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

Nidahamteinsar Papang[1], Priya Sharma[2,3], Bishal Gurung[1], Ibandalin Mawlong[4] and M.S. Sujith Kumar[4]

[1]North Eastern Hill University, Shillong
[2]University of Delhi, Delhi
[3]Fortune Institute of International Business, New Delhi
[4]ICAR-Indian Institute of Rapeseed Mustard Research, Bharatpur

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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 A_5 (IC212031) consistently emerges as the top performer. For the second dataset, VIKOR and COPRAS both placed A_{17} (NRC YS 5-2) at the top and A_{25} (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

Corresponding author: Priya Sharma
E-mail address: priyasharma.du.aor.17@gmail.com

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.

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 $A_i\left(i=1,2,...,n\right)$ based on a multiple criteria set $C_j\left(j=1,2,...,p\right)$

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

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:

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

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:

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

Step 2: Degree of entropy

The degree of entropy for each criterion is calculated using:

$$E_{\mathrm{j}}=-\frac{1}{\ln m}\sum_{\mathrm{i=1}}^{n}\tilde{x}_{\mathrm{ij}}\ln\tilde{x}_{\mathrm{ij}},\ \mathrm{j}=1,2,\ldots,\mathrm{n},\ 0\le E_{\mathrm{j}}\le 1 \quad (3)$$

Step 3: Entropy weight

The deviation degree of entropy is computed as:

$$d_{\mathrm{j}}=1-E_{\mathrm{j}},\quad \mathrm{j}=1,2,\ldots,\mathrm{p} \quad (4)$$

The entropy weight of each criterion is then obtained by:

$$Ew_{\mathrm{j}}=\frac{d_{\mathrm{j}}}{\sum_{\mathrm{j=1}}^{p}d_{\mathrm{j}}} \quad (5)$$

Step 4: Construction of the square matrix

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

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

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

$$a_j = \max_i \tilde{x}_{ij}, \quad j = 1, 2, \ldots, p \tag{7}$$

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:

$$r_{ij} = \frac{a_{jj} - a_{ij}}{a_{jj}}, \quad i, j = 1, 2, \ldots, p, \quad r_{jj} = 0 \tag{8}$$

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:

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

Step 7: Criterion impact loss weight

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

$$Fq^T = 0 \tag{10}$$

where $q = [q_1, q_2, \ldots, q_p]$ 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:

$$w_j = \frac{q_j E w_j}{\sum_{j=1}^{p} q_j E w_j}; \quad j = 1, 2, \ldots, p \tag{11}$$

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* libraryis 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,

$$S(h) = \begin{cases} \dfrac{y(h) - x(h)}{\max\left(x(h), y(h)\right)}, & f\left|C_h\right| > 1 \\ 0, if\left|C_h\right| = 1 \cdot \end{cases} \tag{12}$$

ere $x(h)$ 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

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

isnormalized to remove scale differences. The normalized decision matrix

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

is calculated as:

$$y_{ij} = \frac{x_{ij}}{\sqrt{\sum_{i=1}^{n} x_{ij}^{\,2}}}, \; i = 1, 2, \ldots, n; \; j = 1, 2, \ldots, p \tag{13}$$

Step 2: Weighted normalized decision matrix

The weighted normalized decision matrix

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

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

$$v_{ij} = w_j y_{ij}, \; i = 1, 2, \ldots, n; \; j = 1, 2, \ldots, p \tag{14}$$

Step 3: Positive and negative ideal solutions

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

$$S^{+} = \left\{ v_1^{+}, v_2^{+}, \ldots, v_p^{+} \right\} = \left\{ \max_i v_{ij}, j \in B; \min_i v_{ij}, j \in C \right\} \tag{15}$$

$$S^{-} = \left\{ v_1^{-}, v_2^{-}, \ldots, v_p^{-} \right\} = \left\{ \min_i v_{ij}, j \in B; \max_i v_{ij}, j \in C \right\} \tag{16}$$

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

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

Step 5: Relative closeness to the ideal solution

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

$$C_i = \frac{D_i^{-}}{D_i^{+} + D_i^{-}}, \quad i = 1, 2, \ldots, n \tag{19}$$

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:

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

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

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

Step 8: Weighted normalize decision matrix

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

is obtained as:

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

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:

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

Step 11: Calculation of quantitative utility and ranking of alternatives

The utility degree of each alternative is computed as:

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

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 KriterijumsaOptimizacija I KompromisnoResenje)

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 $X_{n\times p} = \left[x_{ij} \right]_{n\times p}$, determine best and worst criterion values using **Eq. 26**

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

Step 14: Compute utility and regret measures

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

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

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

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

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

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

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

Cj	Criteria	Cj	Criteria	Cj	Criteria	Cj	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

