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Multi-trait selection indices for identifying elite rice genotypes in rice breeding programs

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Abstract

Rice (*Oryza sativa* L.) serves as a staple food for nearly half of the global population, with rising demand necessitating significant advancements in productivity. Traditional selection methods that focus solely on yield often fail to account for the complex interplay of agronomic and grain quality traits. The integration of multiple selection indices in breeding enhances efficiency by simultaneously evaluating important traits, aiding in informed decision-making, balancing desirable traits, and accelerating the development of high-performing varieties. This study aimed to evaluate the efficiency of various multi-trait selection indices, namely the Multi-Trait Genotype-Ideotype Distance Index (MGIDI), Genotype by Yield and Trait biplot (GYT), Linear Phenotypic Selection Index (LPSI), and the Elston Index, in identifying elite rice genotypes for breeding programs. A total of 110 genetically diverse rice germplasm lines were evaluated using a randomized block design during the Rabi season of 2023–24. Key agronomic and grain quality traits were assessed, with statistical analyses, including ANOVA and correlation studies, conducted to interpret the result. Among the indices, MGIDI demonstrated the highest selection gains (16.9%) for yield, while other indices demonstrated variable efficiencies across different traits. Traits such as the number of grains per panicle and productive tillers exhibited positively correlations with yield, whereas negative selection for plant height and days to maturity posed challenges. Notably, genotypes BMDK-2-2-8-2, JR 13, A 67, and CR 4376-1-1-1-2-2-1 were consistently selected across indices, reflecting their superior trait performance across multiple traits. Combining several indices improves the breeding process by enabling the selection of genotypes with traits such as nutrient-use efficiency and drought tolerance, thereby improving rice yield under challenging conditions, such as low-fertility soils or drought stress. These findings highlight the importance of multi-trait indices in optimizing genetic gains and improving breeding efficiency. Notably, MGIDI emerged as the most effective tool, providing a comprehensive approach to integrating traits, making it indispensable for rice breeding programs.

Keywords

elston index; genotype by yield and trait biplot (GYT); linear phenotypic selection; multi-trait genotype-ideotype distance index (MGIDI); rice; selection indices

Introduction

Rice (*Oryza sativa* L.) is primary staple food for nearly half of the world's population. Enhancing rice production is crucial to address the growing food shortages (1), as food security plays a vital role in national stability, economic progress, and overall well-being. Rapid population growth and environmental challenges have raised concerns about global food scarcity (2–4). Currently, over 800 million people worldwide experience hunger and food insecurity (5). Increasing rice productivity has become inevitable due to limited arable land for cultivation and the expanding global population (6). Rice plays a pivotal role in alleviating food shortages and enhancing food security (7, 8).

Asia leads the world in rice production and consumption, with China and India contributing approximately 55% of the world's rice supply (9). India ranks as the second-largest producer of rice, both in terms of cultivated area and total production (10). Rice accounts for approximately 20% of the world's daily caloric intake, highlighting its significance for global food security (9).

Increasing seed yield is a primary objective of crop improvement programs. However, this task is challenging due to the complex and quantitative nature of key agronomical traits (11). Various breeding efforts and agronomic strategies have been undertaken to develop superior genotypes that incorporate desirable traits into a single genotype. Traditional breeding often faces limitations in yield stability and adaptability because it primarily focuses on individual traits and provides limited integration of trait interactions. Multi-trait indices, like MGIDI, provide a more comprehensive approach by simultaneously evaluating multiple traits, balancing trade-offs, and optimizing genetic gains. This contrasts with traditional variety trials, which predominantly assess seed yield using metrics like the yield index and yield stability index (12). Yield alone is often insufficient as a reliable metric since high-yielding cultivars may lack stability across different environments or may be vulnerable to drought or lodging-induced yield losses. Thus, a multi-trait approach is necessary to achieve consistently high yields while incorporating additional beneficial traits.

Several multi-trait selection indices have been developed to assist in identifying genotypes with breeding objectives. The ideotype concept involves altering of genotype to its environment through specific morphological and physiological traits, serving as a framework for breeders to identify high-performing genotypes. This ideotype approach enables breeders to move beyond trial-and-error methods, improving breeding efficiency (13).

Simultaneous multi-trait selection is inherently complex. The earliest index for such selection was introduced by (14) in plant breeding and later by (15) in animal breeding. This index aims to maximize the correlation between unknown genetic values and observed phenotypic values by utilizing both phenotypic data and genetic covariances (16). The Smith-Hazel classical index has been widely used, especially for assigning appropriate economic weights to key traits (17, 18). These weights are often determined based on the coefficient of genetic variation (19) and heritability; however, they are sometimes assigned arbitrarily (20, 18).

In multi-trait selection, breeders often face challenges with multicollinearity, which complicates the use of the Smith-Hazel index. This issue can result in misinterpretations, misguided research priorities, and ineffective conservation stratergies (21). Furthermore, this index may not fully capitalize on genetic correlations among traits, potentially limiting its effectiveness. To address these limitations, the MGIDI was introduced (22). This index incorporates factor analysis to enhance multi-trait selection and optimize treatment recommendations. Similarly, GYT approach was introduced which evaluates yield alongside and other critical traits collectively rather than individually (23). This approach is particularly advantageous for crops where grain yield is a key trait, as it enables the identification of genotypes that perform well in yield while excelling in other important traits (24).

Another widely recognized index is the Elston index, a non-parametric and multiplicative index that simplifies genotype selection by eliminating the need for economic weights, making the less complex compared to linear model (25, 26).

Against this backdrop, the present study was undertaken to identify superior rice genotypes by employing various selection indices. The primary objective was to evaluate the effectiveness of these indices in optimizing selection gains and aligning them with the desired ideotype, thereby advancing breeding strategies for rice improvements.

Materials and Methods

Experimental material and design

The present study was conducted at the Department of Rice, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, during the *Rabi* 2023-24. The experimental site is located at 11°N latitude and 77°E longitude, with an elevation of 426.72 meters above mean sea level. A total of 110 genetically diverse rice germplasm, including advanced breeding lines, were evaluated using a Randomized Block Design (RBD) with three replications. The rice genotypes were chosen from the Department of Rice, Tamil Nadu Agricultural University, Coimbatore, and the All-India Coordinated Improvement Project on Rice (AICRP) based on yield potential, duration, growth habit, resistance to major pests and diseases, and drought tolerance, with the aim of developing high-yielding, climate-resilient varieties. The genotypes and their pedigrees are listed in supplementary Table 1.

Seeds of each genotype were sown on a raised bed, and 30-day-old seedlings were transplanted into a well-puddled field with a spacing of 20 x 20 cm. Each genotype was planted in two rows, with each row measuring three meters in length. Standard cultivation practices were followed throughout the cropping season to ensure healthy crop growth.

Observations were recorded for key traits, including days to 50% flowering (DFF), plant height (PH), number of productive tillers per plant (NPTP), panicle length (PL), flag leaf length (FLL), flag leaf breadth (FLB), number of grains per panicle (NOG), spikelet fertility (SF), days to maturity (DM), harvest index (HI), thousand-seed weight (TSW), and single plant yield (SYP). Data were collected from five randomly chosen plants per replication for each genotype, except for days to 50% flowering and days to maturity, where observations were recorded across the entire plot.

Grain quality assessment included both physical and physicochemical traits *viz*., hulling percentage (HLL), milling percentage (MILL), head rice recovery (HRR), kernel length (KL), kernel breadth (KB), length-to-breadth (LB) ratio, gelatinization temperature (GT), gel consistency (GC), and amylose content (AMC).

