Research Article

Multivariate Selection of Doubled Haploid Rice Lines Based on Agronomic Traits and Blast Resistance

Bambang Sapta Purwoko[1*], Iswari Saraswati Dewi[2], Ratna Kartika Putri[1] and Iskandar Lubis[1]

[1]Department of Agronomy and Horticulture, Faculty of Agriculture, IPB University, Bogor, Indonesia; [2]Research Organization of Agriculture and Food, National Research and Innovation Agency (BRIN), Bogor, Indonesia.

Abstract | Breeding high-yielding and blast-resistant rice cultivars is essential to sustain rice production under increasing disease pressure and environmental challenges. Integrating multiple agronomic traits through multivariate approaches and blast-resistance can improve the efficiency of selecting superior genotypes. Therefore, this study aims to evaluate 14 advanced doubled-haploid (DH) rice lines and two check varieties for agronomic performance and blast resistance. Yield trials were conducted under field conditions at Field Experimental Station in Sukabumi, West Java, while Blast resistance screening was performed in a controlled greenhouse environment at Installation for Testing and Development of Agricultural Instrument Standards (IP2SIP), Bogor, West Java, using four distinct races of blast pathogen *Pyricularia oryzae* (033, 073, 133, and 173). Correlation and path analyses identified days to flowering, days to harvest, panicle length, and grain traits as key contributors to yield. These traits were subsequently used in a multi-trait genotype-ideotype distance index (MGIDI) analysis, in which genotypes M7, M9, M11, and M14 were selected based on agronomic performance, showing a 17.5% increase in grain yield compared with the population mean. Blast resistance was evaluated using hierarchical clustering of ordinal disease scores, with the optimal grouping determined by silhouette width. M13 and M14 clustered closely with the resistant check, while M3, M9, M10, M5, M7, M6, M8, M1, M4, and M16 showed similar resistance patterns. In contrast, M11 and M12 clustered with the susceptible check, indicating high susceptibility across races. Considering both agronomic performance and blast resistance, M7, M9, and M14 were identified as the most promising lines, combining high yield potential with favorable resistance profiles for future varietal development and breeding.

Received | November 24, 2025; **Accepted** | February 23, 2026; **Published** | June 04, 2026
***Correspondence** | Bambang Sapta Purwoko, Department of Agronomy and Horticulture, Faculty of Agriculture, IPB University, Bogor, Indonesia; **Email:** bspurwoko@apps.ipb.ac.id
Citation | Purwoko, B.S., I.S. Dewi, R.K. Putri and I. Lubis. 2026. Multivariate selection of doubled haploid rice lines based on agronomic traits and blast resistance. *Sarhad Journal of Agriculture,* 42(2): 975-990.
DOI | https://dx.doi.org/10.17582/journal.sja/2026/42.2.975.990
Keywords | Doubled haploid, Multivariate analysis, *Pyricularia oryzae*, Rice blast, Resistance, Yield

Introduction

Rice (*Oryza sativa* L.) is an important cereal crop that sustains a large proportion of the global population (Atique-ur-Rehman *et al.*, 2022). Despite significant advances in production technologies, global yields remain insufficient to meet the increasing food demand driven by a growing population (Galanakis, 2024). High-yielding rice varieties (HYVs) are important for global food security due to the potential

to increase crop yields and address food shortages. However, increased reliance on a few HYVs can create favourable conditions for the rapid spread of pests and diseases, potentially leading to significant crop losses (Lenné and Wood, 2024). Developing a wider variety of HYVs allows farmers to select seeds best suited to the specific conditions and needs, thereby promoting more sustainable agricultural practices by diversifying crops and reducing reliance on a single type of HYV. This diversification helps mitigate the risks associated with monoculture, such as increased susceptibility to pests and diseases, while also improving long-term soil health. The challenge has also been recently compounded by limited arable land availability and the increasing impact of climate change on biotic and abiotic stresses in rice cultivation (Fahad *et al*., 2019; Bhadouria *et al*., 2019; Jena *et al*., 2023). Among biotic constraints, fungal diseases represent a critical problem, reducing global rice yield by an estimated 14% annually (Anand and Rajeshkumar, 2022).

