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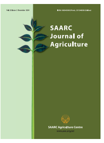

Research Article

Genetic Parameters Estimation and Identification of Promising Rice Genotypes Grown in Rainfed Condition Using Mgidi Index in Rampur, Chitwan

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Abstract

This study evaluated 24 rice genotypes, including 22 pipeline varieties from the National Rice Research Program (NRRP) in Dhanusa and two checks, Bahaguni-2 and Sabitri. The Multi-Trait Genotype-Ideotype Distance Index (MGIDI) was used as selection tool to rank genotypes based on their proximity to an ideal genotype. Broad-sense heritability (h^2) estimates ranged from 0.03 for panicle length to 0.96 for days to 80% maturity, suggesting high potential for selection gains in days to 80% maturity ($h^2 = 0.96$) and plant height ($h^2 = 0.91$), while tiller number and grain yield showed low heritability ($h^2 > 0.5$). Variance analysis indicated substantial genetic control for plant height and days to 80% maturity, while panicle length and grain yield were more influenced by environmental factors. Principal component analysis revealed four factors explaining 76.5% of the trait variation, with FA1 (days to 50% flowering, days to 80% maturity) accounting for the most variation. Selection gains were assessed using MGIDI and FAI-BLUP indexes, with MGIDI achieving a 15.13% gain for targeted traits and FAI-BLUP yielding 1.25%. Selected genotypes from MGIDI included SVIN 127, SVIN 098, SVIN 643, SVIN 084, and IR 18F1085, with SVIN 127 and SVIN 098 also appearing in the FAI-BLUP index, highlighting their potential value for breeding. This research demonstrates the effectiveness of both selection indexes in identifying superior genotypes for enhanced breeding efficiency.

Keywords: Rice, MGIDI, Selection gain, Grain yield, Ideotype

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Introduction

Rice (*Oryza sativa* L.) ranks as the second most crucial cereal crop after wheat and is a staple food for more than half of the world's population. As the global population is expected to reach 8 billion by 2025, there is an increasing need to boost rice production (Mohidem et al., 2022).

Selection gain is a fundamental objective in plant breeding, guiding the development and progress of breeding programs to improve crop performance. Traditionally, breeding efforts have focused on a limited number of traits, but this approach has been recognized as insufficient for achieving comprehensive crop improvement (Sinha et al., 2021). Selecting a few traits in isolation can neglect potential enhancements in other vital characteristics, limiting the overall genetic advancement. Consequently, modern breeding programs seek to combine desirable traits into a single genotype, aiming to create an ideotype-a plant model with optimized traits for superior performance (Donald, 1968).

The concept of ideotype breeding has long been central to crop improvement programs, where the goal is to develop a genotype that integrates a range of traits for optimal agronomic and economic outcomes (Carbajal-Friedrich and Burgess, 2024). However, the complexity of breeding for multiple traits simultaneously poses significant challenges. This is particularly true when accounting for natural correlations between traits, which traditional methods often overlook. In this context, the Multi-Trait Genotype-Ideotype Distance Index (MGIDI) offers a novel approach that addresses these limitations by incorporating data from multiple traits into the selection process (Olivoto and Nardino, 2021). Unlike conventional selection indices, MGIDI leverages multivariate techniques to account for trait correlations and efficiently selects genotypes based on their proximity to an ideal genotype (Alam et al., 2024). MGIDI represents a significant advancement in multivariate selection methodologies, providing a more holistic and effective tool for crop improvement. By computing a weighted Euclidean distance between genotypes and the ideal genotype, MGIDI ranks genotypes according to their overall performance across multiple traits (Olivoto et al., 2022). It applies Principal Component Analysis (PCA) to reduce dimensionality, transforming correlated traits into independent components, thus minimizing redundancy and multicollinearity (Shafizadeh-Moghadam, 2021). This approach enables plant breeders to evaluate genotypes more effectively, considering the strengths and weaknesses of each genotype (Olivoto and Nardino, 2021).

MGIDI offers breeders a powerful approach to achieving genetic gain and improving rice traits holistically by leveraging multivariate data and offering a comprehensive assessment of rice genotype performance. The objective of this study was to evaluate the genetic parameters of key agronomic traits in rice genotypes to enhance the efficiency of breeding programs. This study also explored the application of MGIDI in evaluating rice genotypes, aiming to provide insights into its utility as a selection tool and identify the high potential genotypes.