Ai	**Genotypes**	**Ai**	**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}
A_1	3.12	0.42	0.59	0.42	42.00	12.70	6.30	5.40	66.40	0.63	20.30
A_2	3.03	0.41	0.55	0.38	35.40	10.80	5.10	3.70	55.00	0.64	21.20
A_3	2.94	0.40	0.56	0.38	32.90	9.10	4.70	3.80	50.40	0.64	22.00
A_4	2.99	0.42	0.56	0.41	30.40	9.30	4.60	3.10	47.60	0.64	21.40
A_5	3.36	0.50	0.69	0.46	49.20	14.90	7.70	6.20	77.90	0.62	18.50
A_6	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}
A_1	185.30	39.75	44.98	58.42	80.13	4.45	39.13	45.43	4.44	0.03	0.36
A_2	181.20	39.03	43.30	57.20	80.70	5.37	39.27	44.89	4.84	0.02	0.23
A_3	176.40	41.08	45.60	60.55	86.13	4.12	38.71	45.40	4.92	0.02	0.31
A_4	182.40	39.40	45.28	59.95	83.92	4.45	38.97	44.25	5.09	0.03	0.30
A_5	183.60	39.17	44.02	60.28	83.72	4.00	39.87	46.96	4.81	0.03	0.45
A_6	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 (ρ = 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 (ρ = −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_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	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_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	0.0	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

Cj	Ewj	CILOS wj	Ewj*CILOSwj	Wj	Cj	Ewj	CILOS wj	Ewj*CILOSwj	Wj
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

A6	0.411	0.391	0.378	0.416	0.409	0.443	0.396	0.431	0.417	0.401	0.400
Ai/Cj	**C12**	**C13**	**C14**	**C15**	**C16**	**C17**	**C18**	**C19**	**C20**	**C21**	**C22**
A1	0.415	0.403	0.404	0.395	0.392	0.397	0.407	0.405	0.366	0.418	0.429
A2	0.406	0.395	0.389	0.387	0.395	0.479	0.409	0.400	0.399	0.403	0.273
A3	0.395	0.416	0.410	0.409	0.422	0.368	0.403	0.404	0.405	0.388	0.362
A4	0.408	0.399	0.407	0.405	0.411	0.397	0.405	0.394	0.419	0.434	0.358
A5	0.411	0.397	0.396	0.408	0.410	0.357	0.415	0.418	0.396	0.463	0.528
A6	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)

Ai / Cj	**C1**	**C2**	**C3**	**C4**	**C5**	**C6**	**C7**	**C8**	**C9**	**C10**	**C11**
A1	0.009	0.019	0.027	0.014	0.033	0.040	0.052	0.052	0.038	0.003	0.009
A2	0.008	0.019	0.025	0.013	0.028	0.034	0.042	0.035	0.031	0.003	0.010
A3	0.008	0.018	0.026	0.013	0.026	0.029	0.039	0.036	0.029	0.003	0.010
A4	0.008	0.019	0.026	0.014	0.024	0.029	0.038	0.030	0.027	0.003	0.010
A5	0.009	0.023	0.032	0.016	0.039	0.047	0.063	0.059	0.045	0.003	0.008
A6	0.009	0.019	0.025	0.014	0.031	0.040	0.046	0.047	0.035	0.003	0.009
Ai/Cj	**C12**	**C13**	**C14**	**C15**	**C16**	**C17**	**C18**	**C19**	**C20**	**C21**	**C22**
A1	0.002	0.011	0.008	0.008	0.004	0.032	0.001	0.006	0.011	0.018	0.030
A2	0.002	0.010	0.008	0.008	0.005	0.038	0.001	0.006	0.012	0.017	0.019
A3	0.002	0.011	0.008	0.008	0.005	0.029	0.001	0.006	0.012	0.017	0.026
A4	0.002	0.011	0.008	0.008	0.005	0.032	0.001	0.006	0.013	0.019	0.025
A5	0.002	0.010	0.008	0.008	0.005	0.029	0.001	0.006	0.012	0.020	0.038
A6	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
A1	0.021435	0.0341298	0.614237	2
A2	0.043546	0.01483416	0.254094	4
A3	0.046703	0.01023874	0.179809	5
A4	0.051089	0.00863199	0.144538	6
A5	0.010198	0.05315166	0.839016	1
A6	0.028089	0.02877132	0.506003	3

Table 13. Weighted normalize matrix (VIKOR)