Rice blast disease, caused by the fungal phytopathogen *Pyricularia grisea* (Cooke) Sacc., also called *Pyricularia oryzae* Cavara (anamorph phase) and *Magnaporthe grisea* (teleomorph phase), is recognized as one of the most destructive and widespread diseases affecting rice production globally, with yield losses reaching 70–80% under epidemic conditions (Dean *et al*., 2012; Simkhada and Thapa, 2022). The pathogen infects multiple parts of rice plant, including leaves, nodes, collars, and panicles, resulting in characteristic lesions and severe impairment of grain formation and vigour (Agbowuro *et al*., 2020). Disease severity increases under low to moderate temperatures combined with high humidity, promoting fungal development and spread. Furthermore, mathematical modelling of disease dynamics has shown that climatic factors, particularly temperature and moisture levels, are key determinants in the progression and spatial distribution of blast infection in rice fields (Kirtphaiboon *et al*., 2021).

Globally, rice blast disease is reported in over 101 countries and regions according to recent reports (CABI, 2021). The high adaptability and genetic variability of the pathogen often overcome single resistance genes deployed in cultivars, leading to recurrent disease outbreaks and yield losses ranging from 10% to 30% annually (Kalia and Rathour, 2019). In Indonesia, the spread of rice blast disease and the associated losses among subsistence farmers have become alarming for sustainable production. According to the Indonesian Centre for Plant Pest and Disease Forecasting, rice blast affected approximately 10,993 ha, accounting for about 14.7% of the total 74,921 ha major pest and disease outbreaks recorded during the 2023–2024 cropping season (Indonesian Centre for Plant Pest and Disease Forecasting, 2023).

Studies on rice blast pathogen in Indonesia have shown considerable race diversity and complexity. A total of 201 isolates from diverse rice ecosystems and regions, using 25 international differential varieties (DVs) and the susceptible control Lijiangxintuanheigu (LTH), show high virulence to *Pib*, *Pit*, *Pia, Pik-s*, and *Pi12(t),* classifying the isolates into three cluster groups (Kadeawi *et al*., 2021). Prevalent races in Indonesia, particularly 033, 073, 133, and 173, have been frequently used in resistance screening studies due to the variable virulence patterns (Fitriah *et al*., 2019; Mustikarini *et al*., 2020; Nasution *et al*., 2025).

The development of HYVs is urgently needed to meet the demand of the increasing population and the challenges of a changing climate. Compared to the conventional breeding process, which is lengthy and time-consuming, doubled haploid technology has several advantages, such as shortening the breeding cycle by immediate fixation of homozygosity, offering high-selection efficiency. More importantly, doubled haploid technology has been successfully used to accelerate the development of rice varieties that demonstrate high yield and multiple disease resistance (Samantaray *et al*., 2021). Previous studies have developed advanced doubled-haploid rice lines derived from anther culture of several F_1s (Akbar *et al*., 2018; Akbar *et al*., 2019; Akbar *et al*., 2021).

Potential lines with stable performance and durable blast resistance can be identified efficiently using a multivariate analysis approach, where phenotypic data are analyzed using correlation, path analysis, principal component analysis (PCA), and Multi-trait Genotype-Ideotype Distance Index (MGIDI). More specifically, MGIDI uses PCA to group the traits into factors that represent different dimensions of the data. These factors are used to identify genotypes based on multiple characteristics and avoid redundancy and multicollinearity. The graphical representation derived by MGIDI can help to compare the genotypes with the ideal genotype (Olivoto and Nardino, 2021). Path analysis, when integrated in a multivariate

framework, facilitates modeling and analysis of complex relationships between multiple variables, such as direct and indirect effects, using a series of regression equations. It expands upon traditional regression by incorporating interrelationships among independent variables and enabling the assessment of both direct and indirect influences on a dependent variable (Anshori *et al.*, 2024). MGIDI has been successfully applied to obtain various selection purposes such as high yield combined with pest-and disease resistance and/or rice grain quality (Dewi *et al.*, 2025; Nurhidayah *et al.*, 2025; Feizi *et al.*, 2025). Therefore, this study aims to select advanced doubled-haploid rice lines based on multivariate selection on yield performance, agronomic traits, and resistance to rice blast caused by multiple *P. oryzae* races (033, 073, 133, and 173). The results are expected to support the development of improved rice cultivars capable of maintaining productivity under biotic stress challenges, particularly blast disease, thereby contributing to food security in Indonesia and beyond.

