.2	0.4
C ₄	0.0	0.0	0.1	0.0	0.1	0.2	0.1	0.2	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.1	0.2	0.0
C ₅	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.1	0.0	0.0	0.1	0.2	0.2
C ₆	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.2	0.1	0.0	0.2	0.0	0.1	0.1	0.1	0.1	0.0	0.0	0.0	0.1	0.2	0.3
C ₇	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.1	0.0	0.0	0.1	0.2	0.2
C ₈	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.1	0.0	0.0	0.1	0.2	0.2
C ₉	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.1	0.0	0.0	0.1	0.2	0.2
C ₁₀	0.1	0.2	0.2	0.2	0.4	0.4	0.4	0.5	0.4	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.3	0.5
C ₁₁	0.1	0.2	0.2	0.2	0.4	0.4	0.4	0.5	0.4	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.3	0.5
C ₁₂	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.2	0.1	0.0	0.2	0.0	0.1	0.1	0.1	0.1	0.0	0.0	0.0	0.1	0.2	0.3
C ₁₃	0.0	0.0	0.0	0.0	0.1	0.2	0.1	0.2	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.1	0.2	0.0
C ₁₄	0.0	0.0	0.0	0.0	0.1	0.2	0.1	0.2	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.1	0.2	0.0
C ₁₅	0.0	0.0	0.0	0.0	0.1	0.2	0.1	0.2	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.1	0.2	0.0
C ₁₆	0.1	0.1	0.1	0.1	0.3	0.3	0.3	0.4	0.3	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.2	0.4
C ₁₇	0.1	0.2	0.2	0.2	0.4	0.4	0.4	0.5	0.4	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.3	0.5
C ₁₈	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.2	0.1	0.0	0.2	0.0	0.1	0.1	0.1	0.1	0.0	0.0	0.0	0.1	0.2	0.3
C ₁₉	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.1	0.0	0.0	0.1	0.2	0.2
C ₂₀	0.1	0.1	0.1	0.1	0.3	0.3	0.3	0.4	0.3	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.2	0.4
C ₂₁	0.1	0.0	0.0	0.1	0.2	0.3	0.2	0.4	0.2	0.0	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.0	0.1	0.2	0.0	0.4
C ₂₂	0.0	0.0	0.0	0.0	0.1	0.2	0.1	0.2	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.1	0.2	0.0

Table 8. Weighted system matrix

A _i /C _j	C ₁	C ₂	C ₃	C ₄	C ₅	C ₆	C ₇	C ₈	C ₉	C ₁₀	C ₁₁	C ₁₂	C ₁₃	C ₁₄	C ₁₅	C ₁₆	C ₁₇	C ₁₈	C ₁₉	C ₂₀	C ₂₁	C ₂₂
C ₁	-0.8	0.0	0.0	0.0	0.1	0.0	0.0	0.2	0.1	0.0	0.2	0.0	0.1	0.1	0.1	0.1	0.0	0.0	0.0	0.1	0.2	0.3
C ₂	0.0	-1.1	0.0	0.0	0.1	0.0	0.0	0.2	0.1	0.0	0.2	0.0	0.1	0.1	0.1	0.1	0.0	0.0	0.0	0.1	0.2	0.3
C ₃	0.1	0.1	-1.4	0.1	0.3	0.3	0.3	0.4	0.3	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.2	0.4
C ₄	0.0	0.0	0.1	-1.3	0.1	0.2	0.1	0.2	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.1	0.2	0.0
C ₅	0.0	0.1	0.0	0.1	-3.3	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.1	0.0	0.0	0.1	0.2	0.2
C ₆	0.0	0.0	0.0	0.0	0.1	-3.2	0.0	0.2	0.1	0.0	0.2	0.0	0.1	0.1	0.1	0.1	0.0	0.0	0.0	0.1	0.2	0.3
C ₇	0.0	0.1	0.0	0.1	0.0	0.0	-2.8	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.1	0.0	0.0	0.1	0.2	0.2
C ₈	0.0	0.1	0.0	0.1	0.0	0.0	0.0	-4.9	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.1	0.0	0.0	0.1	0.2	0.2
C ₉	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.0	-3.2	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.1	0.0	0.0	0.1	0.2	0.2
C ₁₀	0.1	0.2	0.2	0.2	0.4	0.4	0.4	0.5	0.4	-0.5	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.3	0.5
C ₁₁	0.1	0.2	0.2	0.2	0.4	0.4	0.4	0.5	0.4	0.0	-2.5	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.3	0.5
C ₁₂	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.2	0.1	0.0	0.2	-0.6	0.1	0.1	0.1	0.1	0.0	0.0	0.0	0.1	0.2	0.3
C ₁₃	0.0	0.0	0.0	0.0	0.1	0.2	0.1	0.2	0.1	0.0	0.1	0.0	-0.5	0.0	0.0	0.0	0.3	0.0	0.0	0.1	0.2	0.0
C ₁₄	0.0	0.0	0.0	0.0	0.1	0.2	0.1	0.2	0.1	0.0	0.1	0.0	0.0	-0.8	0.0	0.0	0.3	0.0	0.0	0.1	0.2	0.0
C ₁₅	0.0	0.0	0.0	0.0	0.1	0.2	0.1	0.2	0.1	0.0	0.1	0.0	0.0	0.0	-0.9	0.0	0.3	0.0	0.0	0.1	0.2	0.0
C ₁₆	0.1	0.1	0.1	0.1	0.3	0.3	0.3	0.4	0.3	0.0	0.1	0.1	0.0	0.0	0.0	-0.8	0.1	0.0	0.0	0.0	0.2	0.4
C ₁₇	0.1	0.2	0.2	0.2	0.4	0.4	0.4	0.5	0.4	0.0	0.0	0.0	0.0	0.0	0.1	0.0	-2.4	0.0	0.1	0.1	0.3	0.5
C ₁₈	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.2	0.1	0.0	0.2	0.0	0.1	0.1	0.1	0.1	0.0	-0.2	0.0	0.1	0.2	0.3
C ₁₉	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.1	0.0	-0.5	0.1	0.2	0.2
C ₂₀	0.1	0.1	0.1	0.1	0.3	0.3	0.3	0.4	0.3	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.1	0.0	0.0	-2.0	0.2	0.4
C ₂₁	0.1	0.0	0.0	0.1	0.2	0.3	0.2	0.4	0.2	0.0	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.0	0.1	0.2	-4.3	0.4
C ₂₂	0.0	0.0	0.0	0.0	0.1	0.2	0.1	0.2	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.1	0.2	-5.4

