Pertanika J. Trop. Agric. Sci. 48 (3): 1019 - 1040 (2025)

TROPICAL AGRICULTURAL SCIENCE

Journal homepage: http://www.pertanika.upm.edu.my/

Brown Plant Hopper Resistance in Promising Doubled Haploid Rice Lines Selected by MGIDI and FAI-BLUP Index

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ABSTRACT

Rice (*Oryza sativa* L.) is the main source of calories for the world's population but faces challenges from climate change and pest infestations, particularly the brown planthopper (BPH) in Indonesia. This study assessed agronomic traits, yield components, and resistance to BPH in 16 rice genotypes, comprising 14 doubled-haploid (DH) lines and two commercial varieties (Ciherang and Inpari 18). Genotype selection involved the Multi-Trait Genotype–Ideotype Distance Index (MGIDI) and Factor Analytic Index-Based Best Linear Unbiased Prediction (FAI-BLUP). Genotype-by-trait (GT) biplots were also utilized to visualize genotype performance across various traits. The response of the DH lines to BPH was assessed using biotypes 1, 2, and 3. The MGIDI-selected genotypes, were M-5, M-7, and M-12, which yielded 9.0-, 8.9-, and 9.6- ton ha^{-1}, respectively. They significantly surpassed yield of the commercial checks. M-5 and M-7 were also selected in the FAI-BLUP, while M-12 was not due to the advantage of trait weighting in the MGIDI analysis. These lines aligned with the selection goals based on the rice ideotype, demonstrating ideal agronomic performance. The effectiveness of both MGIDI and FAI-BLUP in the selection has shown promising results, explaining 100% of the variance among traits and resulting in predicted genetic gains indicating improvements in most traits. Two promising DH lines (M-5 and M-7) showed moderate resistance to BPH biotype 1 and moderately susceptible to biotype 2 while susceptible to biotype 3. This variability highlights the challenge of using these lines in different environments with those two BPH biotypes.

Keywords: Agronomic trait, BPH, doubled-haploid, multivariate selection, selection index

ARTICLE INFO

Article history:
Received: 03 September 2024
Accepted: 30 December 2024
Published: 16 May 2025

DOI: https://doi.org/10.47836/pjtas.48.3.20

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e-ISSN: 2231-8542

INTRODUCTION

Rice (*Oryza sativa* L.) provides 20% of the calorie intake required by humans worldwide and exceeds 70% of human calorie requirements in several Asian countries (Zhao et al., 2020). Of the total global rice production, 90.6% is produced in Asia (Mohidem et al., 2022). The majority of rice consumers were also in Asia, where from 2018 to 2020, the per capita rice consumption reached 77 kg per year. Meanwhile, in Latin America, Africa, Europe, Oceania, and North America, the per capita rice consumption levels were 28.0 kg, 27.4 kg, 13.5 kg, and 6.3 kg per year, respectively (Rahman & Zhang, 2023). According to the Food and Agriculture Organization of the United Nation ([FAO], 2021), rice consumption in low-income Asian countries such as Indonesia is expected to increase from 122 kg per capita per year in 2020 to 129 kg by 2030, following previous trends. According to data released by the United States Department of Agriculture ([USDA], 2023), to meet global rice demand, rice production in 2024 is projected to increase by 8.1 million tons from the previous year, with an estimate of reaching 520.9 million tons of dry paddy rice. However, this projection may not be reached due to production constraints, one of which is global climate change.

The Asian continent is the region most vulnerable to the impacts of global climate change (Queiroz et al., 2021). These impacts include unpredictable pest and disease attacks (Iqbal et al., 2023; Nguyen et al., 2023), which limit agricultural activities and threaten food availability. In 2020, approximately 720 to 811 million people worldwide experienced hunger, mainly due to climate change, conflict, and economic slowdowns (FAO, IFAD, UNICEF, WFP, & WHO, 2021). Global climate change is also leading to increasing water scarcity and land degradation problems, adding complexity to crop production (Hermans & McLeman, 2021). The impact of climate change significantly reduces rice yields (Habib-ur-Rahman et al., 2022). Therefore, the primary focuses in developing superior rice varieties in these conditions are high yields, good quality, resistance to pests and diseases, and tolerance to environmental stress (Rezvi et al., 2023).

Doubled haploid (DH) rice lines derived from anther culture can be used to accelerate the development of new varieties (Hadianto et al., 2023). An efficient selection method using a novel approach for genotype selection and treatment recommendation based on information on multiple traits that overcome the fragility of classical linear indexes called multi-trait genotype–ideotype distance index (MGIDI) has been proposed by Olivoto & Nardino (2021). The lack of varieties resistant to various pests and diseases is one of the main obstacles to achieving high rice production (Fahad et al., 2019). The worsening conditions of climate change and global warming are increasing abiotic stress and affecting the biological processes of biotic factors like pests and diseases, including their development, reproduction, and survival rates, and their interactions with host plants (Wang et al., 2022). Plants respond differently to abiotic factors compared to biotic factors, and most pests and diseases can co-evolve with the host plant, causing the host to remain vulnerable and increasing the potential for epidemics (Bhar et al., 2021). Therefore, developing hosts that are resistant to pests and diseases is considered a practical approach to addressing these challenges (Wang et al., 2021).

On average, 37% of global rice plantations experience yield loss due to pests and diseases every year. In particular, insects significantly limit high rice production (Rasool et al., 2020). The use of insecticides to control insects has reportedly led to an increase in secondary incidences, especially of the brown planthopper (BPH) (*Nilaparvata lugens*), and in the long term, has resulted in consistent resistance (Wu et al., 2018). The BPH, an important pest of rice plants, is widespread in tropical areas, especially in the Asia-Pacific region (Iamba & Dono, 2021). Peak BPH outbreaks in Indonesia occurred during La Nina in 2010 and 2011, affecting 137,481 hectares and 221,832 hectares, respectively, with estimated losses of around Indonesian Rupiah (IDR) 1,102 trillion in 2010 and IDR 1,740 trillion in 2011 (Baehaki & Mejaya, 2014). While the number of BPH attacks in Indonesia was lower in 2023, it is reported that the affected area increased by 1.4% from 6,068.2 hectares in 2022 to 8,511.53 hectares in 2023 (Forecasting Center for Plant Pest Organisms, 2023).