Materials and Methods

The yield performance evaluations were carried out at the experimental station in Sukabumi, West Java, and blast resistance evaluation was conducted at Installation for Testing and Development of Agricultural Instrument Standards (IP2SIP), under the Indonesian Agency for Agricultural Assembly and Modernization (IAASM), Muara, Bogor.

Genetic materials

The genetic materials for the yield trial consisted of 16 rice genotypes, comprising 14 doubled haploid (DH) lines derived from anther culture of several F_1 crosses (coded M) and two commercial checks, Ciherang and Inpari 18 (Table 1). The blast resistance evaluation used the same genotypes, supplemented with two check varieties, Situ Patenggang (resistant) and Kencana Bali (susceptible). Four *Pyricularia oryzae* races (033, 073, 133, and 173) were obtained from the IP2SIP collection.

Yield trial procedure

The experiment was arranged in a randomized complete block design (RCBD) with a single factor (genotype), consisting of 16 genotypes arranged in three replications, resulting in 48 experimental plots. Each plot measured 4 m × 5 m and was planted with 320 plants spaced 25 cm × 25 cm. The procedures included land preparation, seed sowing, transplanting, plant maintenance, observation, and harvesting. Seeds were treated with heat (45 °C for 3 × 24 hours) followed by 2 × 24 hours of incubation before sowing on seedbeds in the field. Subsequently, transplantingwas performed at 21 days after sowing (DAS) with two seedlings per planting hill. Maintenance

Table 1: *Genetic materials and check varieties used in the yield trial.*

No	Field code	DH lines	F_1's parentage
1	M1	CG-8-18-1-1	Inpago 8 × IR8770514-11-B-SKI-12
2	M2	CG-8-18-1-2	Inpago 8 × IR8770514-11-B-SKI-12
3	M3	CG-8-92-1-2	Inpago 8 × IR8770514-11-B-SKI-12
4	M4	CG-9-2-1-5	Inpago 8 × IR83140-B-11-B
5	M5	CG-9-53-1-1	Inpago 8 × IR83140-B-11-B
6	M6	CG-9-53-1-3	Inpago 8 × IR83140-B-11-B
7	M7	CG-9-62-1-1	Inpago 8 × IR83140-B-11-B
8	M8	CG-9-81-1-1	Inpago 8 × IR83140-B-11-B
9	M9	CG-9-81-1-2	Inpago 8 × IR83140-B-11-B
10	M10	CG-12-30-1-2	B1111430D-MR-1-1-PN-3-MR-2-Si-3-PN × IR83140-B-11-B
11	M11	CG-12-30-1-3	B1111430D-MR-1-1-PN-3-MR-2-Si-3-PN × IR83140-B-11-B
12	M12	CG-12-58-1-1	B1111430D-MR-1-1-PN-3-MR-2-Si-3-PN × IR83140-B-11-B
13	M13	CG-12-85-1-2	B1111430D-MR-1-1-PN-3-MR-2-Si-3-PN × IR83140-B-11-B
14	M14	CG-12-85-1-3	B1111430D-MR-1-1-PN-3-MR-2-Si-3-PN × IR83140-B-11-B
Check Varieties used in the yield trial			
15	M15	Ciherang	
16	M16	Inpari 18	

practices included gap filling, fertilization according to recommended doses (Ministry of Agriculture of the Republic of Indonesia, 2022), weed and pest control, as well as irrigation management. Harvesting occurred when approximately 90% of panicles had turned yellow. Agronomic traits and yield components observed include days to flowering (DTF), days to harvest (DTH), plant height (PH), number of vegetative and productive tillers (VTN and PTN), panicle length (PL), filled grains per panicle (FGN), total grains per panicle (TGN), percentage of filled grains (FGP), 1000-grain weight (W1000), and grain yield (Yield) converted to tons per hectare based on plot harvest data.