Materials and Methodology

Experimental Site

The experiment was performed at National Maize Research Program (NMRP) rice research field, Chitwan between June and October 2022. Geographically, the site is positioned at 27°39.27' North latitude and 84°21.28' East longitude, at 228 meters above sea level. The region has a humid, subtropical climate characterized by cool winters, hot summers, over 1500 mm of annual rainfall, a pronounced monsoon season, and sandy loam soils with slight to acidic solid characteristics.

Planting Materials

The experiment involved 24 genotypes (Table 1), comprising 22 pipeline varieties obtained from the National Rice Research Program (NRRP), Dhanusa and two check varieties, Bahaguni-2 and Sabitri.

Table 1. List of twenty-four genotypes of rice used in research.

S.N.	Genotype	Sources
1	HARDINATH-4	NRRP, Dhanusa
2	IR 15L1801	NRRP, Dhanusa
3	IR 16 F 1148	NRRP, Dhanusa
4	IR 16 L 1855	NRRP, Dhanusa
5	IR 16A 5125	NRRP, Dhanusa
6	IR 16F1065	NRRP, Dhanusa
7	IR 16L 1795	NRRP, Dhanusa
8	IR 17L1415	NRRP, Dhanusa
9	IR17A12038	NRRP, Dhanusa
10	IR17A2252	NRRP, Dhanusa
11	NR 2233-3-1-1-3-3	NRRP, Dhanusa
12	P# 14-16-SP #52	NRRP, Dhanusa
13	P# 14-30-SP #27	NRRP, Dhanusa
14	SVIN 028	NRRP, Dhanusa
15	SVIN 060	NRRP, Dhanusa
16	SVIN 064	NRRP, Dhanusa
17	SVIN 095	NRRP, Dhanusa
18	SVIN 098	NRRP, Dhanusa

S.N.	Genotype	Sources
19	SVIN 127	NRRP, Dhanusa
20	SVIN 131	NRRP, Dhanusa
21	SVIN 191	NRRP, Dhanusa
22	SVIN 195	NRRP, Dhanusa
23	SVIN 312	NRRP, Dhanusa
24	SVIN 643	NRRP, Dhanusa

Design of Experiment and Cultural Practices

The experiment followed an alpha-lattice design with three replications and two blocks containing 12 genotypes. Rice seedlings were grown in a wet seedbed for 25 days before being transplanted into well-prepared soil in plots measuring 10 m² (5 m * 2 m), with a spacing of 20 cm * 20 cm. Fertilization was done using 100:40:30 kg NPK per hectare, with half the nitrogen and all phosphorus and potassium applied during field preparation. Additional nitrogen was top-dressed at 20-25 days and 40 days after transplantation.

Data Collection

The data were recorded on individual plants and plotted for nine quantitative traits at the appropriate growth stage of the crop as per Bioversity International et al. (2007). Five plants were randomly selected from each plot. Data was collected on plant height (PH), tiller number (TN), leaf number (LN), panicle per square meter (PASQM), panicle length (PLL), days to 50% flowering (DTF), days to 80% maturity (DTM), chlorophyll content (CC), and grain yield (YD). The final grain yield was adjusted at 12% moisture content, and calculated using the following formula on Equation (1).

$$\text{Grain yield}\left(\frac{\text{ton}}{\text{ha}}\right) = \frac{plot\ yield\ (kg) \times 1000(m^2) \times (100-MC)}{(100-Adjusted\ MC) \times Plotarea\ in\ Sq.m} \quad (1)$$

Where, MC= Moisture content of grain (%) just before weighing the bulk

Y= Net plot yield (kg)

A= Net plot area (m^2)

(100-MC)/(100-Adjusted MC) = Conversion factor for grain yield at adjusted moisture content.

1000/A= Conversion factor for the actual harvested area into hectare basis.

This formula was also adopted by Paudel et al. (1995) to adjust the grain yield (ton ha^{-1}) at 12% moisture content.

Statistical Analysis

The data were processed using the software MS-excel and analyzed through R-Studio. The MGIDI index theory is based on four key steps: (i) standardizing all traits to a range of 0 to 100, (ii) applying factor analysis to capture the correlation structure and reduce the data's dimensionality, (iii) designing an ideal genotype using known or desired trait values, and (iv) calculating the distance between each genotype and the designed ideotype (Olivoto and Nardino, 2021).