The severity of BPH attacks tends to increase under the conditions of global climate change (Ali et al., 2014). Continuous high temperatures caused by climate change affect the growth, fecundity, and reproductive fitness of the BPH. Such conditions may drive BPH migration to more suitable areas, potentially exacerbating damage in those environments (Yang et al., 2021). A study by Surmaini et al. (2024) models the impact of climate variability on the distribution of BPH in Indonesia, forecasting an increase in BPH-damaged areas from 2024 to 2060. Higher temperatures and rainfall during the dry season, especially linked to La Niña events, significantly influence BPH dynamics. Horgan et al. (2021) found that high temperatures reduce the effectiveness of anti-herbivore resistance in rice, affecting BPH distribution to suitable environments. The study also shows that resistant varieties lower adult survival at 20–25°C and nymph weight gain at 25°C, aligning with optimal temperatures for survival and development. Thereby enhancing rice production in changing climates.

Direct damage is caused by BPH-sucking plant fluids, leading to the drying and death of plants (hopper burn). Additionally, brown planthoppers are vectors that spread viruses, which cause extended yield losses and crop failure in rice plants (Jeevanandham et al., 2023). Therefore, it is important to develop high-yielding rice varieties with good agronomic performance and resistance to BPH in anticipation of the outburst of BPH attacks due to climate change. This research discussed the yield, important agronomic traits, and resistance of the DH rice lines to BPH.

MATERIAL AND METHODS

Yield Trial

Plant Material

A yield trial was conducted in Indramayu, West Java, in December 2023. The genetic material used in the yield trial was 14 DH rice lines (M-1 to M-14) and 2 check commercial varieties (M-15: Ciherang and M-16: Inpari 18), as listed in Table 1. Doubled haploid lines were obtained from anther culture of several F1s, specifically F1: Inpago 8 × IR8770514-11-B-SKI-12 (M-1 to M-3); F1: Inpago 8 × IR83140-B-11-B (M-4 to M-9); F1: B1111430D-MR-1-1-PN-3-MR-2-Si-3-PN × IR83140-B-11-B (M-10 to M-14).

Methods

The yield trial was arranged in a randomized complete block design (RCBD) with one factor, namely, the genotype, with 16 levels and three replications. The experimental unit was a plot measuring 4 m × 5 m, with a population density of 320 rice hills per plot. Maintenance included replanting, irrigation arrangements, fertilization, and pest and disease control. Harvesting occurred when 90% of the panicles in one plot were yellow.

Observation

Observations included agronomic traits and yield components, including vegetative (VPH) and generative plant heights (GPH), the number of vegetative tillers (NVT) and productive tillers per hill (NPT), the ages at flowering (FA) and harvest (HA), the number of filled (NFG) and unfilled grains (NUG), the weight of 1000 grains (W1000), and productivity (PRD). Observations were carried out on ten hills of sample plants per experimental unit.

Data Analysis

Genotype selection was performed based on simultaneous multiple traits selection using several approaches to compare the effectiveness of each selection method. The traits include all observed agronomic and yield component traits. The methods include the Multi-Trait Genotype–Ideotype Distance Index (MGIDI) (Olivoto & Nardino, 2021) and Factor Analytic Index-Based Best Linear Unbiased Prediction (FAI-BLUP) (Rocha et al., 2018). In addition, the Genotype by Trait (GT) biplot was utilized to visualize the relationships between genotypes and their performance across various traits. Analysis of variance (ANOVA) and posthoc LSD tests were conducted using SAS On Demand for Academics, while genotype selection analysis was performed using the metan R package (Olivoto & Lúcio, 2020). Genetic gains were compared using those analyses to determine the most effective approaches for selecting genotypes based on multiple trait selection using MGIDI and FAI-BLUP. This comparison contributes to more informed decision-making in breeding programs to improve crop performance.

Multi-Trait Genotype–Ideotype Distance Index (MGID) in this study was conducted with a selection percentage of 30% across multiple traits. Consequently, genotypes with lower MGIDI closer to the ideotype were chosen. The MGIDI index theory revolves around four steps, which were rescaled of the traits to a uniform range of 0 to 100, factor analysis to address the correlation structure and reduce data dimensionality, planning the ideotype based on the known or desired trait values, and finally, calculating the distance between each genotype and the planned ideotype (Olivoto & Nardino, 2021). In this study, the rescaled traits considered the desired direction of selection (increase or decrease) aligned with breeding objectives. The traits designated as increasing include NVT, NPT, PL, NFG, W1000, and PRD. Productivity (PRD) was given a weighting of (+) 3, considering productivity is a crucial target trait in rice breeding programs. Meanwhile, traits designated for the decrease were VPH, GPH, FA, HA, and NUG. In the biplot genotype ranking results from the MGIDI, the selected genotypes are those closest to the cut point according to the selection pressure. Strength and weakness plots were then used to analyze the proportion of MGIDI values.

Factor Analytic Index-Based Best Linear Unbiased Prediction (FAI-BLUP) was also conducted with a selection percentage of 30%, assigning maximum and minimum values for traits based on their desirable and undesirable traits, in alignment with the rice New Plant Type (NPT) ideotype. This approach mirrors the methodology used in MGIDI. Specifically, traits such as NVT, NPT, PL, NFG, W1000, and PRD were designated as desirable for maximum values (undesirable for minimum values). Conversely, traits including VPH, GPH, FA, HA, and NUG were considered desirable for minimum values (undesirable for maximum values). The analysis utilized best linear unbiased prediction (BLUP) values to rank genotypes based on their performance, incorporating factor analysis to capture the correlation structure among traits. The ideotype was then designed using factorial scores adjusted to reflect the ideal trait values (Rocha et al., 2018). Subsequently, the spatial probability was estimated using the genotype-ideotype distance to facilitate the ranking of genotypes.

The GT biplot was one of the GGE biplot methods used to study genotype-trait interaction data (Shojaei et al., 2022). An analysis was carried out to explore the interactions between genotypes and their performance across the various evaluated traits. This analysis provided insights into how specific traits contributed to overall performance and highlighted genotypes that were consistently superior or exhibited particular strengths of traits. In biplot analysis based on traits, genotypes were considered as lines and traits as testers, enabling the visualization of genotype performance and ranking genotypes with each trait.

Brown Plant Hopper (BPH) Evaluation

Plant Material

The Brown plant hopper evaluation was conducted at the Indonesian Center for Rice Standard Testing (ICRIST) greenhouse in Sukamandi, West Java, Indonesia. The same genetic material as in the Yield Trial was used (Table 1), adding BPH checks (PTB33 and IR74 as resistant and TN-1 as susceptible checks). BPH biotypes 1, 2, and 3 were used in the resistance evaluation. BPH biotypes were grouped according to their virulency to differential varieties (Chaerani et al., 2021).