Blast resistance evaluation procedure

The experiment was arranged in a randomized complete block design (RCBD) and conducted separately for each blast race, and all 18 rice genotypes were tested in three replications. One experimental unit consisted of a single row of 20–25 rice seedlings planted in a soil-filled tray. The genotypes were randomized in each replication to reduce environmental bias. The evaluation procedure consisted of genotype establishment and disease scoring, inoculum preparation and inoculation, and data analysis.

Genotype establishment and disease scoring

Seeds were sown in 40 cm × 3 cm × 8 cm trays filled with sieved and pulverized soil. Before sowing, the soil was amended with fertilizer and Carbofuran 3% as a preventive crop protection measure to maintain uniform seedling establishment, applied at recommended agronomic dosages and in accordance with local regulations, followed by irrigation. Each row was sown with 20–25 seeds per genotype and covered with a thin soil layer, while trays were protected with wire mesh to prevent rodents. Daily maintenance included watering and manual weeding.

Inoculum preparation and inoculation procedure

Blast inoculum was prepared using oatmeal agar (OMA) media, following the protocol established in a previous study (Hayashi *et al.*, 2009). Small fragments of each pathogen race mycelia were placed on the solidified OMA media and incubated at 25°C. The first scraping was performed on day 10, using a brush to gently release conidia into sterile water containing 0.01 gL^{-1} streptomycin. The resulting liquid was discarded, and plates were returned to the incubator. About 48 hours after the initial scraping, a second scraping was performed by adding sterile water with 0.02% Tween 20 to release conidia and facilitate attachment to the inoculated rice plants. The conidial suspension was filtered through muslin cloth and adjusted to a concentration of 5×10^4 conidia mL^{-1} using a haemocytometer. Inoculation was conducted by spraying 3.5 mL of the suspension per plant using a glass sprayer attached to a compressor. Seedlings aged 21 days after sowing (DAS) were sprayed in a controlled inoculation chamber. After inoculation, plants were kept in a humidity chamber (100% RH, 25.5°C) for 24 hours, then transferred to a mesh-covered greenhouse with regular misting to maintain humidity. Blast resistance evaluation was conducted 7 days after inoculation, following Standard Evaluation System (SES) for Rice from IRRI (IRRI, 2013) and (Hayashi *et al.*, 2009).

Data analysis

Agronomic and yield performance data were first subjected to analysis of variance (ANOVA) to assess the significance of differences among genotypes. Prior to ANOVA, the assumptions of normality and homogeneity of variance were evaluated using the Shapiro–Wilk and Levene's tests, respectively, and the data were considered suitable for further analysis. Means were then compared using the Least Significant Difference (LSD) test at a 5% significance level. Correlation and path analyses were conducted to identify key traits influencing yield and to clarify relationships among agronomic traits. Traits showing meaningful associations with yield were subsequently included in the MGIDI analysis. The MGIDI approach is based on factor analysis, which groups correlated variables into latent factors, thereby reducing redundancy and minimizing the effect of multicollinearity among traits during genotype selection.

The distribution of disease scores was visualized using bar plots to provide an overview of genotype responses across different blast races. To classify genotypes based on ordinal disease scores, hierarchical clustering was applied using a dissimilarity matrix appropriate for ordinal data. The optimal number of clusters was determined using silhouette width analysis prior to dendrogram cutting, and genotypes were then grouped accordingly to represent similarity in resistance responses.