Table 9. IDOCRIW weights

C _j	E _{wj}	CILOS w _j	E _{wj} *CILOS _{wj}	W _j	C _j	E _{wj}	CILOS w _j	E _{wj} *CILOS _{wj}	W _j
C ₁	0.007	0.045	0.000	0.021	C ₁₂	0.001	0.062	0.000	0.004
C ₂	0.022	0.033	0.001	0.048	C ₁₃	0.005	0.083	0.000	0.026
C ₃	0.027	0.037	0.001	0.066	C ₁₄	0.006	0.050	0.000	0.020
C ₄	0.016	0.032	0.001	0.034	C ₁₅	0.007	0.045	0.000	0.020
C ₅	0.095	0.012	0.001	0.075	C ₁₆	0.003	0.066	0.000	0.011
C ₆	0.116	0.012	0.001	0.091	C ₁₇	0.038	0.032	0.001	0.080
C ₇	0.126	0.014	0.002	0.116	C ₁₈	0.000	0.154	0.000	0.003
C ₈	0.206	0.008	0.002	0.109	C ₁₉	0.003	0.073	0.000	0.014
C ₉	0.106	0.012	0.001	0.085	C ₂₀	0.017	0.027	0.000	0.031
C ₁₀	0.001	0.149	0.000	0.007	C ₂₁	0.038	0.017	0.001	0.043
C ₁₁	0.011	0.031	0.000	0.023	C ₂₂	0.150	0.007	0.001	0.071

Table 10. Updated normalize matrix (TOPSIS)

A _i /C _j	C ₁	C ₂	C ₃	C ₄	C ₅	C ₆	C ₇	C ₈	C ₉	C ₁₀	C ₁₁
A ₁	0.411	0.401	0.413	0.416	0.444	0.440	0.446	0.475	0.446	0.407	0.402
A ₂	0.400	0.391	0.385	0.376	0.374	0.374	0.361	0.325	0.370	0.414	0.420
A ₃	0.388	0.382	0.392	0.376	0.348	0.315	0.333	0.334	0.339	0.414	0.435
A ₄	0.394	0.401	0.392	0.406	0.321	0.322	0.326	0.273	0.320	0.414	0.423
A ₅	0.443	0.477	0.482	0.455	0.520	0.516	0.545	0.545	0.523	0.401	0.366

A ₆	0.411	0.391	0.378	0.416	0.409	0.443	0.396	0.431	0.417	0.401	0.400
A _i /C _j	C ₁₂	C ₁₃	C ₁₄	C ₁₅	C ₁₆	C ₁₇	C ₁₈	C ₁₉	C ₂₀	C ₂₁	C ₂₂
A ₁	0.415	0.403	0.404	0.395	0.392	0.397	0.407	0.405	0.366	0.418	0.429
A ₂	0.406	0.395	0.389	0.387	0.395	0.479	0.409	0.400	0.399	0.403	0.273
A ₃	0.395	0.416	0.410	0.409	0.422	0.368	0.403	0.404	0.405	0.388	0.362
A ₄	0.408	0.399	0.407	0.405	0.411	0.397	0.405	0.394	0.419	0.434	0.358
A ₅	0.411	0.397	0.396	0.408	0.410	0.357	0.415	0.418	0.396	0.463	0.528
A ₆	0.414	0.437	0.442	0.443	0.418	0.438	0.411	0.428	0.459	0.331	0.451

Table 11. Weighted normalized matrix (TOPSIS)

A _i / C _j	C ₁	C ₂	C ₃	C ₄	C ₅	C ₆	C ₇	C ₈	C ₉	C ₁₀	C ₁₁
A ₁	0.009	0.019	0.027	0.014	0.033	0.040	0.052	0.052	0.038	0.003	0.009
A ₂	0.008	0.019	0.025	0.013	0.028	0.034	0.042	0.035	0.031	0.003	0.010
A ₃	0.008	0.018	0.026	0.013	0.026	0.029	0.039	0.036	0.029	0.003	0.010
A ₄	0.008	0.019	0.026	0.014	0.024	0.029	0.038	0.030	0.027	0.003	0.010
A ₅	0.009	0.023	0.032	0.016	0.039	0.047	0.063	0.059	0.045	0.003	0.008
A ₆	0.009	0.019	0.025	0.014	0.031	0.040	0.046	0.047	0.035	0.003	0.009
A _i /C _j	C ₁₂	C ₁₃	C ₁₄	C ₁₅	C ₁₆	C ₁₇	C ₁₈	C ₁₉	C ₂₀	C ₂₁	C ₂₂
A ₁	0.002	0.011	0.008	0.008	0.004	0.032	0.001	0.006	0.011	0.018	0.030
A ₂	0.002	0.010	0.008	0.008	0.005	0.038	0.001	0.006	0.012	0.017	0.019
A ₃	0.002	0.011	0.008	0.008	0.005	0.029	0.001	0.006	0.012	0.017	0.026
A ₄	0.002	0.011	0.008	0.008	0.005	0.032	0.001	0.006	0.013	0.019	0.025
A ₅	0.002	0.010	0.008	0.008	0.005	0.029	0.001	0.006	0.012	0.020	0.038
A ₆	0.002	0.012	0.009	0.009	0.005	0.035	0.001	0.006	0.014	0.014	0.032

Table 12. Final ranking (TOPSIS)

A _i	S _i ⁺	S _i ⁻	C _i	R _i
A ₁	0.021435	0.0341298	0.614237	2
A ₂	0.043546	0.01483416	0.254094	4
A ₃	0.046703	0.01023874	0.179809	5

A _i	S _i ⁺	S _i ⁻	C _i	R _i
A ₄	0.051089	0.00863199	0.144538	6
A ₅	0.010198	0.05315166	0.839016	1
A ₆	0.028089	0.02877132	0.506003	3

Table 13. Weighted normalize matrix (VIKOR)