Table 1
List of DH lines and check varieties

No	Genotype	No	Genotype
1.	M-1	9.	M-9
2.	M-2	10.	M-10
3.	M-3	11.	M-11
4.	M-4	12.	M-12
5.	M-5	13.	M-13
6.	M-6	14.	M-14
7.	M-7	15.	M-15
8.	M-8	16.	M-16

Note. DH lines obtained from another culture of several F_1s crosses F_1: Inpago 8 × IR8770514-11-B-SKI-12 (M-1 to M-3); F_1: Inpago 8 × IR83140-B-11-B (M-4 to M-9); F_1: B1111430D-MR-1-1-PN-3-MR-2-Si-3-PN × IR83140-B-11-B (M-10 to M-14). Check varieties: M-15: Ciherang; M16: Inpari 18

Methods

Brown plant hopper biotypes were propagated on susceptible rice plants (IR 42) in insect-rearing cages. The maintenance involved fertilizing, watering, weeding, and collecting egg masses to obtain adult BPHs for multiplication. Egg-laying occurred 40–45 days after transplanting (DAT) by transferring 25 pairs of male and female planthoppers to new plants in mylar buckets for 48 hours, after which they were returned to the stock cage. The eggs were kept until evaluation. One week later, 2–3 instar planthoppers were harvested for resistance evaluation. Genotypes were sown in plastic boxes filled with NPK-treated soil, with each furrow containing 25 seeds based on the genotype being planted.

The experiment was conducted with three replications. At the age of seven days, the plants were infested with two or three BPH nymph instars, with a density of eight individuals per stem. Observations were conducted when the susceptible check variety showed 90% death by calculating the level of damage based on International Rice Research Institute Standard Evaluation System (IRRI SES) as presented in Table 2. The

Table 2
Response of rice plants to brown planthopper attack

Score	Damage	Category
0	No damage	Resistant (R)
1	Very slight damage	Resistant (R)
3	First and 2nd leaves of most plants partially yellowing	Moderately resistant (MR)
5	Pronounced yellowing and stunting, or about 10% to 25% of plants wilting or dead, and remaining plants severely stunted or dying	Moderately susceptible (MS)
7	More than half of the plants are dead	Susceptible (S)
9	All the plants are dead	Highly susceptible (HS)

Source: IRRI SES (2013)

collected data were analyzed descriptively to compare the resistance of each genotype to the BPH biotype.

RESULTS AND DISCUSSIONS

Agronomic Performance and Yields of Tested Genotypes

The agronomic traits and yields of the tested genotypes varied (Table 3). The tested DH lines exhibited some characteristics of a new plant type, characterized by the high number of grains per panicle, productive tillers, sturdy stems, early harvest, and moderate plant height. Plant height modulated susceptibility to lodging and photosynthetic efficiency, and it had a relationship with environmental factors and cultivation management, as modeled by Confalonieri et al. (2011). Plant height also contributed to the canopy characteristics of rice plants, which was an essential aspect of plant protection against pests and diseases (Jing et al., 2023). Therefore, plant height is a focus in developing superior varieties. Eight DH lines, M-3, M-5 to M-7, and M-10 to M-13 had plant heights in the 80–125 cm range, which was ideal and equivalent to the commercial variety Inpari 18 (99.7 cm). The other DH lines had plant heights above 125 cm, but their height was still similar to Ciherang.

The tested DH lines had sufficient productive tillers, ranging from 15 to 19 per hill. The DH lines with productive tillers equivalent to Ciherang and Inpari 18 were M-1 to M-8. A high number of productive tillers in rice plants significantly increases yields and production efficiency because more panicles could increase the grains per unit of land area and the total yield. A tiller behavior study found that more panicles in tillers produced higher yields (Srimathi & Subramanian, 2022). In addition, a study by Huang et al. (2020) revealed that around 85% of the variation in the total grain number was caused by the primary tiller grain yield, which was positively related to primary tiller panicles.

Plant age was another critical characteristic that was taken into account. Ideally, superior rice varieties mature between 105 and 124 days after sowing (DAS). Based on flowering and harvesting age observations, Inpari 18 had early flowering and harvesting ages of 74 DAS and 107 DAS, respectively. The M-4 line was identified as having a harvest age equivalent to Inpari 18, namely 107 DAS, with a flowering age close to 77 DAS. All the tested DH lines were classified as having early maturity, and some outperformed Ciherang (119 DAS).

A rice plant's yield is determined by the sink size, which includes the number of grains, the percentage of filled grains, and the weight of 1000 grains (Mai et al., 2021). A high weight of 1000 grains means that each grain of rice has a greater mass, indicating good yields if other factors are ideal. Nine of the tested DH lines, namely, M-3 and M-7 to M-14, had significantly higher numbers of filled grains than the two check varieties. Most DH lines showed 1000-grain weights in the 25–30 g range, with one line, M-12, having a significantly higher weight of 34 g for 1000 grains than the check varieties.

Table 3
Agronomic performance and yield of 16 rice genotypes

Genotype	**VPH**	**GPH’**	**NVT**	**NPT**	**FA**	**HA**	**PL**	**NUG’**	**NFG**	**W1000**	**PRD**
M-1	92.8	150.3	20.2	17.9	85.7	122.0	27.3	29.9	111.2	31.0	6.5
M-2	85.6	134.2	21.2	19.7	87.0	121.0	27.3	30.3	110.4	30.0	8.4
M-3	85.4	112.5	21.4	19.4	86.3	121.0	26.5	40.3	162.1	26.7	7.6
M-4	84.5	139.9	21.3	18.8	77.7	107.0	26.9	62.2	110.0	27.0	3.2
M-5	65.1	93.2	21.6	18.0	79.0	111.0	27.0	25.8	157.1	26.0	9.0
M-6	65.2	92.6	22.0	18.6	79.0	111.0	25.4	22.0	153.8	24.0	7.9
M-7	89.0	119.5	20.0	17.8	82.0	113.0	28.5	24.3	175.0	27.7	8.9
M-8	92.8	142.5	19.4	16.9	82.7	116.0	29.8	32.7	177.1	25.3	7.9
M-9	99.0	151.3	18.4	16.2	81.0	114.3	31.7	35.6	184.2	26.7	7.5
M-10	78.8	112.5	20.2	15.2	90.3	121.3	27.8	35.1	169.4	26.0	8.1
M-11	84.5	113.3	19.8	15.4	83.3	118.0	25.8	32.1	186.7	27.7	9.0
M-12	84.0	114.6	19.4	15.8	83.3	115.7	25.9	34.8	174.4	34.0	9.6
M-13	92.0	120.0	19.7	15.7	90.3	118.0	28.1	37.2	184.8	26.3	7.0
M-14	95.8	127.9	18.9	15.9	92.0	118.0	27.0	42.1	183.1	26.3	6.1
M-15	76.5	141.7	22.6	19.8	85.0	119.7	25.8	24.7	127.2	26.0	7.2
M-16	82.9	99.7	20.4	18.3	74.0	107.0	25.6	29.9	137.5	32.3	7.5
Average	84.6	122.9	20.4	17.5	83.7	115.9	27.3	33.7	156.5	27.7	7.6
Pr> F	<0.001**	0.0001**	<0.001**	<0.001**	<0.001**	<0.001**	<0.001**	0.0004**	<0.001**	<0.001**	<0.001**
CV (%)	2.1	2.6	3.1	5.8	1.8	0.4	2.2	6.2	7.9	3.1	8.0
LSD	2.9	31.6	1.0	1.7	1.65	0.78	1.0	11.8	20.5	1.4	1.0