Statistical Analysis

Analysis of variance (ANOVA) and correlation analyses were conducted using ‘R Studio’ to evaluate the associations between yield and yield contributing traits. Pearson’s correlation coefficients were computed based on the mean performance of each trait, with grain quality traits as considered as dependent variables and other traits as independent variables. Correlation plots were generated using the “metan” package in ‘R Studio’. Heritability (h^2) was estimated for all traits and subsequently used to calculate the selection differential (k) and predict selection gains for genotypes selected through various selection indices.

A method was proposed for estimating economic weights for the traits under investigation; however, the exact assignment of these weights varies depending on the trait (27). In this study, equal positive weights were allocated to yield and yield-related traits due to their direct impact on plant productivity, while equal negative weights were assigned to days to 50% flowering, plant height, and kernel length-to-breadth ratio. This approach was employed to prioritize the selection of early-maturing, dwarf plant types with fine grains.

The study utilizes four distinct selection indices: MGIDI, GYT, LPSI, and Elston to identify superior genotypes. The MGIDI integrates multiple traits into a comprehensive evaluation, while the GYT focuses on yield potential under specific conditions. The LPSI focuses on performance in low-input or stress environments, while the Elston index prioritizes the most influential into a single value for overall performance prioritization. Each index serves a distinct function, MGIDI offers a balanced, multi-trait approach, while the other indices focus on specific breeding objectives.

Statistical analyses were performed using various R software packages (28): “Rindsel” for the Linear Phenotypic Selection Index (29); “st4gi” for the Elston Index (30); and “metan” for the Multi trait Genotype Ideotype Distance Index (MGIDI), GYT, coincidence index, and rank correlation (22).

Selection indices

Liner Phenotypic Selection Index (LPSI)

The Linear Phenotypic Selection Index (LPSI) is based on the assumption that traits are independent. It is calculated by estimating the phenotypic and genotypic covariance matrices, with economic weights assigned to each trait (17, 31, 61). The primary objectives of the LPSI are to predict the net genetic merit of genotypes, maximize the selection response, and enhance the expected genetic gains for each trait (or achieve a multi-trait selection response).

The equation for the LPSI is expressed as:

$$l_B = w'y$$

Where, w’ = the vector of economic value, y = the vector of phenotypic value.

Elston index

The Elston Index is based on the principle of integrating various traits by assigning relative economic weights, enabling breeders to enhance multiple traits simultaneously (25). Regarding the weight-free index and associated parameters (25), the multiplicative selection index is estimated using the following equation:

$$\prod_j (x_j - k_j)$$

Where x_j = the genotype value for the i^{th} trait; k_j lower bound option

Multi-trait Genotype Ideotype Distance Index (MGIDI)

The construction of the MGIDI index involves four key steps. First, an ideotype is defined by specifying target values for traits based on known or desired characteristics. Next, the scale of each trait is adjusted to ensure that all values range uniformly from 0 to 100, facilitating consistent comparison and interpretation across traits. Following this, a factor analysis approach is employed, similar to the FAI-BLUP index methodology (32). This includes the use of varimax rotation, as described by (33), to estimate the final loadings effectively. Finally, the MGIDI is calculated using the following formula (22):

$$MGIDI_I = \sqrt{\left[\sum_{j=1}^{f} (Y_{ij} - Y_j)^2\right]}$$

Where $MGIDI_i$ = the distance index for the i^{th} genotype; Y_{ij} = the score of the i^{th} genotype on the j^{th} fac-tor (i = 1, 2, …., g;j = 1,2,…,f); f = the number of factors; Y_j = the score of the j^{th} ideotype.

Genotype by yield and trait biplot (GYT)

GYT analysis was performed using the theoretical framework introduced by (23). This analytical method is based on the use of phenotypic averages. Before performing the GYT analysis, data standardization was performed to ensure that the mean for each trait was appropriately adjusted. The standardization process was carried out using the following equation below:

$$P_{ij} = \left(T_{ij} - \overline{T} / S_j\right)$$

Where P_{ij} = standardized value of genotype *i* for the specific variable or the combination of grain yield and trait *j*; T_{ij} = the original value of genotype *i* for the specific variable or the combination of grain yield and trait j in the GT or GYT table. $\overline{T}$ = mean value across all genotypes for the specific variable or the combination of grain yield and trait *j*. S_j = standard deviation for the specific variable or the combination of grain yield and trait *j*.

The GYT biplot employed the first two principal components (PCs), which were derived through singular value decomposition (SVD). Prior to performing simultaneous selection, all data were standardized. The SVD conducted on the GYT table was then transformed into genotype eigenvalues, trait eigenvalues, and singular values.

The average tester coordinate's view of the GYT biplot was generated with the following parameters: scaling set to 1, centering set to 2, and singular value proportion (SVP) set to 3.

Evaluation of selection index efficiencies

To evaluate the efficiencies of the selection indices, a selection intensity of 15% was applied, resulting in the selection of the top 16 genotypes across all indices consideration.

Selection gains

The selection gains for each trait across various selection indices were estimated following the methodology outlined by (34) and were expressed as percentage gains (SGperc) using the following formula:

$$SG_i = \left(\left(\frac{X_s - X_p}{X_p}\right) \times 100\right) \times h_i^2 = SD_{perc} \times h_i^2$$

Where SG_i = the expected selection gains for the i^{th} trait; *Xs* = the mean of the selected genotypes for the i^{th} trait; *Xp* = the mean of the entire population for the i^{th} trait; SD_i = the selection differential; and = the heritability for the i^{th} trait.

Coincidence index

The effectiveness and relationships among the selection indices were analyzed using the coincidence index established by (35).

$$IC = \frac{(A - C)}{(M - C)} \times 100$$

Where A = number of lines that coincide in both strategies, M = total number of selected lines; C = number of random coincidences assigned, reflecting the selection intensity.

The rankings of various indices were evaluated using Spearman's rank correlation coefficients (36). This will evaluate the relationships among genotype rankings.

Results

Analysis of variance (ANOVA)

The analysis of variance (Table 1) revealed a highly significant level of genetic variability (P = 0.01) among the 110 rice genotypes for all traits taken for the study.

Table 1. Analysis of variance (ANOVA) for agro morphological and grain quality traits in 110 rice germplasm

Source of variation	Genotypes	Replication	Error
	(*df*=109)	**(*df*=2)**	**(*df*=218)**
DFF	133.45**	1	5.16
PH	288.28**	1.45	5.24
NPTP	22.66**	1.21	3
PL	14.35**	0.82	2.95
FLL	37.86**	0.82	2.95
FLB	0.02**	0.02	0.01
NOGP	1762.13**	0.4	2.96
SF	132.93**	1.48	2.99
DM	105.92**	0.4	2.96
BY	450.33**	0.82	2.95
HI	302.5**	1.2	2.82
TGW	6.62**	5.5	2.12
SYP	57**	0.82	2.95
HLL	35.55**	1.37	2.32
MILL	22.11**	3.5	1.67
HRR	199.1**	0.3	1.56
KL	0.69**	0.01	0.14
KB	0.1**	0.003	0.003
LB	0.41**	0.01	0.01
GT	4.23**	0.011	0.014
GC	713.89**	0.37	0.89
AMC	1507.05**	0.11	0.66

** = $p<0.05$:Days to 50% flowering (**DFF**), Plant height (**PH**), Number of productive tillers per plant (**NPTP**), Panicle length (**PL**), Flag leaf length (**FLL**), Flag leaf breadth (**FLB**), Number of grains per panicle (**NOG**), Spikelet fertility (**SF**), Days to maturity (**DM**), Harvest index (**HI**), Thousand-grain weight (**TSW**), Single plant yield (**SYP**), Hulling percent (**HLL**), milling percent (**MILL**), Head rice recovery (**HRR**), Kernel length (**KL**), Kernel breadth (**KB**), Length breadth ratio (**LB** ratio)), Gelatinization Temperature (**GT**), Gel consistency (**GC**) and Amylose content (**AMC**)

Correlation analysis

Fig. 1 presents the correlations among various traits. Correlation analysis showed that single plant yield exhibited positive and significant correlations with the number of productive tillers per plant (0.70), the number of grains per panicle (0.57), harvest index (0.37), and spikelet fertility (0.23). However, it showed a negative correlation with flag leaf length (-0.20). A strong positive correlation was also observed between days to 50% flowering and days to maturity (0.80) as well as between the number of grains per panicle and the number of productive tillers per plant (0.56).