A _i / C _j	C ₁	C ₂	C ₃	C ₄	C ₅	C ₆	C ₇	C ₈	C ₉	C ₁₀	C ₁₁
A ₁	0.012	0.039	0.044	0.017	0.029	0.035	0.052	0.028	0.032	0.004	0.011
A ₂	0.016	0.043	0.061	0.034	0.055	0.064	0.097	0.088	0.064	0.000	0.005
A ₃	0.021	0.048	0.057	0.034	0.065	0.091	0.112	0.084	0.077	0.000	0.000
A ₄	0.018	0.039	0.057	0.021	0.075	0.088	0.116	0.109	0.085	0.000	0.004
A ₅	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.023
A ₆	0.012	0.043	0.066	0.017	0.042	0.033	0.079	0.046	0.045	0.007	0.012
A _i /C _j	C ₁₂	C ₁₃	C ₁₄	C ₁₅	C ₁₆	C ₁₇	C ₁₈	C ₁₉	C ₂₀	C ₂₁	C ₂₂
A ₁	0.000	0.022	0.014	0.017	0.011	0.054	0.002	0.010	0.031	0.015	0.028
A ₂	0.002	0.026	0.020	0.020	0.010	0.000	0.002	0.012	0.020	0.020	0.071
A ₃	0.004	0.013	0.012	0.012	0.000	0.073	0.003	0.010	0.018	0.024	0.046
A ₄	0.001	0.024	0.013	0.014	0.004	0.054	0.003	0.014	0.013	0.010	0.047
A ₅	0.001	0.026	0.018	0.013	0.005	0.080	0.000	0.004	0.021	0.000	0.000
A ₆	0.000	0.000	0.000	0.000	0.002	0.027	0.001	0.000	0.000	0.043	0.022

Table 14. Final ranking (VIKOR)

A_i	S_i	Q_i	R_i
A ₁	0.506	0.253	5
A ₂	0.733	0.788	3
A ₃	0.806	0.968	2

A_i	S_i	Q_i	R_i
A ₄	0.809	1.000	1
A ₅	0.197	0.210	6
A ₆	0.495	0.444	4

Table 15. Normalize matrix (COPRAS)

A_i / C_j	C ₁	C ₂	C ₃	C ₄	C ₅	C ₆	C ₇	C ₈	C ₉	C ₁₀	C ₁₁
A ₁	0.168	0.164	0.169	0.170	0.184	0.182	0.185	0.199	0.185	0.166	0.164
A ₂	0.163	0.160	0.158	0.154	0.155	0.155	0.150	0.137	0.153	0.169	0.172
A ₃	0.158	0.156	0.160	0.154	0.144	0.131	0.138	0.140	0.140	0.169	0.178
A ₄	0.161	0.164	0.160	0.166	0.133	0.134	0.135	0.114	0.132	0.169	0.173
A ₅	0.181	0.195	0.198	0.186	0.215	0.214	0.226	0.229	0.217	0.164	0.150
A ₆	0.168	0.160	0.155	0.170	0.169	0.184	0.165	0.181	0.173	0.164	0.163
A_i / C_j	C ₁₂	C ₁₃	C ₁₄	C ₁₅	C ₁₆	C ₁₇	C ₁₈	C ₁₉	C ₂₀	C ₂₁	C ₂₂
A ₁	0.169	0.165	0.165	0.161	0.160	0.163	0.166	0.165	0.150	0.171	0.179
A ₂	0.166	0.162	0.159	0.158	0.161	0.197	0.167	0.163	0.163	0.165	0.114
A ₃	0.161	0.170	0.167	0.167	0.172	0.151	0.164	0.165	0.166	0.159	0.151
A ₄	0.167	0.163	0.166	0.166	0.168	0.163	0.166	0.161	0.172	0.178	0.149
A ₅	0.168	0.162	0.162	0.167	0.167	0.147	0.169	0.171	0.162	0.190	0.220
A ₆	0.169	0.179	0.181	0.181	0.171	0.180	0.168	0.175	0.188	0.136	0.188

Table 16. Weighted normalize matrix (COPRAS)

A_i / C_j	C ₁	C ₂	C ₃	C ₄	C ₅	C ₆	C ₇	C ₈	C ₉	C ₁₀	C ₁₁
A ₁	0.004	0.008	0.011	0.006	0.014	0.017	0.022	0.022	0.016	0.001	0.004
A ₂	0.003	0.008	0.010	0.005	0.012	0.014	0.017	0.015	0.013	0.001	0.004
A ₃	0.003	0.008	0.011	0.005	0.011	0.012	0.016	0.015	0.012	0.001	0.004
A ₄	0.003	0.008	0.011	0.006	0.010	0.012	0.016	0.012	0.011	0.001	0.004
A ₅	0.004	0.009	0.013	0.006	0.016	0.019	0.026	0.025	0.018	0.001	0.003
A ₆	0.004	0.008	0.010	0.006	0.013	0.017	0.019	0.020	0.015	0.001	0.004
A_i / C_j	C ₁₂	C ₁₃	C ₁₄	C ₁₅	C ₁₆	C ₁₇	C ₁₈	C ₁₉	C ₂₀	C ₂₁	C ₂₂
A ₁	0.001	0.004	0.003	0.003	0.002	0.013	0.001	0.002	0.005	0.007	0.013
A ₂	0.001	0.004	0.003	0.003	0.002	0.016	0.001	0.002	0.005	0.007	0.008
A ₃	0.001	0.004	0.003	0.003	0.002	0.012	0.001	0.002	0.005	0.007	0.011
A ₄	0.001	0.004	0.003	0.003	0.002	0.013	0.001	0.002	0.005	0.008	0.011
A ₅	0.001	0.004	0.003	0.003	0.002	0.012	0.001	0.002	0.005	0.008	0.016
A ₆	0.001	0.005	0.004	0.004	0.002	0.014	0.001	0.002	0.006	0.006	0.013

Table 17. Comparative ranking results obtained using TOPSIS, COPRAS, and VIKOR methods

	TOPSIS		COPRAS		VIKOR	
A_i	C_i	R_i	U_i	R_i	Q_i	R_i
A ₁	0.614237	2	82.97948	2	0.252642	5
A ₂	0.254094	4	66.9448	4	0.787583	3
A ₃	0.179809	5	61.85938	5	0.967661	2
A ₄	0.144538	6	60.58803	6	1	1
A ₅	0.839016	1	100	1	0.209925	6
A ₆	0.506003	3	75.49117	3	0.443835	4