Note. ’= Data have been transformed using the logarithm (log[x]). *Pr> F*= Probability of *F* value in the ANOVA test, *CV*= Coefficient of variation (%), ** highly significant difference at α= 0.01, ^{ns}= not significantly different at α= 0.05, *LSD*= critical value of *LSD* test to determine the significance of the difference between the means at α= 0.05. VPH= vegetative plant height (cm), GPH= generative plant height (cm), NVT= number of vegetative tillers per hill, NPT= number of productive tillers per hill, FA= flowering age (day after sowing), HA= harvesting age (day after sowing), PL= panicle length (cm), NUG= total number of unfilled grains, NFG= number of filled grains, W1000= 1000-grain weight (g), PRD= productivity (t ha^{-1})

As one of the essential traits in evaluating the performance of genotypes, panicle length was studied in this research. The panicle lengths of the DH lines M-3, M-6, M-11, and M-12 were equivalent to those of the two check varieties. In comparison, the other DH lines had improved panicle lengths significantly longer than those of the two check varieties, ranging from 26.9 to 31.7 cm.

Productivity is the primary consideration because the ideal variety must produce high yields per unit land area. In general, the productivity of the tested DH lines varied. The rice lines M-2, M-5, M-7, M-11, and M-12 showed significantly higher productivity than Ciherang. Except for M-2 (equivalent to Inpari 18), these lines also exhibited significantly higher productivity than Inpari 18. Selection to identify potential high-yield DH lines with desirable ideotypes could be done using simultaneous multi-trait selection methods based on agronomic traits and yield components (Baraki et al., 2024; Olivoto & Nardino, 2021).

In this study, genotype selection was performed using the MGIDI described by Olivoto and Nardino (2021) and FAI-BLUP by Rocha et al. (2018). The Multi-Trait Genotype–Ideotype Distance Index (MGIDI) and the Factorial Analysis of Interaction Best Linear Unbiased Prediction (FAI-BLUP) explained 100% of the variance among the traits through the principal components PC1-PC11 (Table 4). There were slight differences in the proportions of variance explained by each principal component, which were negligible. Thus, the overall explanatory power of both methods remained comparable. This indicated that while specific components might capture varying amounts of variance, the methods effectively represented the underlying data structure across all traits, reflecting their robustness in genotype selection.

Table 4
Principal components, eigenvalues, and cumulative variance in MGIDI and FAI-BLUP

MGIDI			**FAI-BLUP**		
PC	**Eigenvalue**	**Cum. var (%)**	**PC**	**Eigenvalue**	**Cum. var (%)**
PC1	3.90	35.4	PC1	3.87	35.22
PC2	2.38	57.1	PC2	2.37	56.75
PC3	1.70	72.5	PC3	1.69	72.16
PC4	1.31	84.4	PC4	1.33	84.23
PC5	1.06	94.1	PC5	1.07	93.99
PC6	0.25	96.3	PC6	0.23	96.07
PC7	0.20	98.2	PC7	0.22	98.07
PC8	0.11	99.2	PC8	0.12	99.15
PC9	0.06	99.7	PC9	0.06	99.68
PC10	0.03	99.9	PC10	0.03	99.89
PC11	0.01	100.0	PC11	0.01	100.00

Note. PC= principal component, Cum.var= cumulative variance

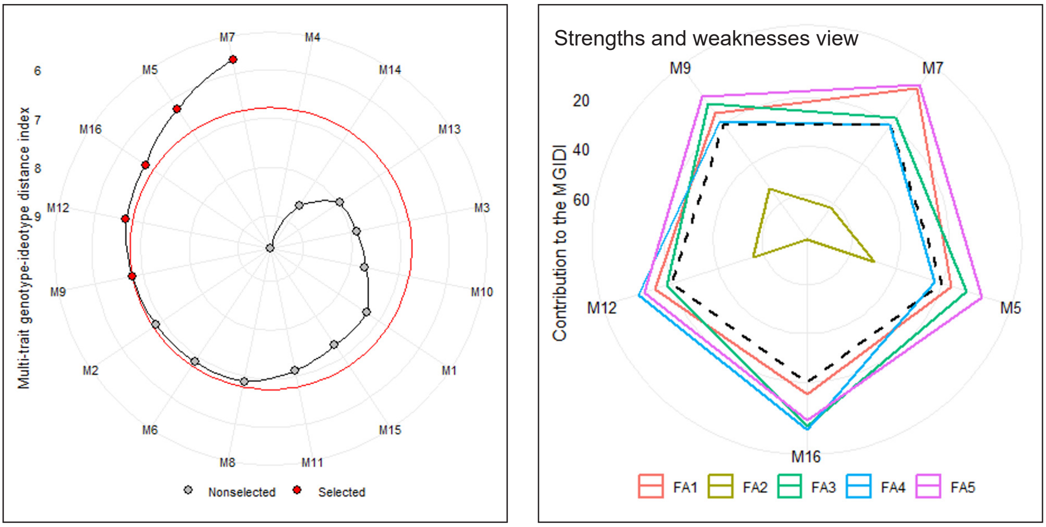
In both MGIDI and FAI-BLUP analyses, the observed traits were grouped into five factors (FA), as shown in Table 5. The MGIDI index selected the genotypes M-7, M-5, M-12, M-16 (Inpari 18), and M-9 (Figure 1[a]). Among these selected genotypes, MGIDI shares three lines with the FAI-BLUP index, which were M-7, M-16, and M-5. The genotypes selected by FAI-BLUP were M-7, M-16, M-5, M-8, and M-6 (Figure 2). Based on the predicted genetic gain, MGIDI demonstrated superior performance compared to FAI-BLUP for traits expected to increase in value, such as panicle length, productivity, W1000, number of vegetative and productive tillers, and number of filled grains. This is evident from the higher total increase in predicted genetic gain values for these traits, as shown in Table 5. Conversely, for traits where the selection goal is to decrease, FAI-BLUP outperformed MGIDI, with a higher total decrease in predicted genetic gain across traits such as vegetative and generative plant height, number of unfilled grains, flowering age, and harvesting age.