Genetic gains and selection differential across various indices

The estimates for broad-sense heritability (h^2), expected selection gains, and selection differential percentages for various traits across different indices are presented in Table 2.

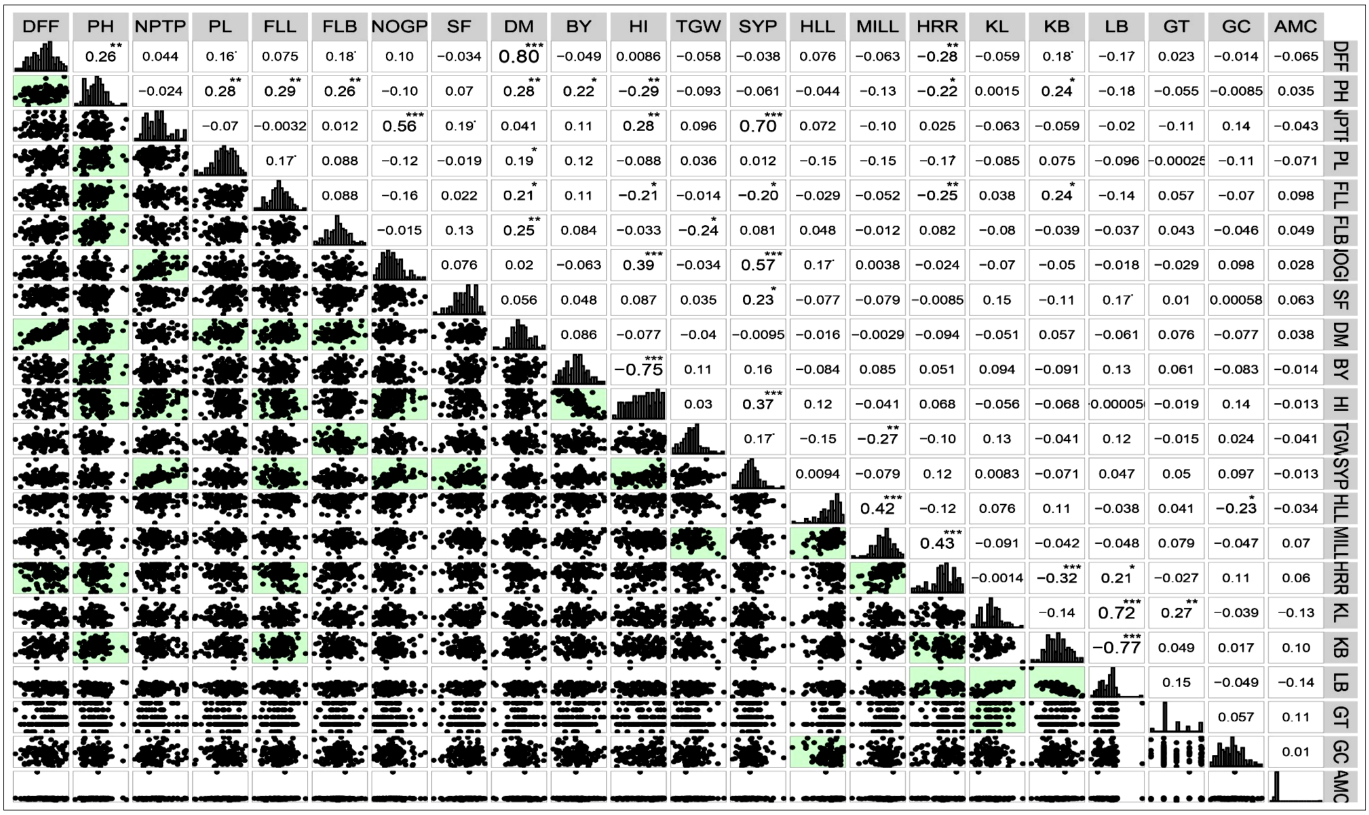

Fig. 1. Correlation analysis among all the traits for 110 rice genotypes.

Table 2. Predicted genetic gain for the effective traits in the different selection indices over base population

Sl.No.	Trait	SD (%)				SG (%)				h²	Sense
		MGIDI	GYT	Elston	LPSI	MGIDI	GYT	Elston	LPSI		
1	DFF	-1.39	0.00	-0.03	-1.69	-1.34	0.00	-0.03	-1.62	0.96	decrease
2	PH	-0.21	-0.03	-0.01	-2.26	-0.20	-0.03	-0.01	-2.22	0.98	decrease
3	NPTP	8.54	0.23	0.12	17.80	7.41	0.20	0.10	15.43	0.87	increase
4	PL	-2.93	-0.04	0.00	-3.10	-2.33	-0.03	0.00	-2.46	0.79	increase
5	FLL	5.64	-0.05	-0.01	-7.53	5.20	-0.05	-0.01	-6.94	0.92	increase
6	FLB	0.60	-0.01	-0.01	-0.27	0.29	-0.01	0.00	-0.13	0.48	increase
7	NOG	1.69	0.18	0.18	27.60	1.69	0.18	0.18	27.54	1.00	increase
8	SF	3.87	0.02	0.02	2.97	3.78	0.02	0.02	2.90	0.98	increase
9	DM	4.44	0.01	-0.02	0.03	4.32	0.01	-0.02	0.03	0.97	decrease
10	BY	6.89	0.06	-0.03	-0.37	6.84	0.06	-0.03	-0.37	0.99	increase
11	HI	6.99	0.14	0.13	12.80	6.93	0.14	0.13	12.68	0.99	increase
12	TGW	1.59	-0.01	0.02	-1.35	1.08	-0.01	0.01	-0.92	0.68	increase
13	SYP	17.90	0.28	0.15	16.90	16.90	0.27	0.15	16.02	0.95	increase
14	HLL	0.83	0.02	0.01	0.73	0.77	0.02	0.01	0.68	0.94	increase
15	MILL	1.36	0.01	0.01	2.34	1.26	0.01	0.01	2.16	0.92	increase
16	HRR	5.92	0.04	0.09	9.90	5.87	0.04	0.09	9.82	0.99	increase
17	KL	-0.39	0.00	0.01	-0.17	-0.38	-0.01	0.01	-0.17	0.98	increase
18	KB	2.12	0.00	0.00	-0.95	2.05	0.00	0.00	-0.92	0.97	decrease
19	LB	-2.55	-0.01	0.00	0.56	-2.48	-0.01	0.00	0.54	0.98	decrease
20	GT	18.30	0.11	0.12	5.67	18.20	0.11	0.12	5.65	1.00	increase
21	GC	0.52	0.06	0.18	24.10	0.52	0.06	0.18	24.08	1.00	increase
22	AMC	52.10	-0.08	0.54	45.30	52.10	-0.08	0.54	45.30	0.99	increase

MGIDI: Multi trait Genotype Ideotype Distance Index; **GYT**: Genotype Yield Trait Biplot; **LPSI**: Linear Phenotypic Selection Index; Days to 50% flowering (**DFF**), Plant height (**PH**), Number of productive tillers per plant (**NPTP**), Panicle length (**PL**), Flag leaf length (**FLL**), Flag leaf breadth (**FLB**), Number of grains per panicle (**NOG**), Spikelet fertility (**SF**), Days to maturity (**DM**), Harvest index (**HI**), Thousand-grain weight (**TSW**), Single plant yield (**SYP**), Hulling percent (**HLL**), Milling percent (**MILL**), Head rice recovery (**HRR**), Kernel length (**KL**), Kernel breadth (**KB**), Length breadth ratio (**LB** ratio)), Gelatinization Temperature (**GT**), Gel consistency (**GC**) and Amylose content (**AMC**).