Rescaling the Trait

Consider a two-way table with i rows representing genotypes and j columns representing traits. The rescaled value (⍰X_{ij}) for the ith row and jth column was expressed as Equation (2).

$$X_{ij} = \frac{n_{nj}-\varphi_{nj}}{n_{oj}-\varphi_{oj}} \times (\theta_{ij} - \eta_{oj}) + \eta_{nj} \qquad (2)$$

In this context, η_{nj} and φ_{nj} represent the new maximum and minimum values for trait j after rescaling. At the same time, η_{oj} and φ_{oj} are the original maximum and minimum values of trait j. The symbol θ_{ij} refers to the original value of the jth trait for the ith genotype or treatment. The values for η_{nj} and φ_{nj} are selected based on the desired direction of gains: if negative gains are preferred, η_{nj}=o and φ_{nj} =100 are applied; if positive gains are preferred, η_{nj} =100 and φ_{nj} = 0 are used instead. After rescaling, the values in the two-way table (⍰X_{ij}) fall within a 0 – 100 range, considering the preferred direction of selection (whether to increase or decrease). This process also preserves the correlation structure of the original set of variables.

Factor analysis

The next step involved performing an exploratory factor analysis with (rX_{ij}) to group the correlated traits into factors. Afterward, the factorial scores for each row, genotype, or treatment are calculated as Equation (3).

$$X = \mu + Lf + \epsilon \qquad (3)$$

In this context, X represents a $p\times1$ vector of rescaled observations, while μ represents a $p \times1$ vector of standardized means. L is $p \times$f of factor loadings, with f being a $p \times1$ vector of common factors. ϵ represents the $p\times1$ vector of residuals, where p is the number of traits and f corresponds to the number of retained common factors. Eigen values and Eigen vectors are derived from the correlation matrix. The initial factor loadings are selected based on Eigen values more significant than one, and the final loadings are calculated using varimax rotation (Kaiser, 1958). Factor scores are then computed accordingly as per Equation (4).

$$F = Z\,(A^T R^{-1})^T \qquad (4)$$

In this case, F is a $g\times f$ matrix containing the factor scores, and Z is a $g\times p$ matrix of (rescaled) standardized means. A refers to a $p\times f$ matrix of canonical loadings, while R represents the $p\times p$ correlation matrix between traits. Here, *g, p, and f* denote the number of rows (genotypes or treatments), retained factors, and traits analyzed, respectively.

Ideotype Planning

According to the definition in Equation (2), the ideotype was characterized by having the highest rescaled value (100) across all traits analyzed. Therefore, the ideotype can be represented by $1 \times p$ vector I such that I = [100, 100, …, 100]. The scores for the ideotype were also calculated as per Equation (4).

The MGIDI Index

The final step involved calculating the multi-trait genotype–ideotype distance index (MGIDI) as per Equation (5).

$$\mathrm{MGIDI}_i = [\sum_{j=1}^{f} (\gamma_{ij} - \gamma_j)^2]^{0.5} \tag{5}$$

In this context, MGIDI_i represented the multi-trait genotype–ideotype distance index for the i^{th} row/genotype/treatment, while γ_{ij} denotes the score of the i^{th} row/genotype/treatment for the j^{th} factor (i=1, 2,…,g; j=1,2,…, f), where g and f are the total number of rows/genotypes/treatments and factors, respectively. γ_j represents the score of the ideotype for the j^{th} factor. The row/genotype/treatment with the smallest MGIDI value is closest to the ideotype and thus exhibits the most desirable values across all p traits. The proportion of the MGIDI index for the i^{th} row/genotype/treatment explained by the j^{th} factor (ω_{ij}) is calculated to highlight the strengths and weaknesses of each genotype/treatment as per Equation (6).

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=1}^{f} \sqrt{D_{ij}^2}} \tag{6}$$

Here, D_{ij} represented the distance between the i^{th} genotype/treatment and the ideotype for the j^{th} factor. A lower contribution from a factor suggests that the traits associated with that factor are closer to the ideotype.