Table 19. List of the genotype evaluation criteria

C_j	Criteria
C ₁	Total glucosinolates
C ₂	Phytic acid
C ₃	Crude fiber (%)
C ₄	Erucic acid (%)

Table 18. List of the suitable genotype alternatives

A_i	Genotype	A_i	Genotype
A ₁	RB 50	A ₂₃	PT-30
A ₂	RH 781	A ₂₄	TS-36
A ₃	RH 819	A ₂₅	Anuradha
A ₄	RH 0406	A ₂₆	KBS 3
A ₅	RH 0749	A ₂₇	KOS 1
A ₆	NRCDR 2	A ₂₈	DRMR-82
A ₇	NRCHB 101	A ₂₉	DRMR-973
A ₈	DRMR IJ-31	A ₃₀	DRMR-388
A ₉	Swarna	A ₃₁	GSL 1
A ₁₀	NPJ-112	A ₃₂	Sheetal
A ₁₁	DRMR-1288	A ₃₃	Neelam
A ₁₂	Basanti	A ₃₄	GSC-5
A ₁₃	CS-52	A ₃₅	GSL-2
A ₁₄	RCC-4	A ₃₆	Kiran
A ₁₅	RGN-73	A ₃₇	PC 5
A ₁₆	YSH 401	A ₃₈	Pusa Aditya
A ₁₇	NRC YS 5-2	A ₃₉	PC5-17
A ₁₈	Ragini	A ₄₀	Pusa Swarnim
A ₁₉	Jhumka	A ₄₁	RTM 314
A ₂₀	Benoy	A ₄₂	T 27
A ₂₁	Bhavani	A ₄₃	DRMR-171
A ₂₂	PT 303	A ₄₄	DRMR-173
		A ₄₅	TMLC-2

Table 20. Original decision matrix

A_i / C_j	C ₁	C ₂	C ₃	C ₄	A_i	C ₁	C ₂	C ₃	C ₄
A ₁	141.42	0.3	10.34	19.97	A ₂₃	204.77	2.58	9.07	41.36
A ₂	137.85	0.2	12.67	27.82	A ₂₄	156.99	1.2	9.03	33.24
A ₃	118.83	0.54	9.91	37.32	A ₂₅	200.02	5.86	9.91	33.94
A ₄	130.13	0.21	13.39	42.9	A ₂₆	160.2	5.07	10.44	38.94
A ₅	94.23	0.35	10.11	43.99	A ₂₇	172.2	2.2	12.63	34.19
A ₆	118.48	0.69	12.54	36.54	A ₂₈	199.18	0.82	10.94	4013
A ₇	113.13	0.8	10.14	34.72	A ₂₉	167.33	2.88	10.42	39.77
A ₈	103.38	0.46	11.31	41.43	A ₃₀	150.93	1.99	10.51	35.37
A ₉	72.48	0.65	6.85	35.65	A ₃₁	165.55	2.4	10.65	27.76
A ₁₀	159.84	2.58	9.73	31.56	A ₃₂	141.06	2.44	10.49	21.94
A ₁₁	179.57	2.25	11.44	38.75	A ₃₃	137.26	3.54	10.82	14.12
A ₁₂	164.59	2.6	11.57	41.7	A ₃₄	155.32	3.36	10.72	17.72
A ₁₃	169.35	1.58	10.69	35.12	A ₃₅	110.51	2.38	9.54	22.03
A ₁₄	187.42	3.03	11.41	37.93	A ₃₆	157.94	2.61	8.58	35.22
A ₁₅	180.05	1.76	11.25	40.3	A ₃₇	75.81	2.96	10.85	33.62
A ₁₆	139.28	0.55	8.15	48.51	A ₃₈	69.74	3.32	7.01	26.92
A ₁₇	160.91	0.31	8.34	43.64	A ₃₉	175.41	3.27	10.25	36.09
A ₁₈	152.59	6.15	7.79	41.31	A ₄₀	138.21	4.39	6.69	36.73
A ₁₉	148.07	2	6.43	31.18	A ₄₁	134.52	1.24	10.01	39.99

A ₂₀	122.52	1.33	6.66	37.01	A ₄₂	144.86	3.39	12.17	30.65
A ₂₁	137.73	0.53	12.44	37.38	A ₄₃	92.09	4.46	12.63	33.32
A ₂₂	164.48	0.64	13.1	32.37	A ₄₄	92.57	2.69	8.78	42.34
					A ₄₅	131.2	3.41	9.89	41.44

Table 21. Normalized matrix

A _i / C _j	C ₁	C ₂	C ₃	C ₄	A _i / C _j	C ₁	C ₂	C ₃	C ₄
A ₁	0.022	0.003	0.023	0.004	A ₂₃	0.032	0.026	0.020	0.007
A ₂	0.021	0.002	0.028	0.005	A ₂₄	0.024	0.012	0.020	0.006
A ₃	0.018	0.006	0.022	0.007	A ₂₅	0.031	0.060	0.022	0.006
A ₄	0.020	0.002	0.029	0.008	A ₂₆	0.025	0.052	0.023	0.007
A ₅	0.015	0.004	0.022	0.008	A ₂₇	0.027	0.022	0.028	0.006
A ₆	0.018	0.007	0.027	0.007	A ₂₈	0.031	0.008	0.024	0.723
A ₇	0.018	0.008	0.022	0.006	A ₂₉	0.026	0.029	0.023	0.007
A ₈	0.016	0.005	0.025	0.007	A ₃₀	0.023	0.020	0.023	0.006
A ₉	0.011	0.007	0.015	0.006	A ₃₁	0.026	0.024	0.023	0.005
A ₁₀	0.025	0.026	0.021	0.006	A ₃₂	0.022	0.025	0.023	0.004
A ₁₁	0.028	0.023	0.025	0.007	A ₃₃	0.021	0.036	0.024	0.003
A ₁₂	0.026	0.027	0.025	0.008	A ₃₄	0.024	0.034	0.023	0.003
A ₁₃	0.026	0.016	0.023	0.006	A ₃₅	0.017	0.024	0.021	0.004
A ₁₄	0.029	0.031	0.025	0.007	A ₃₆	0.025	0.027	0.019	0.006
A ₁₅	0.028	0.018	0.025	0.007	A ₃₇	0.012	0.030	0.024	0.006
A ₁₆	0.022	0.006	0.018	0.009	A ₃₈	0.011	0.034	0.015	0.005
A ₁₇	0.025	0.003	0.018	0.008	A ₃₉	0.027	0.033	0.022	0.007
A ₁₈	0.024	0.063	0.017	0.007	A ₄₀	0.021	0.045	0.015	0.007
A ₁₉	0.023	0.020	0.014	0.006	A ₄₁	0.021	0.013	0.022	0.007
A ₂₀	0.019	0.014	0.015	0.007	A ₄₂	0.023	0.035	0.027	0.006
A ₂₁	0.021	0.005	0.027	0.007	A ₄₃	0.014	0.046	0.028	0.006
A ₂₂	0.026	0.007	0.029	0.006	A ₄₄	0.014	0.027	0.019	0.008
					A ₄₅	0.020	0.035	0.022	0.007