Heritability

The broad-sense heritability (h^2) estimates ranged from 0.48 for flag leaf breadth to 0.99 for biological yield, harvest index, gel consistency, amylose content, gelatinization temperature, and head rice recovery. High heritability was observed for all traits studied, except for flag leaf breadth, which demonstrated moderate heritability (0.48).

Targeted traits for positive gains

In this study, all traits were targeted for positive selection gains except for days to 50% flowering, days to maturity, plant height, kernel breadth, and length-to-breadth ratio. Negative selection for plant height and kernel breadth posed challenges due to limited genetic variability and their correlations with key traits. However, leveraging diverse genetic resources, advanced breeding tools, and multi-environment trials can help overcome these issues. Positive correlations between single plant yield and yield-contributing traits facilitated the selection process through the use of indices.

Single plant yield demonstrated percentage selection gain (SGperc) across different indices, ranging from 0.14% for the Elston index to 16.90% for MGIDI, with GYT and LPSI showing gains of 0.26% and 16.02%, respectively. Productive tillers per plant showed SGperc values from 2.53% (GYT) to 0.96% (MGIDI), while the Elston and LPSI indices resulted in gains of 1.30% and 1.99%, respectively. For the number of grains per panicle, LPSI showed the highest increase at 32.34%, followed by GYT (21.29%), the Elston index (20.62%), and MGIDI with the lowest increase at 1.98%. The harvest index recorded gains of 6.71% in GYT, 6.28% in the Elston index, and 6.14% in LPSI, with MGIDI showing the smallest gain at 3.35%.

Grain quality traits, such as gel consistency, recorded SGperc ranging from 0.25% in MGIDI to a maximum of 11.79% in LPSI. For head rice recovery, LPSI led with a 5.94% gain, followed by the Elston index at 5.69%, MGIDI at 3.55%, and GYT at 2.15%. Among the selection indices, MGIDI showed a notable gain of 5.20% for flag leaf length, although it achieved only a minimal gain of 0.29% for flag leaf breadth, falling short of desired outcomes.

Certain traits recorded negative gains under specific indices. For instance, the harvest index showed negative gains in LPSI (-0.37%) and the Elston index (-0.03%). Thousand-grain weight also experienced negative gains in LPSI (-0.91%) and GYT (-0.01%). Regarding grain quality traits, amylose content showed a decrease under GYT (-0.07%), while kernel length exhibited negative gains under MGIDI (-0.38%), LPSI (-0.16%), and GYT (-0.01%), failing to meet the selection goals.

Targeted traits for negative gains

The traits targeted for reduction through negative selection include days to 50% flowering, days to maturity, plant height, kernel breadth, and length-to-breadth ratio. The objective of the selection indices is to reduce the values of these traits across the selected genotypes. The correlations between traits are essential in determining in shaping selection gains and determining the outcomes achievable through various indices.

For days to 50% flowering, negative gains were ranging from -0.01% (GYT) to -1.62% (LPSI), with MGIDI and the Elston index showing reduction of -1.34% and -0.03%, respectively. Plant height showed the most significant negative gain with LPSI (-2.21%), while the Elston index indicated the smallest gaits at -0.14%.

The success of a selection index in breeding programs depends on its ability to achieve selection goals across traits, irrespective of correlations between those traits. The selection in this case targets significant increases in single plant yield and its related traits, such as the number of grains per panicle, the number of productive tillers per plant, and spikelet fertility.

Additionally, grain quality attributes, such as hulling, milling, head rice recovery, and amylose content are prioritized, while maintaining negative gains for days to 50% flowering, days to maturity, plant height, kernel breadth and length-to-breadth ratio.

The positive association between days to maturity and grain yield poses a challenge in achieving the desired reductions. Three of the four selection indices: MGIDI (4.32%), LPSI (0.02%), and GYT (0.007%), did not achieve negative gains for this trait. Likewise, LPSI (0.54%) and the Elston index (0.004%) for length-to-breadth ratio showed positive gains, and for kernel breadth, MGIDI (2.05%) and the Elston index (0.001%) failed to achieve the target reductions.

Selection of genotypes using different indices at a 15% selection intensity

Sixteen genotypes with the highest index values were selected as the top candidates for further improvement, representing a selection intensity of 15% (Table 3 and Fig. 2). Across all indices, a total of 31 unique genotypes were selected, with some being common to multiple indices.

Table 3. Genotypes selected at 15% selection intensity by each selection index

RANK	Selection Indices			
	MGIDI	GYT	ELSTON	LPSI
1	G39	G3	G3	G39
2	G3	G43	G25	G108
3	G25	G20	G103	G67
4	G92	G31	G101	G88
5	G41	G60	G39	G103
6	G1	G44	G92	G3
7	G10	G88	G44	G107
8	G29	G41	G107	G25
9	G76	G25	G60	G109
10	G60	G34	G104	G104
11	G85	G82	G30	G70
12	G43	G67	G43	G31
13	G56	G47	G108	G92
14	G47	G85	G58	G101
15	G44	G92	G29	G43
16	G2	G1	G88	G20

MGIDI: Multitrait Genotype Ideotype Distance Index; **GYT**: Genotype Yield Trait Biplot; **LPSI**: Linear Phenotypic Selection Index.