FAI-BLUP

The FAI-BLUP index (Rocha et al., 2018) was used to evaluate genotypes based on their proximity to a desired ideotype (DI). The DI was defined by assigning "min" values for traits where lower values are preferred and "max" values for traits where higher values are desired. The distance to the DI was calculated using the Euclidean distance formula for each genotype. These distances were then transformed into spatial probabilities by taking the inverse of the distance, with probabilities normalized to sum to 1. Genotypes were ranked based on their normalized spatial probabilities, with higher values indicating more excellent proximity to the ideal as demonstrated in Equation 7.

$$P_{ij} = \frac{\frac{1}{dij}}{\sum_{i=1;j=2}^{i=n;j=m} \frac{1}{dij}} \quad (7)$$

In this context, P_{ij} represents the likelihood of the ith genotype (where i=1, 2,………..,n) being similar to the jth ideotype (where j=1,2,……………..,m). The term d_{ij} refers to the distance between the i thgenotype and the jth ideotype, calculated using the standardized mean Euclidean distance.

Genotype Selection in Breeding Programs

The index was illustrated using a real dataset obtained from a trial involving 24 genotypes. Nine agronomic traits were evaluated. The selection of genotypes focused on identifying those with lower values (negative gains) for DTF, PH, and DTM, while aiming for higher values (positive gains) for YD, PLL, PASQM, CC, TN, and LN.

Each trait was analyzed using the gamem () function from the R package metan, which utilizes the mixed-effects model represented by Equation 8.

$$\mathrm{y} = \mathrm{Xb} + \mathrm{Zu} + \mathrm{e} \quad (8)$$

where y is an $n = [\sum_{j=1}^{r}(gr)] \times 1$ vector of response variable, i.e. the response of the ith genotype in the jth block (*i=1,2,…..,g; j=1,2,…..,r;* $\mathrm{y} = [y_{11}, y_{12}, \dots, y_{gr}]'$); b is an $1 \times r$ vector of unknown and unobservable fixed effects of block $\mathrm{b} = [\gamma_1, \gamma_2, \dots, \gamma_r]'$; u is an $m[= 1 \times g]$ vector of unknown and unobservable random effects of genotype $\mathrm{u} = [\alpha_1, \alpha_2, \dots, \alpha_g]'$; X is an n × r design matrix of 0s and 1s relating y to b; Z is an n × m design matrix of 0s and 1s relating y to u; and e is an *n ×1* vector of random errors $\mathrm{e} = [y_{11}, y_{12}, \dots, y_{gr}]'$;The variance components obtained from the analysis were utilized to calculate the broad-sense heritability (h^2) based on the mean of the genotypes, as shown below in Equation 9.

$$h^2 = \hat{\sigma}_\alpha^2 / (\hat{\sigma}_\alpha^2 + \hat{\sigma}_\epsilon^2 / r) \quad (9)$$

The predicted selection gain obtained with the index, SG (%), was computed for each trait considering a α % selection intensity was expressed in Equation 10.

$$SG(\%) = \frac{(\bar{X}_s - \bar{X}_o) \times h^2}{\bar{X}_o} \times 100 \quad (10)$$

Where $\bar{X}_s$ is the mean of the selected genotypes is, $\bar{X}_o$ is the mean of original population and h^2 is the heritability.

Results

Deviance Analysis, Variance Components, and Genetic Parameters

The deviance analysis using the MGIDI and BLUP methods, with random effects of genotype and fixed effects of replication, revealed significant genotype effects across several agronomic traits (Table 2). Highly significant genotype effects ($p < 0.05$)

were observed for PH, DTF, and DTM, indicating robust genetic control over these traits. Moderately significant genotype effects ($p < 0.05$) were noted for LN, PASQM, and CC suggesting an intermediate genetic influence. In contrast, TN and YD did not show significant genotypic effects.

Broad-sense heritability (h^2) estimates varied across the traits, ranging from 0.03 for PLL to 0.96 for DTM. DTM exhibited high heritability ($h^2 = 0.96$) with an accuracy of 0.98, indicating strong genetic control and potential for selection gains. Similarly, PH also showed high heritability ($h^2 = 0.91$) with an accuracy of 0.96 after DTM. In contrast, TN and YD exhibited low broad-sense heritability values ($h^2 < 0.5$), suggesting a greater environmental influence on these traits.