All statistical analyses were performed using R

Table 2: *Mean agronomic and yield traits of the tested genotypes.*

Genotype	DTF	DTH	VTN	PTN	PH	PL	FGN	TGN	FGP	W1000	Yield
M1	95.0^{ab}	118.0^{ab}	18.0	13.0	142.3^{ab}	24.73^{b}	116.9	140.1	83.5	29.37^{b}	8.19^{a}
M2	97.0^{ab}	118.3^{ab}	21.5^{ab}	13.2	126.2^{ab}	24.70^{b}	111.4	123.8	89.9^{a}	31.87^{a}	9.46^{ab}
M3	90.3^{ab}	120.0^{ab}	20.9^{ab}	14.1	110.2^{b}	25.40^{b}	119.1	134.7	88.3^{a}	28.33^{b}	8.54^{a}
M4	85.0^{ab}	109.3^{ab}	14.8	12.1	110.8^{ab}	24.63^{b}	130.9^{b}	159.0^{b}	82.5	27.47^{b}	3.05^{ab}
M5	85.3^{ab}	109.7^{ab}	15.9	11.7	99.3^{ab}	23.73^{ab}	112.7	149.2	76.0^{b}	24.93^{ab}	3.57^{ab}
M6	86.0^{ab}	120.0^{ab}	19.1	13.1	86.8^{ab}	23.50^{ab}	108.5	131.2	83.2	23.80^{ab}	6.40^{ab}
M7	88.3^{ab}	120.3^{ab}	13.9	11.0	113.6^{ab}	26.33^{b}	154.3^{b}	178.9^{b}	86.2	26.27^{b}	10.12^{b}
M8	89.0^{ab}	123.7^{ab}	17.3	11.4	130.0^{ab}	25.43^{b}	135.3^{b}	157.9^{b}	85.8	25.23^{b}	9.08^{a}
M9	94.0^{ab}	119.7^{ab}	17.1	11.7	142.1^{ab}	26.47^{b}	186.9^{ab}	214.0^{ab}	86.8	25.23^{b}	9.27^{a}
M10	95.0^{ab}	120.7^{ab}	11.3	10.9^{a}	110.5^{b}	24.93^{b}	138.5^{b}	167.1^{b}	83.4	24.30^{ab}	9.80^{b}
M11	99.0^{ab}	125.3^{b}	13.9	11.3	109.2^{b}	24.80^{b}	192.9^{ab}	221.9^{ab}	87.1	26.27^{b}	9.93^{b}
M12	100.0^{ab}	125.3^{b}	11.8	10.1	113.0^{ab}	25.63^{b}	151.7^{b}	231.5^{ab}	65.9^{ab}	26.13^{b}	10.45^{b}
M13	99.0^{ab}	126.0	20.7^{ab}	11.6	119.8^{ab}	23.87^{ab}	124.7	187.6^{b}	66.2^{ab}	27.10^{b}	9.98^{b}
M14	101.3^{b}	124.3^{ab}	15.4	12.1	116.8^{ab}	25.70^{b}	171.2^{ab}	214.3^{ab}	79.6	27.13^{b}	11.28^{b}
Ciherang	100.7^{b}	126.0	15.7	12.9	108.9^{b}	26.13^{b}	122.9	153.2	80.1	27.63^{b}	11.04^{b}
Inpari 18	104.0^{a}	126.7	15.1	11.1	92.5^{a}	21.37^{a}	96.1	114.2	84.3	32.23^{a}	8.04^{a}
Average	94.3	120.8	16.4	12.0	114.5	24.84	135.9	167.4	81.8	27.08	8.64
CV%	0.43	0.44	16.41	11.36	0.93	3.81	15.00	14.53	5.68	5.50	8.63
P	0.00**	0.00**	0.00**	0.07^{ns}	0.00**	0.00**	0.00**	0.00**	0.00**	0.00**	0.00**
LSD	0.68	0.89	4.49	-	1.77	1.58	33.99	40.57	7.75	2.48	1.24

**Notes:DTF = days to flowering (DAS); DTH = days to harvest (DAS); VTN = vegetative tiller number (tillers hill^{-1}); PTN = productive tiller number (tillers hill^{-1}); PH = plant height (cm); PL = panicle length (cm); FGN = filled grain number (grains panicle^{-1}); TGN = total grain number (grains panicle^{-1}); FGP = filled grain percentage (%); W1000 = weight of 1000 filled grains (g); Yield = grain yield (t ha^{-1}); CV = coefficient of variation; P = P value of genotype from ANOVA test at the 95% confidence level; ** = significantly difference at the 99% confidence level; ^{ns} = not-significantly difference at the 95% confidence level; LSD = Least Significant Difference; numbers followed by the letter ^{a} indicate a significantly different from Ciherang and those followed by the letter ^{b} indicate a significantly different from Inpari 18 at LSD test at 95% confidence level.*

software, including correlation analysis, which was conducted using the "corrplot" package (Wei *et al.*, 2017), and path analysis carried out through the "agricolae" package (de Mendiburu, 2023). MGIDI was calculated using the "metan" package (Olivoto and Lúcio, 2020). Disease score distributions were visualized with bar plots generated by the "ggplot2" package (Wickham *et al.*, 2016), while hierarchical clustering and silhouette analysis were performed using the "cluster" and "factoextra" packages. (Kassambara and Mundt, 2016).