Each trait remains important in developing the ideal rice genotype. Thus, both MGIDI and FAI-BLUP can be effectively used to select and provide options for breeders. The higher predicted genetic gain values for traits targeted for enhancement under MGIDI and FAI-BLUP emphasize their advantage in selecting genotypes that better meet breeding objectives. In the context of traits targeted for increase, the more positive total increase in predicted genetic gain, such as 11.48% in MGIDI compared to 4.22% in FAI-BLUP, indicates a stronger addition. Meanwhile, the more negative total decrease in predicted

Table 5
Factor analysis and predicted genetic gain for MGIDI and FAI-BLUP indexes

Trait	**Factor analysis**		**Goal**	**Predicted genetic gain (%)**	
	MGIDI	**FAI-BLUP**		**MGIDI**	**FAI-BLUP**
VPH	FA1	FA1	Decrease	-0.62	-5.61
GPH	FA1	FA1	Decrease	-0.07	-0.10
PL	FA1	FA1	Increase	0.46	-0.03
NUG	FA2	FA2	Decrease	-0.12	-0.19
PRD	FA2	FA2	Increase	0.91	0.64
FA	FA3	FA3	Decrease	-3.80	-4.32
HA	FA3	FA3	Decrease	-3.67	-4.27
W1000	FA4	FA4	Increase	1.65	-0.62
NVT	FA5	FA5	Increase	-0.45	0.26
NPT	FA5	FA5	Increase	-0.24	0.45
NFG	FA5	FA5	Increase	9.14	3.52
Total (Increase)				11.48	4.22
Total (Decrease)				-8.26	-14.49

Note. VPH= vegetative plant height, GPH= generative plant height, PL= panicle length, NUG= number of unfilled grains, PRD= productivity, FA= flowering age, HA= harvesting age, W1000= 1000-grain weight, NVT= number of vegetative tillers per hill, NPT= number of productive tillers per hill, NFG= number of filled grains



(a) (b)

Figure 1. (a) Genotype ranking in ascending order for the MGIDI index with a selection pressure of 30%; the selected genotypes were shown in red dot, and the circle represents the cutpoint according to the selection pressure. (b) The strengths and weaknesses of the selected genotype are shown in the proportion of each factor on the computed multi-trait genotype–ideotype distance index (MGIDI). The factor contributing the most to selection is represented by the polygon closest to the center of the MGIDI. Genotype strength in a specific factor is indicated by the outermost polygon nearest to the genotype. The closer the genotype is to the outer polygon of a factor, the stronger its performance for the traits grouped under that factor. The dashed line shows the theoretical value if all the factors had contributed equally. FA1= vegetative plant height, generative plant height, and panicle length, FA2= number of unfilled grains and productivity, FA3= flowering age and harvesting age, FA4= 1000 grain weight, FA5= number of vegetative tillers and productive tillers per hill and number of filled grains

genetic gain, such as -14.49% in FAI-BLUP compared to -8.26% in MGIDI, reflects a stronger reduction, aligning with the selection goal. These results further support the effectiveness of both methods in achieving breeding objectives.

When examining the differences, MGIDI showed a slightly higher predicted genetic gain than FAI-BLUP, with MGIDI being 1.02% higher than FAI. These results were consistent with Olivoto and Nardino (2021), which demonstrated that the performance of the MGIDI index in selecting superior genotypes based on multi-trait data surpassed that of classical indices,

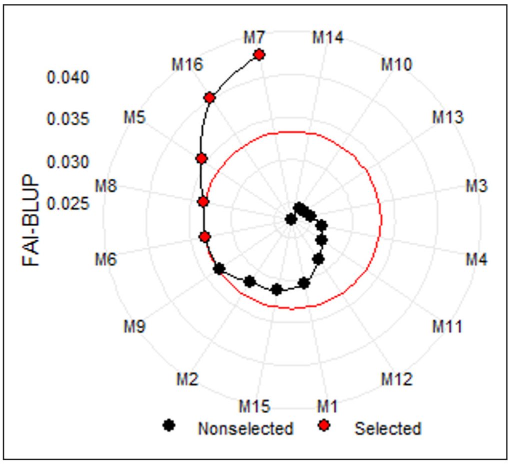


Figure 2. Genotype ranking based on the FAI-BLUP method with a selection percentage of 30%. The selected genotypes were highlighted with red dots, and the circle indicates the cut point corresponding to the selection pressure applied

including the Smith-Hazel (SH) index, a widely-used base linear phenotypic selection index, as well as modern methods like FAI-BLUP, thereby aiding practitioners in making more effective strategic decisions for multivariate selection in biological experiments. Various researchers have used MGIDI and revealed its effectiveness in selecting superior genotypes while simultaneously considering multiple traits (Al Mamun et al., 2024; Baraki et al., 2024; Klein et al., 2023; Mamun et al., 2022; Pallavi et al., 2024; Raj et al., 2024).

Multi-Trait Genotype–Ideotype Distance Index (MGIDI) is considered superior to FAI-BLUP for several reasons. First, in MGIDI, the breeder could lead the direction of selection for each trait by assigning 'h' (high) for traits intended to increase and 'l' (low) for traits intended to decrease (Olivoto et al., 2022; Debnath et al., 2024). Although FAI-BLUP can also specify the direction of selection by assigning "max" and "min" for traits that are desired to increase and decrease, MGIDI offered an additional advantage by allowing breeders to apply weightings to traits based on their economic importance or alignment with breeding goals. For example, in this study, a trait like productivity (PRD) was given higher weight than other traits to reflect its importance in the rice breeding program. In contrast, FAI-BLUP does not provide this option for weighting traits, which limits its customization for specific breeding priorities. This explained the two genotypes not selected by FAI-BLUP but selected by MGIDI, i.e., M-12 and M-9, due to their superior traits. The productivity trait was given a higher weight than other traits (+3) in the MGIDI analysis, so M-12 was selected due to its high productivity. As a result, this genotype performed better under the MGIDI index. M-9, due to its high number of filled grains, was selected following the predicted genetic gain for the goal of an increase in MGIDI. The number of filled grains had a predicted genetic gain of 9.14% compared to only 3.52% in FAI-BLUP.