The analysis of variance components further elucidated the contributions of genetic and environmental factors to trait variation, as presented in Table 3. PH and DTM showed substantial genotypic variances relative to residual variances, indicating predominant genetic control. In contrast, PLL and YD exhibited higher residual variances, underscoring their sensitivity to environmental factors.

Table 2. Deviance analysis and genetic parameters for agronomic traits evaluated in 24 rice genotypes.

Traits	h^2	Accuracy	Cvg	CV_r	p-value
PH	0.91	0.96	10.2	4.59	6.92E-15
TN	0.2	0.45	6.5	18.5	3.77E-01
LN	0.55	0.74	11.8	15.2	3.09E-03
PASQM	0.44	0.71	5.47	7.88	1.05E-02
DTF	0.55	0.74	7.93	10.3	3.49E-03
DTM	0.96	0.98	5.7	1.81	5.85E-21
PLL	0.03	0.15	0.79	7.36	9.27E-01
CC	0.66	0.82	7.09	7.24	9.45E-05
YD	0.23	0.48	5.76	15.3	3.19E-01

Table 3. Estimated variance components.

Traits	Genotypic Variance	Residual Variance	Genotypic Variance (%)	Residual Variance (%)
PH	140	28.3	83.2	16.8
TN	0.43	3.42	11	89
LN	31.3	52.1	37.5	62.5
PASQM	185	385	32.5	67.5
DTF	42.6	72.3	37.1	62.9

Traits	Genotypic Variance	Residual Variance	Genotypic Variance (%)	Residual Variance (%)
DTM	40.4	4.07	90.8	9.16
CC	5.04	5.27	48.9	51.1
PLL	0.04	3.03	1.11	98.9
YD	0.06	0.36	12.5	87.5

Eigenvalues and Varimax Factor Loadings

The eigenvalue analysis and varimax factor loadings identified four principal components with eigenvalues greater than 1, collectively explaining 76.5% of the total trait variation (Table 4). Post-varimax rotation enhanced interpretability, with an average communality (h) of 0.76 across traits. Communalities ranged from 0.58 for PH to 0.85 for PLL, indicating that the factors captured a substantial portion of each trait's Variance. The nine traits analyzed were grouped into four factors (FA): FA1 (DTF, DTM), FA2 (YD, PASQM), FA3 (TN, LN), and FA4 (PLL, CC). FA1, encompassing DTF and DTM, accounted for the highest variation in the dataset, highlighting its significance in identifying genotypes suitable for further breeding.

Table 4. Eigenvalues, explained Variance, factorial loading after varimax rotation, and communalities

Traits	FA1	FA2	FA3	FA4
PH	-0.23	0.04	0.59	0.58
DTF	-0.92	-0.07	-0.13	0.18
DTM	-0.91	-0.05	-0.14	0.03
TN	0.14	-0.14	0.77	-0.23
LN	0.42	0.23	0.7	-0.09
PLL	-0.07	0.06	0.08	-0.85
PASQM	0.1	-0.89	-0.04	0.01
CC	0.36	0.05	0.29	-0.69
YD	0.25	0.81	-0.03	-0.07
Eigenvalues	2.93	1.46	1.41	1.09
Variances	32.5	16.2	15.6	12.2
Accumulated	32.5	48.7	64.3	76.5

Predicted Selection Gain

The selection gains (SG) comparison between the MGIDI and FAI-BLUP indexes indicated that both indexes effectively achieved desired gains across all evaluated traits (Table 5). Specifically, the MGIDI index demonstrated an overall selection gain of 15.13% for traits targeted for improvement and -0.42% for traits requiring reduction. Among the traits, LN showed the highest selection gain with 6.41%, followed by chlorophyll content with 4.32% for MGIDI. For FAI-BLUP, the overall selection gain was 1.25% for traits targeted for improvement and -11.09% for traits requiring reduction. The highest selection gain for FAI-BLUP was observed for CC with 1.07%, followed by YD with 0.17%. These results underscore the efficacy of both indexes in enhancing breeding objectives and achieving balanced genetic improvements across multiple traits.