Results and Discussion

Phenotypic variation, trait relationships, and genotype selection

Morphological and yield-related traits are widely used as a criterion to evaluate phenotypic variability for improving rice yield potential (Kakar *et al.*, 2021). In this study, significant differences were found in mean values among genotypes, except for productive tiller number (Table 2), which indicates substantial phenotypic diversity across most observed traits, offering valuable opportunities for selecting superior genotypes.. The coefficients of variation (CVs) for all traits were in a low range, indicating relatively low variability around the mean. This suggests that the observed data were relatively consistent and reliable.

Agronomic and yield component traits reflect the plant morphological and physiological performance, playing a crucial role in determining a genotype adaptability, stability, and productivity, specifically during climate change. This has been well documented in previous studies for traits such as flowering and harvest time (Liang *et al.*, 2024), plant height (Zhang *et al.*, 2017), panicle architecture (Fei *et al.*, 2019), as well as panicle length, grain number per panicle, seed-setting rate, and 1000-grain weight (Li *et al.*, 2019). Therefore, the phenotypic diversity observed in

this study provides a foundation for identifying and selecting promising rice genotypes.

Most DH lines exhibited earlier maturity than the check varieties, except M13, which showed a comparable maturity duration. Early maturity is advantageous for avoiding late-season stresses and improving cropping efficiency (Shanmugam *et al*., 2023; Noviana *et al*., 2021; Saminadane *et al*., 2024; Musa *et al*., 2023). Earliness also supports faster production cycles and earlier economic returns for farmers (Sao *et al*., 2022). These results suggest that several DH lines are suitable for cultivation in stress-prone or short-season environments. Previous breeding programs have also demonstrated that early-maturing cultivars can combine favorable yield, grain quality, and disease resistance, highlighting the importance of this trait in modern rice breeding (Wang *et al*., 2022; Zhu and Pan, 1990).

Plant height (PH) varied among genotypes, with several DH lines showing comparable stature to the check varieties. Lines M5 and M6 were significantly shorter, while M10 and M11 were similar to Ciherang. This variation indicates flexibility for selecting genotypes with optimal plant architecture that balance lodging resistance and yield potential. Appropriate plant height has been associated with improved lodging resistance while maintaining grain yield stability (Huang *et al*., 2022).

Vegetative tiller number (VTN) varied slightly among genotypes, with M2, M3, and M13 showing higher values than the check varieties. The formation efficiency of productive tillers is generally associated with yield formation in rice (Takai, 2024). However, productive tiller number (PTN) showed limited variation, suggesting that tillering was not a primary determinant of yield in this population. According to SES for rice (IRRI, 2013), DH lines appear to have moderate tillering ability. The number of productive tillers among genotypes of DH lines was similar, with an average of 12 tillers hill^{-1}. Panicle length (PL) showed meaningful variation, with several DH lines, particularly M5, M6, and M9, producing longer panicles than both check varieties. This trait is closely associated with spikelet formation and yield potential (Parida *et al*., 2022; Kim and Vergara, 1991).

Yield component traits further distinguished the DH lines. Lines M9, M11, and M14 produced significantly higher filled grain numbers (FGN) than the check varieties, while several other lines surpassed Inpari 18. Similarly, total grain number was highest in M11, M9, M12, and M14. These results indicate strong sink capacity and reproductive performance, which are critical determinants of yield formation (Meng *et al*., 2021). Filled grain percentage (FGP) was higher in M2 and M3, while most lines showed values comparable to the checks. For 1000-grain weight, most DH lines were similar to Ciherang, while M2 showed a significantly higher value, indicating superior grain size.