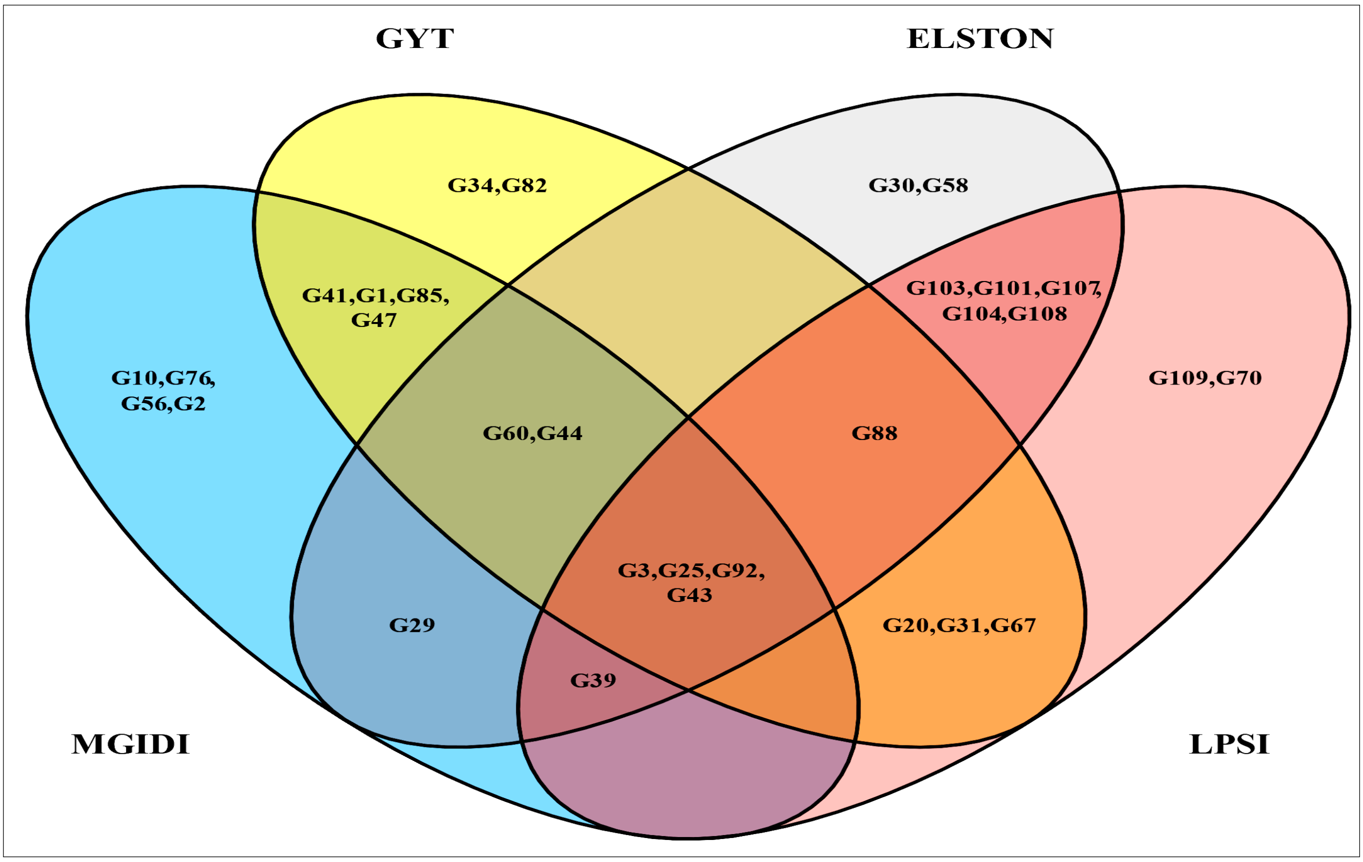

Fig. 2. Venn diagram of selected genotypes across all selection indices in 110 rice genotypes. (**MGIDI**: Multi-trait Genotype Ideotype Distance Index; **GYT**: Genotype by yield and trait biplot ; **LPSI**: Linear Phenotypic Selection Index).

Notably, genotypes G3, G25, G92, and G43 were consistently selected across all four indices. Genotypes G39, G60, G44, and G88 appeared in at least three indices. Meanwhile, G41, G1, G29, G85, G47, G20, G31, G67, G103, G101, G107, G104, and G108 were selected by at least two indices.

Some genotypes were unique to individual indices: MGIDI selected G10, G76, G56, and G2; G34 and G82 were only in the GYT index; G30, G58, and G29 were only in the Elston index; and G109 and G70 in LPSI index.

The rankings of the genotypes across the four indices are detailed in Supplementary Table 2. Fig. 3 depicts

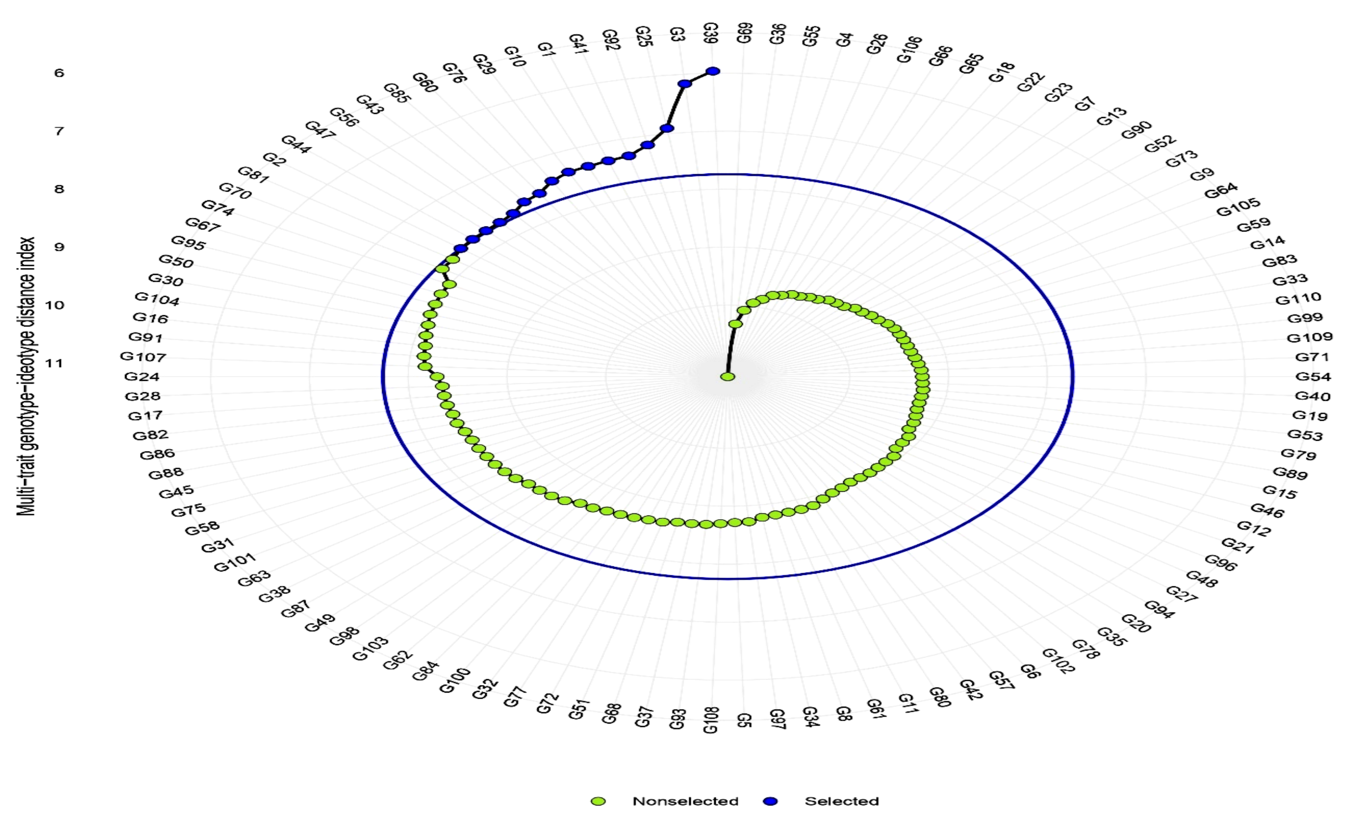

Fig. 3. Genotype ranking for MGIDI index.

the MGIDI index, where the top 16 genotypes meeting the selection threshold are highlighted in blue. The GYT biplot (Fig. 4) visually represents genotype performance, illustrating the "which-won-where" pattern (Fig. 5) derived from the GYT biplot. In these figures, blue denotes rice genotypes, while green represents traits, highlighting the associations between specific genotypes and traits.