Moreover, MGIDI offers a visualization of the strengths and weaknesses of each selected genotype through factor analysis (Figure 1[b]), which allows breeders to understand why certain genotypes were selected (Olivoto & Nardino, 2021). This visual representation could clarify specific traits that contributed to the genotypes' selection, providing deeper insights into their overall performance. FAI-BLUP, on the other hand, lacks this further visualization and only identifies which genotypes were selected. Therefore, MGIDI is a more powerful tool for breeders, as it allows customization through trait weighting and provides visual insights to support the selection process.

The selected genotypes by MGIDI were M-7, M-5, M-12, M-16 (Inpari 18), and M-9. In Figure 1(b), it can be seen that FA2 (NUG and PRD) made the largest contribution to the MGIDI. The strengths of these lines are as follows: M-5 is strong in PRD, FA, HA, VPH, and GPH; M-7 is strong in PRD, VPH, GPH, NFG, FA, HA, and W1000; M-12 demonstrates strength in PRD, W1000, NFG, VPH, GPH, FA, and HA; and M-9 is strong in NFG, HA, FA, and PL. M-16 (Inpari 18) is slightly weaker in FA1 (VPH, GPH, and PL). This finding aligns with the description of the Inpari 18 variety, known for its relatively shorter plant height, approximately ±93 cm (in this study, it measured 99.7 cm).

Biplot genotype by trait (GT) biplot type 3, also known as the "which-won-where" biplot, visualizes the interaction of traits with genotypes (Figure 3). The polygon formed connects the outer genotype (those with the most extended vectors from the center of the polygon) in all directions. Dashed lines drawn from the center of the polygon divide the traits into sections. The genotypes on the outer edges of the polygon indicate extreme performance in specific traits. In contrast, genotypes near the center of the polygon are generally more stable. Genotypes M5 and M6 are among the outer corner of the polygon and demonstrate good performance in specific traits, with M5 leaning towards PRD (evidenced by a PRD value of 9.0 t ha^{-1}) and M6 leaning towards NVT, indicated by its high value corresponding to their positions on the polygon. Genotype M-9 is another outer genotype in the area with PL, FA, HA, and VPH traits. Among these traits, M-9 is closest to PL, highlighting M-9's superiority in PL. Genotype M-12 is the outermost genotype closest to PRD (demonstrated by the highest PRD among all genotypes), followed by genotypes M-11 and M-7, which also exhibit high PRD and tend to be closer to the center of the polygon, indicating consistently average performance across all traits. These results do not precisely align with the strengths and weaknesses observed in MGIDI, as MGIDI considers various factors that may not be fully reflected in the two principal components (PC1 and PC2) of this biplot, which together explain approximately 57.1% of the total variance among traits.

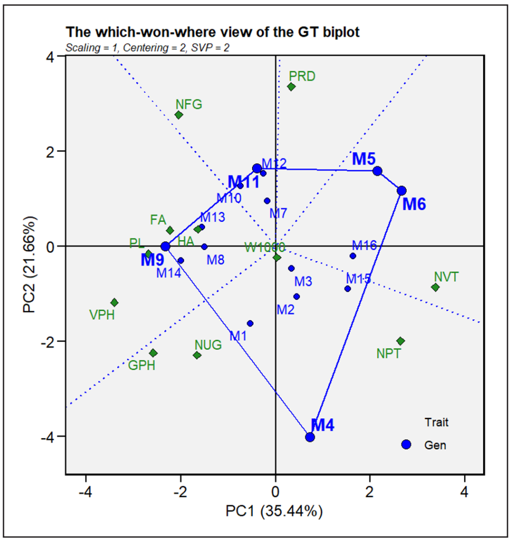


Figure 3. Which-won-where view of the genotype by trait biplot. Genotypes are labeled with blue circles, and traits with green diamonds. The biplot captures 57.1% of the total variance among traits, with PC1 accounting for 35.44% and PC2 for 21.66%. GT= genotype by trait, SVP= singular value partitioning, PC= principal component

Resistance of Tested Genotypes to Brown Planthoppers

Several DH lines (M-2 to M-9) demonstrated moderate resistance to biotype 1 brown planthopper (BPH) but exhibited varied responses to biotypes 2 and 3 (Figure 4). Specifically, resistance levels ranged from moderately resistant (M-2, M-3, and M-4) to moderately susceptible (M-5, M-6, M-7, M-8, and M-9) against biotype 2, and from moderately susceptible (M-2, M-3, and M-6) to susceptible against biotype 3. The tested DH lines mostly exhibited better resistance to BPH biotypes 1 and 2 than to biotype 3. This variation in resistance underscores the challenges of deploying these lines in diverse environments where different biotypes may dominate. However, their ability to resist BPH biotypes 1 and 2 offers hope for protecting rice plants from BPH attacks. Lines with varying susceptibility require careful consideration, including thorough surveys to identify prevalent biotypes, which is essential for selecting suitable resistant varieties. In the future, farmers can reduce yield losses from BPH infestations and enhance overall productivity by using BPH-resistant varieties derived from the lines.

Varying resistance levels to brown planthopper (BPH) biotypes pose a significant challenge in developing durable resistant rice varieties (Baehaki & Mejaya, 2014). Those responses underscore the complex interactions between host plant genetics and BPH biotype characteristics. Zheng et al. (2021) note that resistance variations reflect the differing virulence of BPH among rice varieties, which depends on the specific resistance genes present in host plants. Currently, 70 BPH-resistant gene loci have been identified in rice, and 17 genes have been successfully cloned (Yan et al., 2023). Four BPH biotypes have been identified and correspond to specific resistance genes with the prefix *Bph/bph* genes. BPH biotype 1 could not infest plants with major resistance genes, while biotype 2 could infest plants with the *Bph*$_1$ gene.