Grain yield reflects the combined effects of all observed agronomic and yield-related components. In this study, several doubled haploid (DH) lines, including M2, M7, M10, M11, M12, M13, and M14, demonstrated significantly higher yields than Inpari 18. Moreover, M7, M10, M11, M12, M13, and M14 lines achieved yields comparable to Ciherang, which recorded a high productivity of 11.04 t ha^{-1}, further underscoring the potential as promising candidates. This result supports the view that high yield does not solely depend on the number of tillers. According to a previous study (Kim and Vergara, 1991), rice plants have to possess strong sink strength, large panicles with a greater number of spikelets, and higher grain weight to achieve a high grain yield.

The favourable agronomic performance and yield components indicate that the evaluated doubled haploid lines are suitable candidates for further selection. Multi-trait evaluation using MGIDI enables simultaneous identification of superior genotypes by integrating agronomic and yield-related traits (Olivoto and Nardino, 2021). Prior to index construction, correlation and path analyses were used to identify key traits influencing yield and to minimize redundancy among variables, as recommended in multivariate breeding frameworks (Anshori *et al*., 2024).

Based on the correlation matrix (Figure 1), several traits such as days to flowering (DTF), days to harvest (DTH), plant height (PH), panicle length (PL), filled grain number (FGN), and total grain number (TGN) showed significant and positive correlations with grain yield. The result indicates that the increase in these traits tends to be followed by elevated yield, suggesting the potential as a selection criterion. In contrast, traits-demonstrated insignificant correlations with yield,

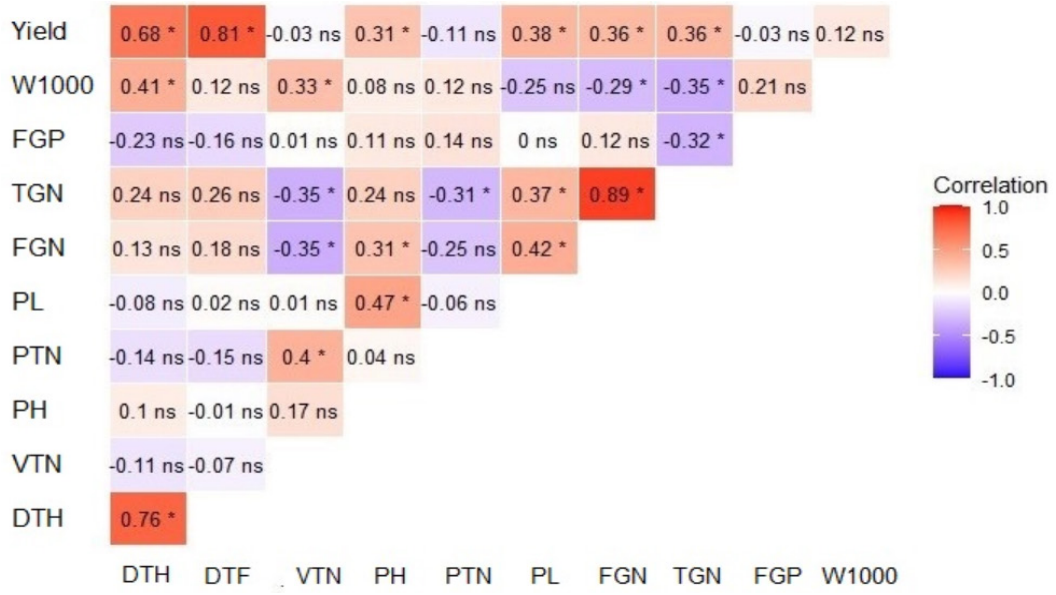

Figure 1: *Pearson correlation matrix among agronomic and yield-related traits.*
DTF = days to flowering; DTH = days to harvest; VTN = vegetative tiller number; PTN = productive tiller number; PH = plant height; PL = panicle length; FGN = filled grain number; TGN = total grain number;FGP = filled grain percentage; W1000 = weight of 1000 filled grains; Yield = grain yield.