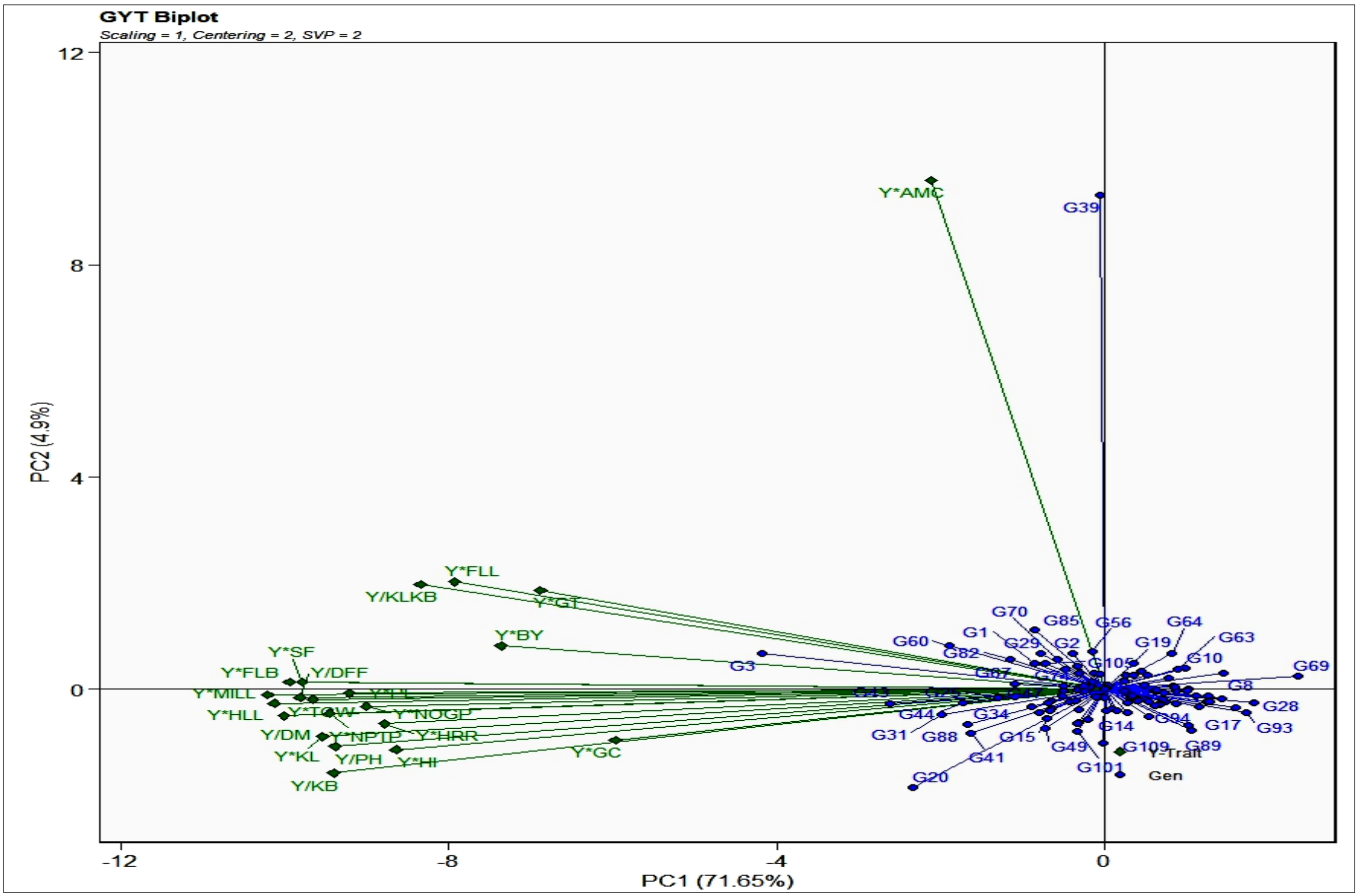

Fig. 4. Genotype-by-yield trait plot for 110 rice genotypes across all traits.

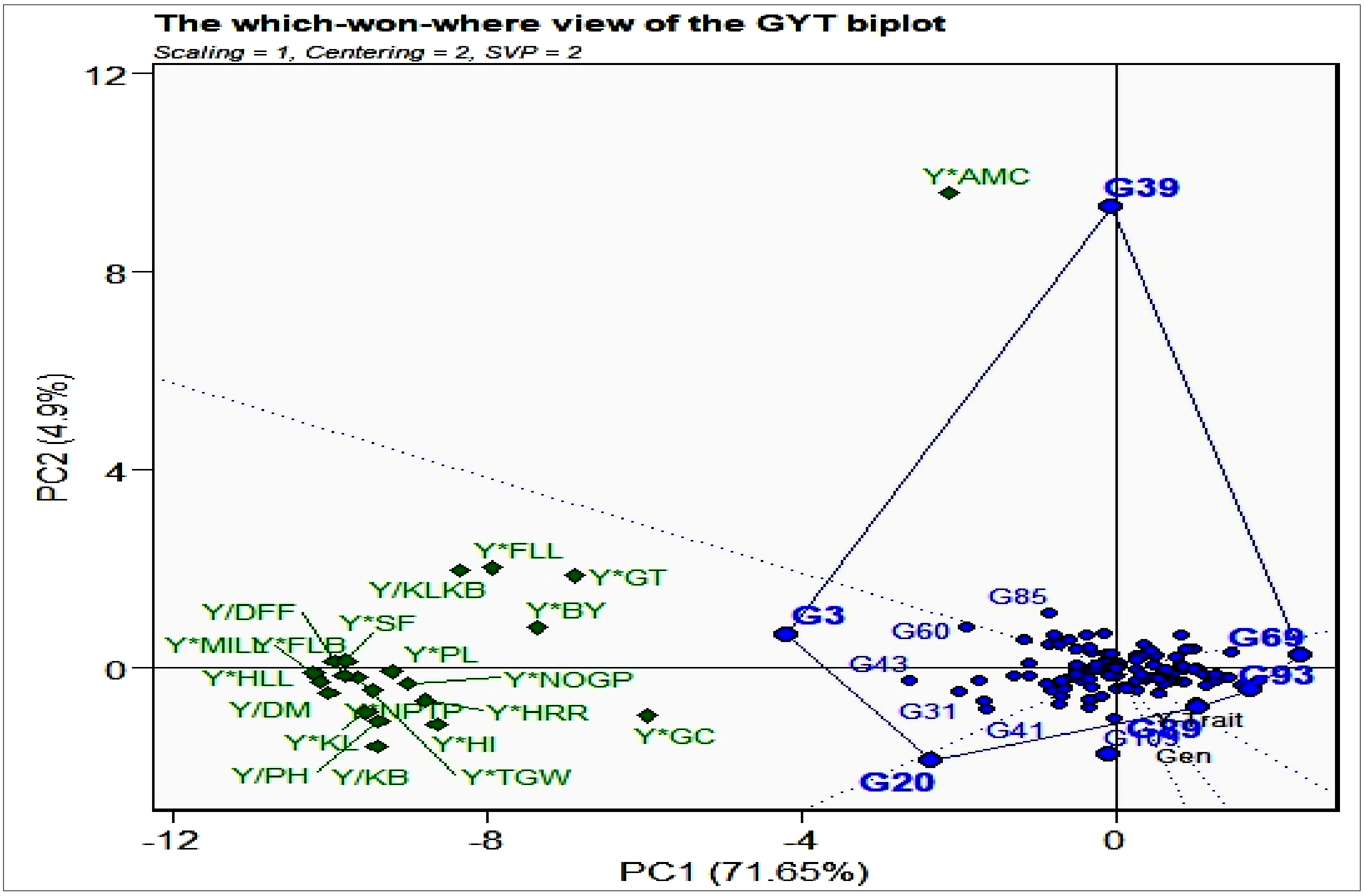

Fig. 5. Genotype-by-yield trait "which-won-where" pattern for 110 rice genotypes across all traits.