Table 5. Selection Gain Percentage of MGIDI and FBI-BLUP

Traits	Factor	Goal	Selection Gain (%)	
			MGIDI	FBI-BLUP
DTF	FA1	Decrease	1.43	-2.52
DTM	FA1	Decrease	2.1	-3.82
PASQM	FA2	Increase	-0.21	-1.74
YD	FA2	Increase	0.1	0.17
PH	FA3	Decrease	-0.21	-1.42
TN	FA3	Increase	0.76	-0.31
LN	FA3	Increase	6.41	-1.28
PLL	FA4	Increase	0.01	0.01
CC	FA4	Increase	4.32	1.07
Total (Increase)			15.13	1.25
Total (Decrease)			-0.42	-11.09

Selected Genotypes by MGIDI Index and BLUP

The genotypes selected by the MGIDI Index include SVIN 127, SVIN 098, SVIN 643, SVIN 084, and IR 18F1085 (Fig. *1*). Notably, three of these genotypes: SVIN 127, SVIN 098, and SVIN 643—are also selected by the FAI-BLUP index, indicating consistency in their selection criteria (Fig. *2*). SVIN 127 and SVIN 098 were found near the cutoff point in the MGIDI index, whereas Hardinath-4 was found near the cutoff point in the FBI-BLUP index, suggesting they possess potentially valuable traits that warrant further investigation. MGIDI and FAI-BLUP indexes demonstrate effectiveness in identifying superior genotypes, contributing to balanced trait selection and enhancing breeding efficiency.

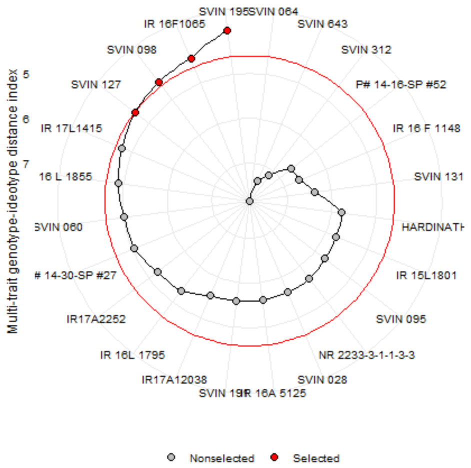

Fig. 1. Genotype ranking in ascending order for the MGIDI index. The selected genotypes are shown in red in the electronic version of the article. The circle represents the cut-point according to the selection pressure.

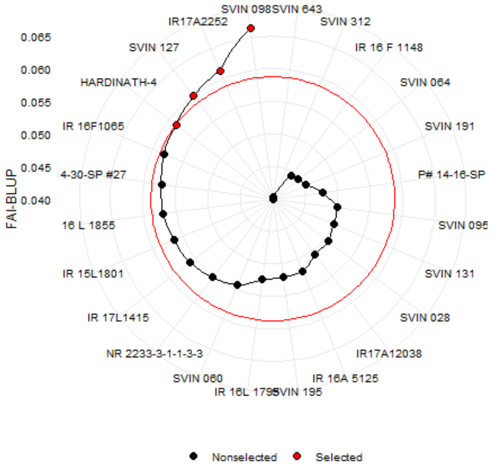

Fig. 2. Genotype ranking in ascending order for the FAI-BLUP. The selected genotypes are shown in red in the electronic version of the article. The circle represents the cut point according to the selection pressure.

MGIDI and FAI-BLUP Comparison

The comparison revealed that the MGIDI and FAI-BLUP achieved the desired gains across all evaluated traits. Specifically, the MGIDI index demonstrated a higher overall selection gain, with an improvement of 15.13% for traits targeted for enhancement and a reduction of -0.42% for traits requiring minimization. In contrast, the FAI-BLUP index improved by 1.25% for traits seeking enhancement and a reduction of -11.09% for traits needing minimization. This suggests that both indexes effectively meet breeding objectives, with MGIDI showing a more pronounced impact on enhancing desirable traits, while FAI-BLUP offers substantial reductions in traits requiring minimization.

Strength and Weakness view

The radar plot visualizes the strengths and weaknesses of various rice genotypes based on four factors (FA1, FA2, FA3, and FA4) contributing to the MGIDI index (Fig. *3*). FA1 includes DTF, DTM, and YD. FA2 encompasses PASQM and PH. FA3 covers TN and LN. FA4 includes PLL and CC.