Table 22. Final square matrix

C _j	C ₁	C ₂	C ₃	C ₄
C ₁	1	0.06024	0.91726	0.52452
C ₂	0.5059	1	0.5075	0.50755
C ₃	0.471	0.1	1	0.45285
C ₄	0.5081	0.0565	0.59427	1

Table 23. Relative impact loss matrix

C _j	C ₁	C ₂	C ₃	C ₄
C ₁	0	0.93976	0.08274	0.47548
C ₂	0.49409	0	0.4925	0.49245
C ₃	0.52901	0.9	0	0.54715
C ₄	0.49191	0.9435	0.40573	0

Table 24. Weighted system matrix

C _j	C ₁	C ₂	C ₃	C ₄
C ₁	-1.515	0.93976	0.08274	0.47548
C ₂	0.4941	-2.7833	0.4925	0.49245
C ₃	0.529	0.9	-0.981	0.54715
C ₄	0.4919	0.9435	0.40573	-1.5151

Table 25. IDOCRIW weights

C _j	Ew _j	CILOS w _j	Ew _j *CILOS w _j	W _j
C ₁	0.271	0.197	0.053	0.271
C ₂	0.263	0.197	0.052	0.263
C ₃	0.272	0.197	0.053	0.272
C ₄	0.194	0.197	0.038	0.194

Table 26. TOPSIS

Original decision matrix					Normalise				
A_i/C_j	C_1	C_2	C_3	C_4	A_i/C_j	C_1	C_2	C_3	C_4
A ₁₀	159.84	2.58	9.73	31.56	A ₁₀	2.43	0.041	0.718	0.746
A ₁₁	179.57	2.25	11.44	38.75	A ₁₁	2.37	0.027	0.88	1.039
A ₁₂	164.59	2.6	11.57	41.7	A ₁₂	2.04	0.073	0.688	1.394
A ₁₃	169.35	1.58	10.69	35.12	A ₁₃	2.24	0.028	0.929	1.603
A ₁₄	187.42	3.03	11.41	37.93	A ₁₄	1.62	0.047	0.702	1.644
A ₁₅	180.05	1.76	11.25	40.3	A ₁₅	2.04	0.094	0.87	1.365
A ₁₇	160.91	0.31	8.34	43.64	A ₁₇	1.94	0.109	0.704	1.297
A ₁₈	152.59	6.15	7.79	41.31	A ₁₈	1.78	0.062	0.785	1.548
A ₂₂	164.48	0.64	13.1	32.37	A ₂₂	1.25	0.088	0.475	1.332
A ₂₃	204.77	2.58	9.07	41.36	A ₂₃	2.75	0.35	0.675	1.179
A ₂₄	156.99	1.2	9.03	33.24	A ₂₄	3.09	0.305	0.794	1.448
A ₂₅	200.02	5.86	9.91	33.94	A ₂₅	2.83	0.353	0.803	1.558
A ₂₆	160.2	5.07	10.44	38.94	A ₂₆	2.91	0.214	0.742	1.312
A ₂₇	172.2	2.2	12.63	34.19	A ₂₇	3.22	0.411	0.792	1.417
A ₂₉	167.33	2.88	10.42	39.77	A ₂₉	3.09	0.239	0.781	1.506
A ₃₀	150.93	1.99	10.51	35.37	A ₃₀	2.39	0.075	0.566	1.813
A ₃₁	165.55	2.4	10.65	27.76	A ₃₁	2.77	0.042	0.579	1.631
A ₃₄	155.32	3.36	10.72	17.72	A ₃₄	2.62	0.834	0.541	1.544
A ₃₆	157.94	2.61	8.58	35.22	A ₃₆	2.55	0.271	0.446	1.165
A ₃₉	175.41	3.27	10.25	36.09	A ₃₉	2.11	0.18	0.462	1.383
Weighted normalised matrix					Euclidean distance				
A_i/C_j	C_1	C_2	C_3	C_4	A_i	S_i^+	S_i^-	Q_i	R_i
A ₁₀	0.659	0.011	0.195	0.145	A ₁₀	0.37	0.33	0.472	13
A ₁₁	0.642	0.007	0.239	0.202	A ₁₁	0.35	0.331	0.488	12
A ₁₂	0.554	0.019	0.187	0.271	A ₁₂	0.39	0.259	0.398	16
A ₁₃	0.606	0.007	0.252	0.311	A ₁₃	0.34	0.342	0.499	11
A ₁₄	0.439	0.012	0.191	0.319	A ₁₄	0.49	0.213	0.305	19
A ₁₅	0.552	0.025	0.236	0.265	A ₁₅	0.39	0.272	0.413	14
A ₁₇	0.527	0.029	0.191	0.252	A ₁₇	0.41	0.23	0.358	17
A ₁₈	0.482	0.016	0.213	0.301	A ₁₈	0.45	0.231	0.342	18
A ₂₂	0.338	0.023	0.129	0.259	A ₂₂	0.59	0.115	0.163	20
A ₂₃	0.745	0.092	0.183	0.229	A ₂₃	0.23	0.429	0.651	7
A ₂₄	0.837	0.08	0.216	0.281	A ₂₄	0.17	0.531	0.763	2
A ₂₅	0.767	0.093	0.218	0.303	A ₂₅	0.18	0.475	0.73	4
A ₂₆	0.789	0.056	0.201	0.255	A ₂₆	0.21	0.474	0.689	6
A ₂₇	0.873	0.108	0.215	0.275	A ₂₇	0.14	0.568	0.802	1
A ₂₉	0.839	0.063	0.212	0.293	A ₂₉	0.18	0.533	0.752	3
A ₃₀	0.649	0.02	0.154	0.352	A ₃₀	0.32	0.375	0.543	10
A ₃₁	0.75	0.011	0.157	0.317	A ₃₁	0.26	0.448	0.63	8
A ₃₄	0.711	0.22	0.147	0.3	A ₃₄	0.2	0.457	0.695	5
A ₃₆	0.69	0.071	0.121	0.226	A ₃₆	0.3	0.367	0.552	9
A ₃₉	0.571	0.047	0.126	0.269	A ₃₉	0.38	0.267	0.413	15