Comparative analysis of similarities among various selection indices

The similarities among the selection indices are summarized in Table 4, with the upper diagonal displaying Spearman's rank correlation coefficeint and the lower diagonal showing the coincidence index across the four selection indices.

Table 4. Analysis of similarities among various selection indices

INDEX	MGIDI	GYT	ELSTON	LPSI
MGIDI	**1**	0.43	0.56	0.49
GYT	55.88	**1**	0.35	0.65
ELSTON	41.17	33.82	**1**	0.34
LPSI	19.11	41.17	63.23	**1**

MGIDI: Multi-trait Genotype Ideotype Distance Index; **GYT**: Genotype by yield and trait biplot; **LPSI**: Linear Phenotypic Selection Index; Upper diagonal displaying Spearman's rank correlation and the lower diagonal showing the Coincidence index across the four selection indices.

Assessment of Spearman's rank correlation

Spearman's rank correlation coefficient was used to compare the rankings of genotypes across different selection indices. The correlation coefficients (r) varied from 0.34 to 0.65, all of which were statistically significant. Among the indices, GYT was most closely aligned with LPSI, with a correlation of 0.65, while it was least similar to the Elston index, with correlation of 0.35.

The MGIDI index showed consistent correlations with all indices, with values of 0.43 for GYT, 0.56 for the Elston index, and 0.49 for LPSI. In contrast, the Elston index exhibited the least correlation with LPSI ($r = 0.34$). Overall, MGIDI had moderate to high correlations ($r > 0.40$) with all other indices, reflecting a consistent similarity in genotype rankings across the different selection methods (Table 4).

Assessment of coincidence index

The coincidence index (CI) was used to measure the similarity across selection indices when genotypes were identified under a fixed selection intensity of 15%. In this study, CI values ranged from 19.11% to 63.23%, which represents the percentage of overlap in selected genotypes between indices.

The highest coincidence index, 63.23%, was observed between the Elston index and LPSI, indicating the strongest alignment in genotype selection between these indices. MGIDI and GYT showed a moderate similarity, with a CI of 55.88%. In contrast, the Elston index and GYT had a lower similarity, with a CI of 33.82%.

The CI between GYT and LPSI, as well as between the Elston index and LPSI, was 41.17%, indicating a fair level of alignment in genotype selection. The lowest CI, 19.11%, was found between MGIDI and LPSI, showing a clear difference in genotype selection between these two indices (Table 4).

Discussion

Plant breeders strive to develop or select a superior genotype, or ideotypes, that shows genetic progress by incorporating multiple desirable traits (37). Breeders often aim to bring together various desirable agronomic traits into a single high-performing genotype. Several selection indices have been proposed over time to achieve it (38).

Traditional indices like the Smith-Hazel (SH) index (14, 15) and the ideotype-design method (39), have notable limitations. These include challenges in assigning economic values to traits and translating these values into practical weightings for selection. Such challenges complicate the optimization of breeding decisions that consider both genetic potential and economic outcomes.

To address these issues, advanced multi-trait selection indices have been developed, like MGIDI, GYT, Elston index, and LPSI. These indices have demonstrated effectiveness in selecting superior genotypes when multiple traits are involved. Additionally, incorporating predicted genotypic values using best linear unbiased predictors (BLUPs) has been shown to increase the precision of selection index efficiency.

The gains achieved in trait-specific depend on the genetic correlations between traits. In this study, the BLUPs of genotypes were used to estimate selection differences and predict the expected gains, providing a more precise framework for multi-trait selection.

The analysis of variance (ANOVA) showed significant differences (P value=0.01) among the rice genotypes for all traits studied, indicating substantial variability among the genotypes. Similar findings were reported in earlier studies (40, 41, 37). Correlation coefficients, which measure the association between two variables, can be influenced by genetic linkages, pleiotropy, or environmental factors. Understanding the correlation between seed yield and its components allow plant breeders to identify traits that enhance yield, thereby enabling the development of effective selection strategies (42).

In this study, a significant and positive correlation was recorded between single-plant yield and traits such as the number of productive tillers and grains per panicle, suggesting these traits play a major role in determining yield. Moderate and positive correlations with the harvest index and spikelet fertility, suggest that these traits provide additional, though smaller, contributions to yield improvement. A strong correlation between days to 50% flowering and days to maturity highlights their potential in synchronizing crop development for early-maturing varieties. In contrast, the nonsignificant negative correlations of days to 50% flowering, days to maturity, and plant height with seed yield suggest these traits have little effect on yield. Although days to 50% flowering and days to maturity are important for developing early maturing varieties, their low correlation with yield indicates that selecting reduced maturity or shorter plant stature may not significantly enhance yield.

To manage conflicting selection goals, breeders can use strategies like multi-trait indices, which balance traits with strong positive correlations (e.g., productive tillers) alongside those with weaker associations (e.g., maturity). The finding suggest that reduced crop duration and shorter plant stature have minimal effect on yield potential consistent with previous studies (43- 46). Prioritizing traits like productive tillers and grains per panicle, which directly impact yield, aligns with earlier findings (47 – 50).

The high broad-sense heritability observed for single plant yield, the number of productive tillers per plant, and the number of grains per panicle indicates strong genetic stability, making these traits ideal for selection in rice breeding programs (51). Similarly, grain quality traits also had high heritability, highlighting the potential for simultaneous improvements in yield and grain quality. High heritability suggests significant genetic gains can be made, as traits with high heritability are less affected by environmental changes (55). This ensures a larger part of the observed variation is due to heritable factors, making it easier to select reliably superior genotypes based on phenotypic characteristics (52 – 54).

Predicted gains from selection index provide a useful tool for evaluating selection efficiency. A key requirement for any selection index is its ability to improve predicted gains for the primary trait of interest, like seed yield, while meeting desired standards for secondary traits outlined in the ideal plant ideotype. This study aimed to achieve both positive and negative selection gains for various traits in rice genotypes to optimize yield and grain quality. Traits like single plant yield, the number of productive tillers per plant, and the number of grains per panicle were targeted for positive gain, with MGIDI and LPSI showing the highest yield gains.

At the same time, negative selection was applied to reduce traits like days to 50% flowering and plant height, but achieving negative gains for days to maturity proved challenging. Grain quality traits, including gel consistency and head rice recovery, showed positive gains, especially under LPSI. However, traits like panicle length and flag leaf breadth showed either minimal or negative gains, indicating the difficulty in improving these attributes. Negative selection targeting traits such as days to 50% flowering, days to maturity, plant height, and kernel traits (e.g., breadth and length-to-breadth ratio) proved partially successful. LPSI and MGIDI indices demonstrated the greatest reductions in plant height and days to 50% flowering, but achieving targeted reductions for days to maturity and kernel breadth remained difficult. All indices reflected negative gains for panicle length, further illustrating the challenges in improving this trait. The GYT-biplot analysis revealed a general positive correlation among yield components, even when individual variables were negatively correlated (24). This underscores the importance of earliness and grain type traits as key selection criteria in rice ideotype development. To create genetic variability, crossing these genotypes is essential for obtaining segregating populations with higher potential for yield and precocity (56). The GYT model, a multiplicative framework, combines seed yield with other traits, prioritizing yield improvement. The effectiveness of the GYT model depends on the associations between traits. Similarly, the Elston index, while effective, is influenced by multicollinearity, which may affect its performance.