Ai / Cj	**C1**	**C2**	**C3**	**C4**	**C5**	**C6**	**C7**	**C8**	**C9**	**C10**	**C11**
A1	0.012	0.039	0.044	0.017	0.029	0.035	0.052	0.028	0.032	0.004	0.011
A2	0.016	0.043	0.061	0.034	0.055	0.064	0.097	0.088	0.064	0.000	0.005
A3	0.021	0.048	0.057	0.034	0.065	0.091	0.112	0.084	0.077	0.000	0.000
A4	0.018	0.039	0.057	0.021	0.075	0.088	0.116	0.109	0.085	0.000	0.004
A5	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.023
A6	0.012	0.043	0.066	0.017	0.042	0.033	0.079	0.046	0.045	0.007	0.012
Ai/Cj	**C12**	**C13**	**C14**	**C15**	**C16**	**C17**	**C18**	**C19**	**C20**	**C21**	**C22**
A1	0.000	0.022	0.014	0.017	0.011	0.054	0.002	0.010	0.031	0.015	0.028
A2	0.002	0.026	0.020	0.020	0.010	0.000	0.002	0.012	0.020	0.020	0.071
A3	0.004	0.013	0.012	0.012	0.000	0.073	0.003	0.010	0.018	0.024	0.046
A4	0.001	0.024	0.013	0.014	0.004	0.054	0.003	0.014	0.013	0.010	0.047
A5	0.001	0.026	0.018	0.013	0.005	0.080	0.000	0.004	0.021	0.000	0.000
A6	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
A1	0.506	0.253	5
A2	0.733	0.788	3
A3	0.806	0.968	2
A4	0.809	1.000	1
A5	0.197	0.210	6
A6	0.495	0.444	4

Table 15. Normalize matrix (COPRAS)

A_i / C_j	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11
A1	0.168	0.164	0.169	0.170	0.184	0.182	0.185	0.199	0.185	0.166	0.164
A2	0.163	0.160	0.158	0.154	0.155	0.155	0.150	0.137	0.153	0.169	0.172
A3	0.158	0.156	0.160	0.154	0.144	0.131	0.138	0.140	0.140	0.169	0.178
A4	0.161	0.164	0.160	0.166	0.133	0.134	0.135	0.114	0.132	0.169	0.173
A5	0.181	0.195	0.198	0.186	0.215	0.214	0.226	0.229	0.217	0.164	0.150
A6	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	C12	C13	C14	C15	C16	C17	C18	C19	C20	C21	C22
A1	0.169	0.165	0.165	0.161	0.160	0.163	0.166	0.165	0.150	0.171	0.179
A2	0.166	0.162	0.159	0.158	0.161	0.197	0.167	0.163	0.163	0.165	0.114
A3	0.161	0.170	0.167	0.167	0.172	0.151	0.164	0.165	0.166	0.159	0.151
A4	0.167	0.163	0.166	0.166	0.168	0.163	0.166	0.161	0.172	0.178	0.149
A5	0.168	0.162	0.162	0.167	0.167	0.147	0.169	0.171	0.162	0.190	0.220
A6	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	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11
A1	0.004	0.008	0.011	0.006	0.014	0.017	0.022	0.022	0.016	0.001	0.004
A2	0.003	0.008	0.010	0.005	0.012	0.014	0.017	0.015	0.013	0.001	0.004
A3	0.003	0.008	0.011	0.005	0.011	0.012	0.016	0.015	0.012	0.001	0.004
A4	0.003	0.008	0.011	0.006	0.010	0.012	0.016	0.012	0.011	0.001	0.004
A5	0.004	0.009	0.013	0.006	0.016	0.019	0.026	0.025	0.018	0.001	0.003
A6	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	C12	C13	C14	C15	C16	C17	C18	C19	C20	C21	C22
A1	0.001	0.004	0.003	0.003	0.002	0.013	0.001	0.002	0.005	0.007	0.013
A2	0.001	0.004	0.003	0.003	0.002	0.016	0.001	0.002	0.005	0.007	0.008
A3	0.001	0.004	0.003	0.003	0.002	0.012	0.001	0.002	0.005	0.007	0.011
A4	0.001	0.004	0.003	0.003	0.002	0.013	0.001	0.002	0.005	0.008	0.011
A5	0.001	0.004	0.003	0.003	0.002	0.012	0.001	0.002	0.005	0.008	0.016
A6	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 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 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 20. Original decision matrix

A_i / C_j	C_1	C_2	C_3	C_4	Ai	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	Ewj*CILOSw_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**				
$A_i \backslash C_j$	C_1	C_2	C_3	C_4	$A_i \backslash C_j$	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**				
$A_i \backslash C_j$	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**				
$A_i\backslash C_j$	**C_1**	**C_2**	**C_3**	**C_4**	**$A_i\backslash C_j$**	**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	Ri	*Ui*	*Ri*	*Qi*	*Ri*
*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 A_5 (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 A_{17} (NRC YS 5-2) as the top-performing genotype and A_{25} (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.

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REFERENCES

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

Przełęcki, 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-Ghorabaee, 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-Ghorabaee, 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-Ekonomskaistraživanja*, **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., andYoon, 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.