Table 27. VIKOR

Original decision matrix					Weighted normalised matrix					Index				
A _i /C _j	C ₁	C ₂	C ₃	C ₄	A _i /C _j	C ₁	C ₂	C ₃	C ₄	A _i /C _j	S ⁺	S ⁻	Q _i	R _i
A ₁₀	159.8	2.58	9.73	31.6	A ₁₀	0.2	0.16	0.17	0.09	A ₁₀	1	0.23	0.72	7
A ₁₁	179.6	2.25	11.4	38.8	A ₁₁	0.1	0.18	0.09	0.04	A ₁₁	0	0.18	0.29	17
A ₁₂	164.6	2.6	11.6	41.7	A ₁₂	0.2	0.16	0.08	0.02	A ₁₂	0	0.2	0.43	12
A ₁₃	169.4	1.58	10.7	35.1	A ₁₃	0.2	0.21	0.12	0.06	A ₁₃	1	0.21	0.56	10
A ₁₄	187.4	3.03	11.4	37.9	A ₁₄	0.1	0.14	0.09	0.04	A ₁₄	0	0.14	0.09	19
A ₁₅	180.1	1.76	11.3	40.3	A ₁₅	0.1	0.2	0.1	0.03	A ₁₅	0	0.2	0.4	14
A ₁₇	160.9	0.31	8.34	43.6	A ₁₇	0.2	0.26	0.24	0	A ₁₇	1	0.26	0.95	1
A ₁₈	152.6	6.15	7.79	41.3	A ₁₈	0.3	0	0.27	0.02	A ₁₈	1	0.27	0.79	6
A ₂₂	164.5	0.64	13.1	32.4	A ₂₂	0.2	0.25	0	0.08	A ₂₂	1	0.25	0.69	8
A ₂₃	204.8	2.58	9.07	41.4	A ₂₃	0	0.16	0.21	0.02	A ₂₃	0	0.21	0.37	15
A ₂₄	157	1.2	9.03	33.2	A ₂₄	0.2	0.22	0.21	0.08	A ₂₄	1	0.24	0.88	3
A ₂₅	200	5.86	9.91	33.9	A ₂₅	0	0.01	0.16	0.07	A ₂₅	0	0.16	0.09	20
A ₂₆	160.2	5.07	10.4	38.9	A ₂₆	0.2	0.05	0.14	0.04	A ₂₆	0	0.22	0.5	11
A ₂₇	172.2	2.2	12.6	34.2	A ₂₇	0.2	0.18	0.02	0.07	A ₂₇	0	0.18	0.32	16
A ₂₉	167.3	2.88	10.4	39.8	A ₂₉	0.2	0.15	0.14	0.03	A ₂₉	1	0.19	0.42	13
A ₃₀	150.9	1.99	10.5	35.4	A ₃₀	0.3	0.19	0.13	0.06	A ₃₀	1	0.27	0.9	2
A ₃₁	165.6	2.4	10.7	27.8	A ₃₁	0.2	0.17	0.13	0.12	A ₃₁	1	0.2	0.57	9
A ₃₄	155.3	3.36	10.7	17.7	A ₃₄	0.2	0.13	0.12	0.19	A ₃₄	1	0.25	0.85	4
A ₃₆	157.9	2.61	8.58	35.2	A ₃₆	0.2	0.16	0.23	0.06	A ₃₆	1	0.24	0.8	5
A ₃₉	175.4	3.27	10.3	36.1	A ₃₉	0.1	0.13	0.15	0.06	A ₃₉	0	0.15	0.25	18

Table 28. COPRAS

Original decision matrix					Normalise				
A _i /C _j	C ₁	C ₂	C ₃	C ₄	A _i /C _j	C ₁	C ₂	C ₃	C ₄
A ₁₀	159.84	2.58	9.73	31.56	A ₁₀	0.047	0.047	0.047	0.044
A ₁₁	179.57	2.25	11.44	38.75	A ₁₁	0.053	0.041	0.055	0.054
A ₁₂	164.59	2.6	11.57	41.7	A ₁₂	0.049	0.048	0.056	0.058
A ₁₃	169.35	1.58	10.69	35.12	A ₁₃	0.05	0.029	0.052	0.049
A ₁₄	187.42	3.03	11.41	37.93	A ₁₄	0.055	0.056	0.055	0.053
A ₁₅	180.05	1.76	11.25	40.3	A ₁₅	0.053	0.032	0.054	0.056
A ₁₇	160.91	0.31	8.34	43.64	A ₁₇	0.048	0.006	0.04	0.061
A ₁₈	152.59	6.15	7.79	41.31	A ₁₈	0.045	0.113	0.038	0.058
A ₂₂	164.48	0.64	13.1	32.37	A ₂₂	0.049	0.012	0.063	0.045
A ₂₃	204.77	2.58	9.07	41.36	A ₂₃	0.06	0.047	0.044	0.058
A ₂₄	156.99	1.2	9.03	33.24	A ₂₄	0.046	0.022	0.044	0.046
A ₂₅	200.02	5.86	9.91	33.94	A ₂₅	0.059	0.108	0.048	0.047
A ₂₆	160.2	5.07	10.44	38.94	A ₂₆	0.047	0.093	0.05	0.054
A ₂₇	172.2	2.2	12.63	34.19	A ₂₇	0.051	0.041	0.061	0.048
A ₂₉	167.33	2.88	10.42	39.77	A ₂₉	0.049	0.053	0.05	0.056
A ₃₀	150.93	1.99	10.51	35.37	A ₃₀	0.045	0.037	0.051	0.049
A ₃₁	165.55	2.4	10.65	27.76	A ₃₁	0.049	0.044	0.051	0.039
A ₃₄	155.32	3.36	10.72	17.72	A ₃₄	0.046	0.062	0.052	0.025
A ₃₆	157.94	2.61	8.58	35.22	A ₃₆	0.047	0.048	0.041	0.049
A ₃₉	175.41	3.27	10.25	36.09	A ₃₉	0.052	0.06	0.049	0.05