The MGIDI index provided satisfactory results in selecting for seed yield but was less effective in achieving negative gains for days to maturity. Balancing gains across traits remain critical for selection indices to achieve breeding objectives. While positive gains were achieved for yield -related traits, the mixed results for traits targeted negative selection highlight the challenges of improving yield while simultaneously reducing undesirable traits. MGIDI and LPSI effectively improving yield while simultaneously reducing undesirable attributes. MGIDI and LPSI effectively improved yields while managing reductions in plant architecture and flowering traits; however, further refinement is needed to target days to maturity and grain type. Among these, the MGIDI index was particularly effective, achieving a 71.7% success rate in selecting traits with desired gains (57). Additionally, the GYT biplot provided valuable insights into genotype performance and trait associations, proving crucial for identifying superior genotypes across multiple traits, especially in datasets with low trait correlation (58).

At a selection intensity of 15%, 31 genotypes were identified across all four indices. Among these, the genotypes BMDK-2-2-8-2, JR 13, A 67, and CR 4376-1-1-1-2-2-1 were consistently selected, demonstrating strong performance across various traits. Their repeated selection shows their genetic potential for yield-related traits and grain quality, making them ideal for further breeding programs. The multi-index approach provided a robust and comprehensive method for identifying genotypes with desirable traits for genetic improvement.

In plant breeding, selection indices such as MGIDI, SI, GYT biplot, LPSI and the Elston Index play a crucial role in effective multi-trait selection. MGIDI, in particular, stands out with a 71.7% success rate in achieving desired trait gains, offering a valuable tool for balancing yield with other important traits. The application of MGIDI has resulted in significant genetic gain, making a promising advancement in the field of multivariate selection indices (56 -59). These tools enable breeders to identify genotypes with ideal trait combinations, thereby enhancing genetic gains and crop resilience.

The strong correlations among these indices suggest consistency in genotype rankings, allowing breeders to make selections that align across multiple indices. GYT and LPSI showed a strong correlation due to their shared basis in factor analysis; their gains differed due to variations in genotype selection, as highlighted by the coincidence index. While GYT and LPSI showed the closest alignment in rankings and selections, the Elston index demonstrated less similarity with the others, reflecting its unique selection criteria. The coincidence index supported these findings, revealing the greatest overlap in genotype selection between the Elston and LPSI. Although, MGIDI showed moderate to high correlation with all indices, it diverged significantly from LPSI, highlighting differences in the prioritized traits.

The analysis revealed that indices like GYT and LPSI are closely aligned, whereas MGIDI and LPSI exhibit greater divergence in selection outcomes. Employing both rank correlation and coincidence indices offered valuable insights into the relationships among the selection indices. A Venn diagram showed that genotypes such as BMDK-2-2-8-2, JR 13, A 67, and CR 4376-1-1-1-2-2-1 were consistently selected by all indices. Other genotypes, like RP 5084-58-33-2-2-3-B, NWGR 16058, RNR 28359, and W 225, were chosen by three indices. This suggests that combining multiple indices improve genotype selection by balancing yield improvements with specific trait enhancements.

Selection indices for multiple traits have been extensively utilized to identify suitable genotypes. Although a single genotype rarely meets the ideotype criterion, the expected gain is calculated based on the mean performance of the selected population. These selected genotypes can be used in either as parents to assess their genetic value in hybrid production or as founder lines for population improvement. They may also undergo recurrent selection cycles to improve multiple traits simultaneously, ensuring continuous advancements in breeding programs.

In rice, selection indices are valuable tools for identifying the best genotypes from a set of germplasms. These selected genotypes can be used to develop synthetics or composite varieties after evaluating their combining ability, often without the need for need for further testing. Selection indices based on multiple traits effectively identify best genotypes, although it is rare to find a single genotype to meet all the ideal criteria. Genetic gains are typically estimated based on the average performance of the selected population. The identified genotypes can serve as parent lines for hybrid production or be utilized in recurrent selection programs to improve multiple traits simultaneously. In rice breeding, these indices help to identify superior genotypes that can then be used to develop superior hybrids, provided their combining abilities are thoroughly tested. This approach simplifies breeding processes, improving efficiency, and facilitates the development of superior varieties with targeted traits.

The MGIDI has been highly effective in identifying superior rice genotypes, resulting in significant improvements across multiple traits. MGIDI is widely recognized as one of the most efficient indices x for selecting genotypes with desirable characteristics, highlighting its value in crop improvement programs (560). This innovative multivariate selection index addresses several limitations of traditional indices, especially the problem of multicollinearity. Unlike conventional methods, MGIDI accounts for trait correlations and evaluates all variables comprehensively. This approach helps overcome challenges like poorly conditioned matrices and biased index coefficients, which are commonly encountered in traditional indices like the SH index.

MGIDI aligns with the principles of ideotype breeding by focusing on the genotype and ideotype distance, providing a more holistic and effective strategy for crop improvement (59).

Conclusion

In conclusion, this study has demonstrated the efficacy of multi-trait selection indices, particularly the MGIDI, in optimizing genetic gains and identifying elite rice genotypes for breeding programs. The analysis revealed significant genetic variability among traits, with MGIDI achieving the highest selection gains for yield (16.9%), while other indices like GYT, LPSI, and the Elston Index displayed varied efficiencies across different traits. Key findings highlighted the importance of traits such as the number of grains per panicle and productive tillers, which exhibited positive correlations with yield. However, challenges persisted in achieving negative selection gains for traits such as plant height and days to maturity.

The use of multi-trait indices enabled a more comprehensive selection process, considering complex relationships between traits, which are often missed in single-trait selection. Genotypes such as BMDK-2-2-8-2 and CR 4376-1-1-1-2-2-1 were identified as top performers, making them strong candidates for further improvement to enhance yield and grain quality. This research underscores the broader significance of using advanced indices like MGIDI to balance yield improvements with other agronomic and grain quality traits, contributing valuable insights for ideotype breeding and sustainable crop improvement. By integrating these indices, breeders can achieve more robust and precise trait selections, enhancing both productivity and resilience in rice varieties.

Despite these advancements, the study also identified limitations, such as the difficulty in reducing certain traits like days to maturity and kernel breadth, which highlight areas for further investigation. Future research should focus on refining these indices to address these challenges, exploring their applications in diverse environments, and test their adaptability to other crops. The multi-index approach provides a comprehensive framework for breeding programs, facilitating the development of rice genotypes that meet the growing demands for yield and quality.

Breeders should give priority to traits that directly influence yield, such as grains per panicle and productive tillers, while considering plant height and maturity based on environmental conditions when integrating MGIDI into routine selection processes. Emphasis should also be placed on developing early-maturity and dwarf plant type, particularly in drought-prone areas, to minimize the impact of terminal stress at later stages of growth. MGIDI can be applied in early-generation selection to optimize yield and adaptability. Future research should refine MGIDI, to address challenges associated with traits like maturity and kernel breadth and explore its application to other crops and environments for broader utility.

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Authors' contributions

TAM and DK conceptualized the research. DK and SM conceived of the study and participated in its design and supplied the necessary materials . TAM conducted the experiments and participated in the datasets. TAM carried out the analyses and drafted the manuscript. DK, SM, SR, NMB, SN and BNN participated in reviewing the draft. All authors revised the paper and approved the final version of the manuscript.

Compliance with Ethical Standards

Conflict of interest: **:** The authors have no competing interests to declare that are relevant to the content of this article.

Ethical issues: None

Supplementary data

Supplementary Table 1. The list of genotypes with their pedigree and sources

Supplementary Table 2. Index ranks and scores of 110 genotypes across all indices

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