Genotype SVIN 191 exhibited strong overall performance across all traits, particularly excelling in FA1 traits such as DTF, DTM, and YD. In contrast, SVIN 064 showed weaknesses in most traits, demonstrating lower FA1, FA3, and FA4 performance. Genotype SVIN 312 performed well in FA2 traits like PASQM and PH, while IR 18L 1855 showed strengths in FA3 traits such as TN and LN. Additionally, IR 16A 5125 performed consistently well in FA1 and FA2 traits, indicating a balanced genetic potential. Conversely, SVIN 028 and IR 15L 1801 exhibited weak performance across all factors, with slight strengths in specific FA2 and FA4 traits. These insights underscore the utility of the MGIDI index in identifying genotypes with superior trait performances and facilitating targeted breeding strategies.

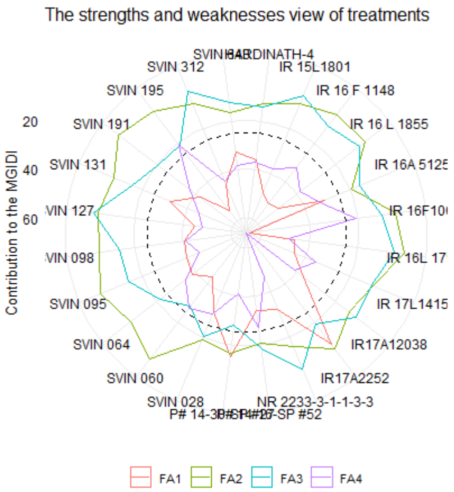

Fig. 3. The strengths and weaknesses of the selected genotypes are shown in the proportion of each factor on the computed multi-trait genotype–ideotype distance index (MGIDI). The most minor the proportion explained by a factor (closer to the external edge),

Discussion

Deviance Analysis, Variance Components, and Genetic Parameters

The findings from Azevedo et al. (2023) aligned with existing research which also showed lower narrow sense heritability for GY and high narrow sense heritability for PH. Additionally, GY is a quantitative trait that is significantly influenced by environmental factors (dos Reis et al., 2015; Li et al., 2018; Zhang et al., 2022) . Higher residual variance was observed in PLL and YD, consistent with Akhouri (2022), which identified higher residual variance in these traits within environments 1 and 2.

The high heritability in PH and DTM indicated their potential for use in breeding programs focused on enhancing adaptation and productivity. Despite the DTM and DTF are usually strongly correlated, their heritability differences can arise due to factors like environmental interactions and specific genetic loci. DTF is often more environmentally sensitive than DTM because flowering initiation is affected by temperature, photoperiod, and other growth conditions (González et al., 2016; Shi et al., 2022). This aligned with the views of De Oliveira Neto et al. (2021), who emphasized the importance of genetic variability in selecting superior genotypes for better agricultural performance. On the other hand, the low heritability and non-significant genotypic effects observed in TN and GY suggest that environmental factors play a more dominant role, supporting studies that highlight the environmental sensitivity of traits such as TN and GY.

Research by Pallavi et al. (2024) and Al-Ashkar et al. (2023) highlighted the importance of genetic factors in trait variation, especially within the MGIDI framework, which focuses on capturing genetic diversity. Their studies stressed the essential role of genotype effects in fostering genetic diversity, supporting the broader goal of improving crop resilience and adaptability through genetic enhancement strategies.

Eigenvalues and Varimax Factor Loadings:

Eigenvalues indicated the amount of variance each factor explains, with FA1 explaining 32.5% of the total Variance, followed by FA2 (16.2%), FA3 (15.6%), and FA4 (12.2%). The cumulative Variance showed that the first two factors explained 48.7% of the variance, and all four factors together explained 76.5%. This highlighted that the factors represent different combinations of traits contributing to the variability in the dataset, with higher eigenvalues indicating more influential factors (Eze et al., 2021). Al Mamun et al. (2024) and Palaniyappan et al. (2024) also reported the factors with Eigen value greater than 1 representing the most variability.

FA1, indicating this factor favored early flowering and maturing genotypes. TN was positively associated with FA3, implying this factor was related to higher tiller numbers. LN showed positive associations with FA1, FA2, and especially FA3, indicating a relationship with increased leaf production. PLL was negatively associated with FA4, suggesting this factor favors shorter panicle lengths. PASQM was strongly negatively associated with FA2, implying this factor favored genotypes with lower PASQM. The CC was positively associated with FA1 and FA3 but negatively with FA4, indicating factors FA1 and FA3 may favor higher chlorophyll content. YD was strongly positively associated with FA2, closely linking this factor to higher yields.