Weighted normalised matrix						Relative Significance Value				
$A_i \backslash C_j$	C_1	C_2	C_3	C_4	$A_i \backslash C_j$	S_i^+	S_i^-	C_i	U_i	R_i
A_{10}	0.013	0.012	0.013	0.009	A_{10}	0.013	0.009	15.429	17.554	8
A_{11}	0.014	0.011	0.015	0.011	A_{11}	0.015	0.011	12.571	14.302	15
A_{12}	0.013	0.013	0.015	0.011	A_{12}	0.015	0.011	11.683	13.292	19
A_{13}	0.014	0.008	0.014	0.01	A_{13}	0.014	0.008	17.257	19.633	6
A_{14}	0.015	0.015	0.015	0.01	A_{14}	0.015	0.01	12.843	14.611	14
A_{15}	0.014	0.009	0.015	0.011	A_{15}	0.015	0.009	15.494	17.628	7
A_{17}	0.013	0.002	0.011	0.012	A_{17}	0.013	0.002	87.895	100	1
A_{18}	0.012	0.03	0.01	0.011	A_{18}	0.03	0.01	12.978	14.765	13
A_{22}	0.013	0.003	0.017	0.009	A_{22}	0.017	0.003	42.585	48.45	2
A_{23}	0.016	0.012	0.012	0.011	A_{23}	0.016	0.011	11.78	13.403	18
A_{24}	0.013	0.006	0.012	0.009	A_{24}	0.013	0.006	22.715	25.844	4
A_{25}	0.016	0.028	0.013	0.009	A_{25}	0.028	0.009	14.364	12.342	20
A_{26}	0.013	0.025	0.014	0.011	A_{26}	0.025	0.011	12.519	14.244	16
A_{27}	0.014	0.011	0.017	0.009	A_{27}	0.017	0.009	14.247	16.209	9
A_{29}	0.013	0.014	0.014	0.011	A_{29}	0.014	0.011	12.248	13.935	17
A_{30}	0.012	0.01	0.014	0.01	A_{30}	0.014	0.01	13.77	15.666	11
A_{31}	0.013	0.012	0.014	0.008	A_{31}	0.014	0.008	17.541	19.957	5
A_{34}	0.012	0.016	0.014	0.005	A_{34}	0.016	0.005	27.474	31.258	3
A_{36}	0.013	0.013	0.011	0.01	A_{36}	0.013	0.01	13.827	15.732	10
A_{39}	0.014	0.016	0.013	0.01	A_{39}	0.016	0.01	13.497	15.356	12

Table 29. Comparative ranking results obtained using TOPSIS, COPRAS, and VIKOR methods

A_i	TOPSIS		COPRAS		VIKOR	
	Q_i	R_i	U_i	R_i	Q_i	R_i
A_{10}	0.472	13	17.554	8	0.722	7
A_{11}	0.488	12	14.302	15	0.293	17
A_{12}	0.398	16	13.292	19	0.427	12
A_{13}	0.499	11	19.633	6	0.562	10
A_{14}	0.305	19	14.611	14	0.088	19
A_{15}	0.413	14	17.628	7	0.396	14
A_{17}	0.358	17	100	1	0.945	1
A_{18}	0.342	18	14.765	13	0.792	6
A_{22}	0.163	20	48.45	2	0.687	8
A_{23}	0.651	7	13.403	18	0.367	15
A_{24}	0.763	2	25.844	4	0.882	3
A_{25}	0.73	4	12.342	20	0.086	20
A_{26}	0.689	6	14.244	16	0.5	11
A_{27}	0.802	1	16.209	9	0.315	16
A_{29}	0.752	3	13.935	17	0.423	13
A_{30}	0.543	10	15.666	11	0.897	2
A_{31}	0.63	8	19.957	5	0.572	9
A_{34}	0.695	5	31.258	3	0.852	4
A_{36}	0.552	9	15.732	10	0.8	5
A_{39}	0.413	15	15.356	12	0.245	18

5. CONCLUSION

This study demonstrates the effectiveness of a structured MCDM framework for evaluating and selecting genotypes based on multi-criteria performance. By integrating the TOPSIS, VIKOR, and COPRAS methods, the proposed framework enables a transparent, systematic, and robust ranking of genotypes through the simultaneous consideration of multiple evaluation criteria. The results confirm that this approach successfully identifies genotypes exhibiting consistently strong and well-balanced performance across criteria, thereby supporting reliable and informed selection decisions. This study first adopted the IDOCRIW method to objectively derive the criteria weights, these derived weights are seamlessly incorporated into the decision-making framework, further enhancing the reliability and transparency of the ranking of potential genotype alternatives. The use of well-structured and systematically recorded genotype data improves the clarity and interpretability of outcomes, reinforcing the practical applicability of the proposed framework as a decision-support tool in breeding and experimental research. To effectively manage the large number of alternative present in the

second dataset, this study integrates silhouette analysis with the K-means++ clustering algorithm to achieve more meaningful and reliable groupings. The resulting clusters are subsequently aggregated into cluster-based alternatives (CBAs) and evaluated using an extended decision-making framework. This combined approach enables a clear and consistent identification of the most and least suitable genotypes, highlighting the robustness and scalability of the proposed methodology. The final rankings were obtained using the TOPSIS, VIKOR, and COPRAS methods. For the first dataset, TOPSIS and COPRAS showed perfect agreement ($\rho = 1.000$), while VIKOR exhibited a complete rank reversal ($\rho = -1.000$), a pattern attributable to its inherently compromise-based decision logic. Based on these findings, genotype A₅ (IC212031) emerges as the top performer, demonstrating stable and superior performance across all evaluated criteria. For the second dataset, both VIKOR and COPRAS consistently identified A₁₇ (NRC YS 5-2) as the top-performing genotype and A₂₅ (Anuradha) as the lowest-performing, aligning with the results of the best-worst method. This agreement at both extremes of the ranking underscores the robustness of the framework in reliably distinguishing between superior and inferior genotypes.

Data availability statement

Data will be made available on request.