Furthermore, the *Bph*$_1$ gene provides resistance to biotypes 1 and 3, the *bph*$_2$ gene offers resistance to biotypes 1 and 2, and *Bph*$_3$, *bph*$_4$, *bph*$_8$, and *Bph*$_9$ confer resistance to all four biotypes, whereas *bph*$_5$, *Bph*$_6$, and *bph*$_7$ provide resistance only to biotype 4 (Cheng et al., 2013). BPH biotypes 1 and 2 are common in East and Southeast Asia, biotype 3 originated from laboratory breeding, and biotype 4 is prevalent in the Indian subcontinent. BPH

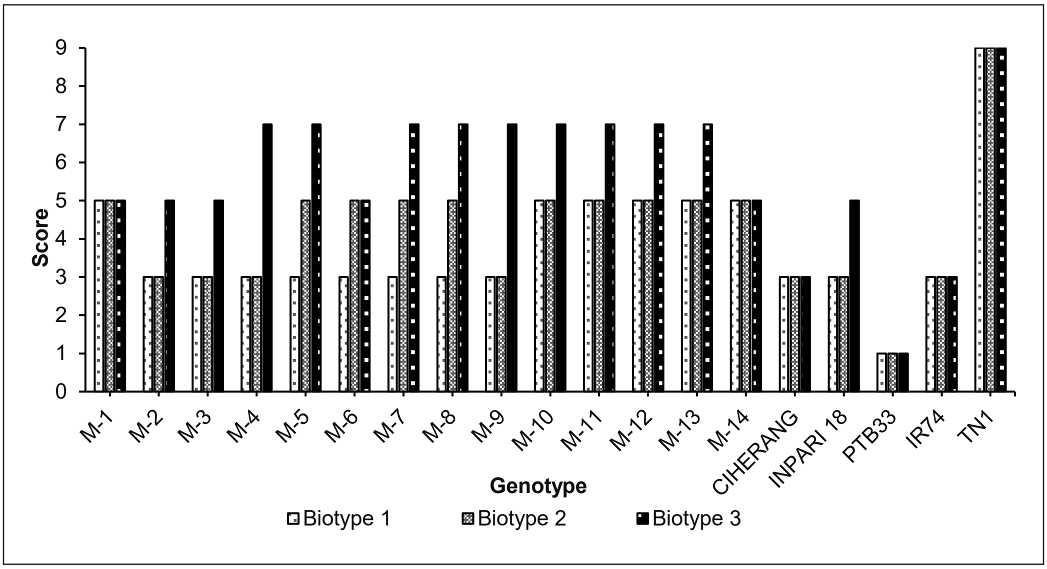


Figure 4. Bar diagram of resistant scoring on test genotypes to brown planthopper biotypes 1, 2, and 3. Score 0-1= resistant, 3= moderately resistant, 5= moderately susceptible, 7= susceptible, 9= highly susceptible. PTB33 and IR74= resistant check, TN1= susceptible check

distribution varies with environmental conditions and agricultural practices, as shown by Surmaini et al. (2024), who modeled BPH biotype distribution based on climate suitability, identifying regions in southern Indonesia as particularly favorable.

The TN-1 variety, serving as a susceptibility check for BPH, exhibited a high susceptibility to the three biotypes of BPHs (Figure 4). This aligns with the findings of Chaerani et al. (2021), who confirmed that TN1 lacks a single *Bph* (brown planthopper) gene, making it susceptible to all biotypes of BPHs. *Bph* is the gene for resistance to brown planthoppers. The resistance check, PTB33, is reported to have three Bph genes, BPH_2, BPH_{17}-*ptb*, and BPH_{32}, causing durable resistance (Nguyen et al., 2021). That aligns with the results of this study, as PTB33 showed resistance to all BPH biotypes tested. IR74 is reported to have the BPH_3 locus, which can overcome Biotype 3 (Jena & Kim, 2010). The evaluation results for IR74 showed moderate resistance to all biotypes and were equivalent to popular rice varieties such as Ciherang. Meanwhile, the commercial variety Inpari 18 showed moderate resistance to Biotypes 1 and 2 but was moderately susceptible to Biotype 3.

Selected DH Lines and Their Resistance to BPH

All DH lines significantly varied in agronomic traits and yield components, with several lines showing promising characteristics. The field performance of the four selected rice genotypes is shown in Figure 5. Three out of the four selected DH lines based on MGIDI significantly outperformed the commercial varieties Ciherang and Inpari 18 in terms of yield, with M-7, M-5, and M-12 yielding 8.9-, 9.0-, and 9.6- ton ha^{-1}, respectively. Among these, M-7 and M-5 were also selected by FAI-BLUP, highlighting their consistent performance across both selection methods. M-12, previously selected by MGIDI, was not chosen by FAI-BLUP, likely due to its higher productivity, which was weighted more heavily in the MGIDI analysis. These three DH lines demonstrated desirable agronomic traits, including ideal plant height (93.2–119.5 cm), a good number of productive tillers, and a high grain number per panicle (Table 3).

Particularly, M-5, M-7, and M-12 showed notable strength based on MGIDI strengths and weaknesses in traits such as PRD, FA, HA, VPH, GPH, NFG, and W1000, making them ideal candidates for future breeding programs focused on improving rice yield and performance (Figure 1[b]). Regarding brown planthopper (BPH) resistance, M-5 and M-7 showed moderate resistance to biotype 1 and moderate susceptibility to biotype 2, while the M-9 line demonstrated moderate resistance to both biotypes 1 and 2. In contrast, M-12 shows susceptibility to biotypes 1 and 2. However, all lines were susceptible to biotype 3 (Table 6). This suggests that although the lines exhibit some resistance, further breeding efforts are necessary to enhance resistance to all BPH biotypes, especially biotype 3. Utilizing suitable resistant varieties for the dominant BPH biotypes in a given environment will help farmers reduce yield losses from brown planthopper (BPH) infestations and enhance overall productivity.

The response of the selected genotypes based on the MGIDI analysis was presented in Table 6, with the selection criteria aligned with the ideal ideotype based on the Rice New Plant Type, characterized by a high number of grains per panicle, productive tillers, early harvest, and moderate plant height, along with BPH resistance. Among these lines, M-5 and M-7 stand out for their superior yields, agronomic performance, and resistance to BPH, as well as their consistent selection in both MGIDI and FAI-BLUP analyses, which aligned with the breeding goals and ideal genotype traits, making them promising candidates for future varietal development. Genotype selection using MGIDI has proven slightly more effective than FAI-BLUP in identifying these superior lines, as it offers the ability to apply trait weighting. Additionally, the biplot genotype by trait (GTB) provided valuable insights into genotype performance. For future studies, it is recommended that additional multi-environment trials be conducted to confirm their stability and adaptability.