In the rice breeding program context, these factors guide genotype selection by highlighting key traits contributing to performance variability. Factors aligning with breeding objectives, such as increasing yield, can be prioritized in the selection process. Retaining principal components with eigenvalues exceeding 1, as suggested by Kaiser (1958) and supported by studies from Prasad et al. (2020), Pallavi et al. (2024), Bermudez and Pinheiro (2020) and Olivoto and Nardino (2021) demonstrates the robustness of factor analysis in distilling numerous traits into significant factors for breeding selection.

Predicted Selection Gain

The observed selection gains validated the robustness of the MGIDI and FAI-BLUP indexes in breeding programs, with significant improvements across evaluated traits. The MGIDI index demonstrated superior performance, particularly in traits like LN and TN, achieving higher overall gains. MGIDI showed a total gain of 15.13% for traits targeted for increase, compared to 1.25% for FAI-BLUP. MGIDI achieved -0.42% for traits targeted for decrease, whereas FAI-BLUP achieved -11.09%. This indicated that MGIDI is slightly more effective, especially for traits needing significant improvement, aligning with the objectives of enhancing genetic diversity and crop adaptability for sustainable agriculture. Similar findings by Olivoto and Nardino (2021) and Al-Ashkar et al. (2023) also reported success of MGIDI in selecting traits with genetic gain.

MGIDI and FAI-BLUP Comparison

The evaluation of MGIDI versus FAI-BLUP revealed that both indices are effective but with notable differences. MGIDI excelled with a 15.13% increase in traits targeted for enhancement and a minimal -0.42% reduction in traits that needed to be minimized, reflecting its robust performance in boosting desirable traits while maintaining others. Conversely, FAI-BLUP showed a smaller 1.25% gain in enhancement traits and a significant -11.09% reduction in traits requiring minimization. The MGIDI index's balanced approach to improving primary traits like grain yield without compromising secondary traits underscores its suitability for modern breeding programs, especially in light of the importance of stress-resilient traits discussed by Nelimor et al. (2020).

Strength and Weakness View

This analysis provided valuable insights for breeders by highlighting the strengths and weaknesses of various rice genotypes using the MGIDI. Genotype SVIN 191's robust performance across key traits, especially within FA1 (DTF, DTM, and YD), positioned it as a top candidate for breeding programs. Conversely, SVIN 064's underperformance across multiple factors, including FA1, FA3, and FA4, indicated areas that need improvement.

The favorable results of genotypes like IR 18L 1855, which exceled in FA3 traits (TN and LN), and IR 16A 5125, which showed balanced performance in FA1 and FA2 traits, underscored their potential to enhance rice production. While exhibiting weak overall performance, Genotypes SVIN 028 and IR 15L 1801 showed some strengths in specific FA2 and FA4 traits, suggesting targeted improvements might be beneficial.

In contrast, the weak performance of SVIN 051 and IR 17L 14 pointed to a need for significant enhancement or reconsideration for breeding use. The detailed evaluation of these strengths and weaknesses highlighted the potential of MGIDI as an effective tool for identifying and selecting genotypes with desirable traits, such as early seedling vigor and high grain yield. These insights were crucial for developing improved rice varieties and making strategic decisions in breeding programs, as emphasized by Pallavi et al. (2024).

Conclusion

This study evaluated genetic variability and heritability of key agronomic traits in rice genotypes using the MGIDI and FAI-BLUP methods. Significant genotype effects were identified for PH, DTF, and DTM, indicating their suitability for breeding programs focused on enhancing adaptability and productivity. High heritability estimates for these traits suggested robust genetic control, while lower heritability for YD and TN highlighted environmental influences. The analysis also demonstrated the MGIDI index superior performance in predicting selection gains, particularly for LN and TN, with selected genotypes like SVIN 191 showing strong potential. These findings underscored the importance of genetic diversity and strategic selection in rice breeding. Overall, the study supported the use of MGIDI as an effective tool for improving crop resilience and quality. Future research should focus on genotype- environment interactions and the application of multivariate techniques to further refine selection strategies.

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