A CONFLICT OF INTERESTS STATEMENT

The authors state that they have no competing financial interests or personal relationships that might have influenced the research presented in this paper.

ACKNOWLEDGEMENTS

The authors are thankful to the reviewers and the Editorial Board for providing constructive suggestions that lead to the improvement over the original version of the paper. We thank Dr. Ibandalin Mawlong and Dr. M.S. Sujith Kumar, ICAR-Indian institute of Rapeseed Mustard Research Bharatpur, India for providing the two data set used in this study.

REFERENCES

Johannsen, W. (1911). The genotype conception of heredity. *The American Naturalist*, **45**(531), 129-159.

- Przelećki, M. (1964). On the concept of genotype. In *Form and Strategy in Science: Studies Dedicated to Joseph Henry Woodger on the Occasion of his Seventieth Birthday* (pp. 315-329). Dordrecht: Springer Netherlands.
- Sur, B., Rout, S., Singla, S., Mandal, R., Nath, S., Maying, B., ...and Roy, S.K. (2023). Evaluation of mustard genotypes [*Brassica juncea* (L.) Czern and Coss] for quantitative criteria and character association of seed yield and yield components at sub Himalayan region of West Bengal (India). *Plant Science Today*, **10**(1), 166-178.
- Rout, S. (2021). *Studies on combining ability for seed yield along with its attributing characters and aphid resistance in mustard [Brassica juncea (L.) Czern&Coss.]* (Doctoral dissertation, UTTAR BANGA KRISHI VISWAVIDYALAYA).
- Gomes, C.F.S., Costa, H.G., and de Barros, A.P. (2017). Sensibility analysis of MCDA using prospective in Brazilian energy sector. *Journal of Modelling in Management*, **12**(3), 475-497.
- Hezer, S., Gelmez, E., & Özceylan, E. (2021). Comparative analysis of TOPSIS, VIKOR and COPRAS methods for the COVID-19 Regional Safety Assessment. *Journal of infection and public health*, **14**(6), 775-786.
- de Matos Lessa, M.S.C., Amaral, T.M., Leão, P.C.S., and Oliva, J.T. (2024). Multi-criteria decision analysis applied to Brazilian grapevine genotype selection. *Journal of Food Composition and Analysis*, **130**, 106126.
- de Oliveira, B.R., Zuffo, A.M., Aguilera, J.G., Steiner, F., Ancca, S.M., Flores, L.A.P., and Gonzales, H.H.S. (2022). Selection of soybean genotypes under drought and saline stress conditions using Manhattan distance and TOPSIS. *Plants*, **11**(21), 2827.
- Mondal, P., Biswas, T., Maji, P., and Majumder, A. (2024). Application of multiple criteria decision-making approach for ranking lentil genotypes. *International Journal of Agricultural and Applied Sciences*, **5**(1), 31-36.
- Gholizadeh Vazvani, M., Dashti, H., SaberiRiseh, R., and Loit, E. (2025). Association analysis of response to take-all disease with agronomic criteria and molecular markers and selection ideal genotypes in bread wheat (*Triticum aestivum* L.) genotypes. *Molecular Breeding*, **45**(4), 36.
- Prakash Kumar, P.K., Bhar, L.M., Paul, A.K., Samarendra Das, S.D., and Roy, H.S. (2018). Development of composite stability measure using Multi Criteria Decisions Making (MCDM) techniques, *Journal of the Indian Society of agricultural Statistics*, **72**(2), 121-127.
- Zavadskas, E.K., and Podvezko, V. (2016). Integrated determination of objective criteria weights in MCDM. *International Journal of Information Technology & Decision Making*, **15**(02), 267-283.
- Rezaei, J. (2015). Best-worst multi-criteria decision-making method. *Omega*, **53**, 49-57.
- Diakoulaki, D., Mavrotas, G., and Papayannakis, L. (1995). Determining objective weights in multiple criteria problems: The critic method. *Computers & operations research*, **22**(7), 763-770.
- Keshavarz-Ghorabae, M., Amiri, M., Zavadskas, E.K., Turskis, Z., and Antucheviciene, J. (2021). Determination of objective weights using a new method based on the removal effects of criteria (MEREC). *Symmetry*, **13**(4), 525.

- Keshavarz-Ghorabae, M., Amiri, M., Zavadskas, E.K., Turskis, Z., and Antucheviciene, J. (2018). Simultaneous evaluation of criteria and alternatives (SECA) for multi-criteria decision-making. *Informatica*, **29**(2), 265-280.
- Trinkūnienė, E., Podvezko, V., Zavadskas, E.K., Jokšienė, I., Vinogradova, I., and Trinkūnas, V. (2017). Evaluation of quality assurance in contractor contracts by multi-criteria decision-making methods. *Economic research-Ekonomska istraživanja*, **30**(1), 1152-1180.
- Alao, M.A., Popoola, O.M., and Ayodele, T.R. (2021). Selection of waste-to-energy technology for distributed generation using IDOCRIW-Weighted TOPSIS method: A case study of the City of Johannesburg, South Africa. *Renewable Energy*, **178**, 162-183.
- Parthasarathy, T.N., Narayanamoorthy, S., Thilagasree, C.S., Marimuthu, P.R., Salahshour, S., Ferrara, M., and Ahmadian, A. (2024). An enhanced fuzzy IDOCRIW-COCOSO multi-criteria decision making algorithm for decisive electric vehicle battery recycling method. *Results in engineering*, **22**, 102272.
- Rousseeuw, P.J. (1987). Silhouettes: a graphical aid to the interpretation and validation of cluster analysis. *Journal of computational and applied mathematics*, **20**, 53-65.
- Hwang, C.L., and Yoon, K. (1981). Methods for multiple criteria decision making. In *Multiple criteria decision making: methods and applications a state-of-the-art survey* (pp. 58-191). Berlin, Heidelberg: Springer Berlin Heidelberg.
- Zavadskas, E.K., Kaklauskas, A., Peldschus, F., and Turskis, Z. (2007). Multi-criteria assessment of road design solutions by using the COPRAS method. *The Baltic journal of Road and Bridge engineering*, **2**(4), 195-203.
- Opricovic, S., and Tzeng, G.H. (2002). Multicriteria planning of post-earthquake sustainable reconstruction. *Computer-Aided Civil and Infrastructure Engineering*, **17**(3), 211-220.