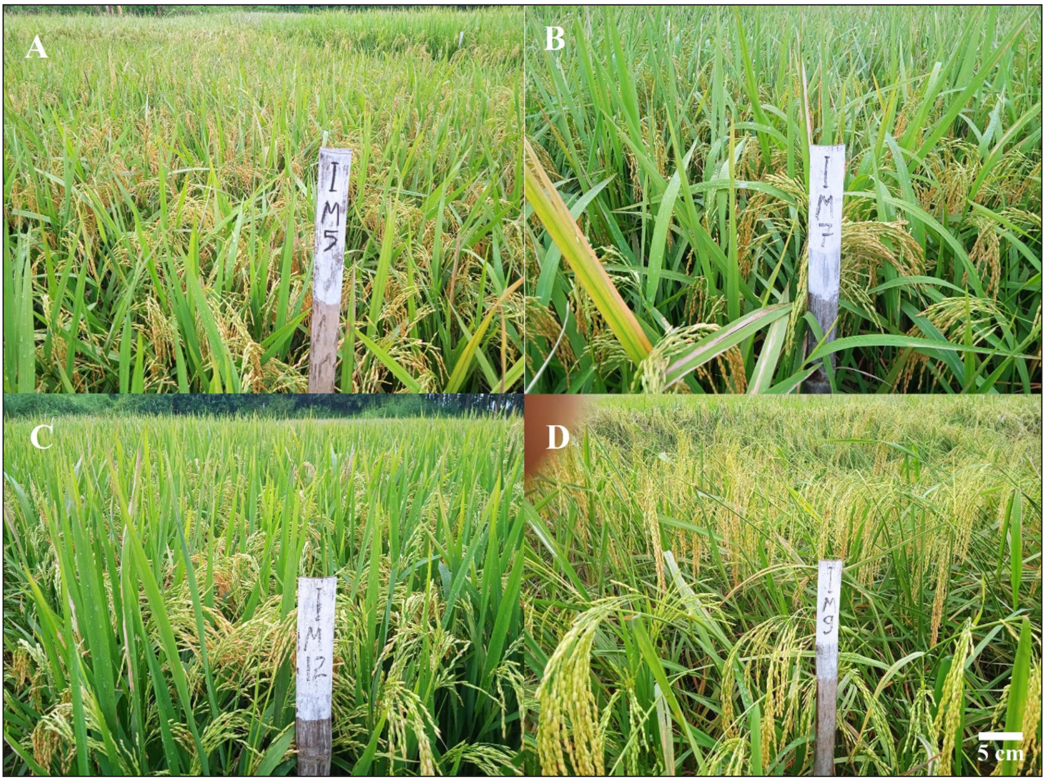


Figure 5. Field performance of four selected rice genotypes: (A) M-7, (B) M-5, (C) M-12, and (D) M-9 based on MGIDI. The photograph illustrates the agronomic appearance of the selected doubled-haploid lines in the field at the reproductive stage

Table 6
Agronomic traits, yield components, and BPH resistance of selected doubled-haploid lines based on MGIDI compared with check varieties

Traits	Doubled-haploid lines				Check variety	
	M-7	M-5	M-9	M-12	M-15	M-16
Agronomic Traits and Yield Components						
GPH	119.5	93.2	151.3	114.6	141.7	99.7
NPT	17.8	18.0	15.8	15.8	19.8	18.3
FA	82.0	79.0	82.0	83.3	85.0	74.0
HA	113.0	111.0	114.3	115.7	119.7	107.0
PL	28.5	27.0	31.7	25.9	25.8	25.6
NFG	175.5	157.1	184.2	174.4	127.2	137.5
NUG	24.3	25.8	35.6	34.8	24.7	29.9
W1000	27.7	26.0	26.7	34.0	26.0	32.3
PRD	8.9	9.0	7.5	9.6	7.2	7.5
Response to Brown Planthopper						
Biotype 1	MR	MR	MR	MS	MR	MR
Biotype 2	MS	MS	MR	MS	MR	MR
Biotype 3	S	S	S	S	MR	MS

Note. M-15= Ciherang, M-16= Inpari 18, GPH= generative plant height (cm), NPT= number of productive tillers per hill, FA= flowering age (days after sowing), HA= harvesting age (days after sowing), PL= panicle length (cm), NUG= total number of unfilled grains, NFG= the number of filled grains, W1000= 1000-grain weight (g), PRD= productivity (t ha^{-1}), MR= moderately resistant, MS= moderately susceptible, S= susceptible

CONCLUSION

The genotypes selected through the MGIDI index exhibited yields exceeding the commercial checks, with M-5, M-7, and M-12 yielding 9.0-, 8.9-, and 9.6- ton ha^{-1}, respectively. M-5 and M-7 were also selected in the FAI-BLUP analysis, while M-12 was not due to the advantage of weighting in the MGIDI analysis. These lines also demonstrate superior agronomic traits and yield components, including ideal plant height, a good number of productive tillers, a high filled grain number per panicle, and early maturity. The effectiveness of both MGIDI and FAI-BLUP in the selection has shown promising results, explaining 100% of the variance among traits and resulting in predicted genetic gains indicating improvements in most traits. The M-5 and M-7 lines show moderate resistance to BPH biotype 1 and moderate susceptibility to biotype 2, marking them as the most promising genotypes. Utilizing suitable resistant varieties based on the dominant BPH biotypes in the field will help farmers reduce yield losses and enhance productivity. However, conducting multi-environment trials to confirm the stability and adaptability of those lines, along with their resistance evaluation to other main rice diseases, is recommended to ensure robust performance across diverse environments.

ACKNOWLEDGMENTS

The authors acknowledge funding support for this research from the National Research and Innovation Agency (BRIN) and the Indonesia Endowment Funds for Education (LPDP) through the Riset dan Inovasi untuk Indonesia Maju (RIIM) Scheme, contract numbers 18/IV/KS/06/2022 and 4830/IT3.L1/PT.01.03/P/B/2022, and from Riset Aksi IPB, contract number 41079/IT3.D10/PT.01.03/P/B/2023. The authors also wish to thank the Indonesian Center for Rice Instrument Standard Testing (ICRIST), Sukamandi, for its assistance in brown plant hopper evaluation.

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