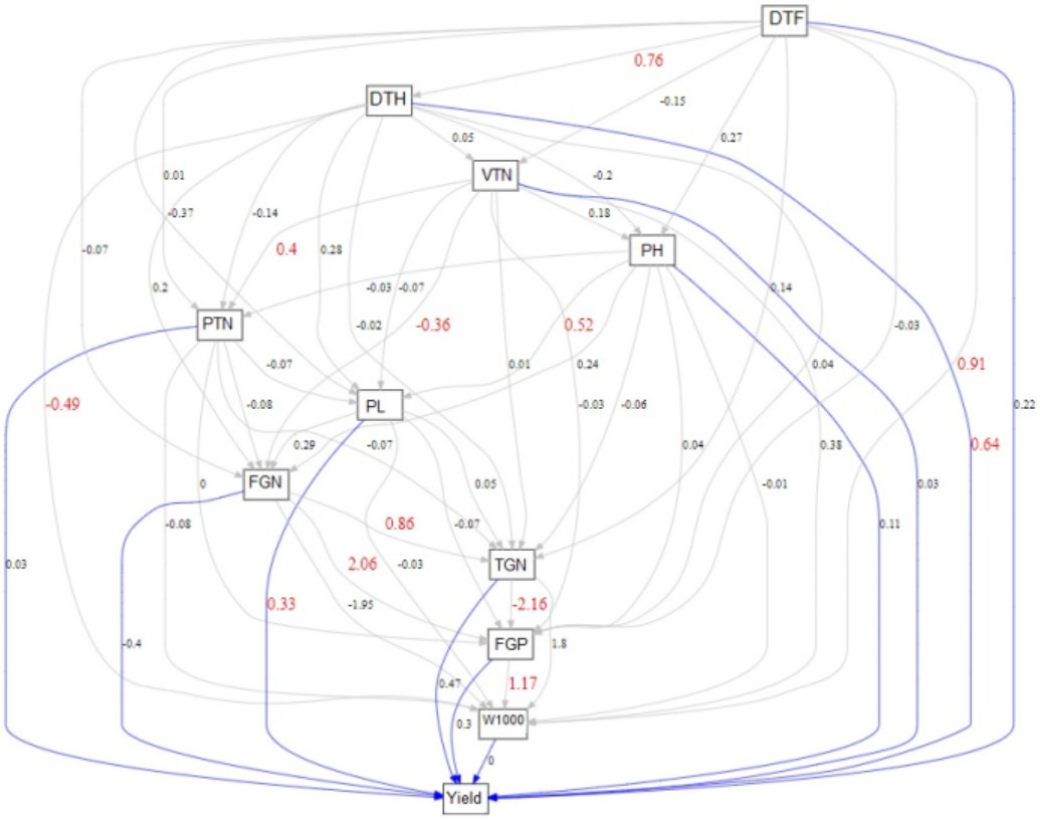

Figure 2: *Path analysis diagram illustrating the direct and indirect effects of agronomic and yield traits of tested genotypes.*
DTF = days to flowering; DTH = days to harvest; VTN = vegetative tiller number; PTN = productive tiller number; PH = plant height; PL = panicle length; FGN = filled grain number; TGN = total grain number; FGP = filled grain percentage; W1000 = weight of 1000 filled grains; Yield = grain yield

such as vegetative tiller number (VTN), productive tiller number (PTN), filled grain percentage (FGP), and 1000-grain weight (W1000), implying limited limited roles as primary selection criteria when evaluated independently.

Path analysis provided a more detailed understanding of the direct and indirect effects of each trait on yield. Traits such as DTH, PL, FGN, TGN, SS, and DTF showed relatively high direct effects on yield (Figure 2). Notably, filled grain number (FGN) exhibited a

Table 3: *Factor loading after rotation and selection differential of selected genotype from MGIDI.*

Factor loadings after rotation				Selection differential				
Var	FA1	FA2	FA3	Var	Factor	X_0	X_s	Sense
DTF	-0.9	-0.03	-0.2	DTF	FA1	94.3	95.7	decrease
DTH	-0.94	0.07	-0.09	DTH	FA1	121	122	decrease
PL	0	-0.86	-0.21	PL	FA2	24.8	25.8	increase
FGN	0.16	-0.92	0.03	FGN	FA2	136	176	increase
TGN	0.21	-0.85	0.45	TGN	FA2	167	207	increase
FGP	-0.1	-0.01	-0.96	FGP	FA3	81.8	84.9	increase
Yield	0.87	-0.4	-0.09	Yield	FA1	8.64	10.1	increase
Comunality mean			0.89					

Notes: Var= variable; FA = days to flowering; DTH = days to harvest; Yield = grain yield; PL = panicle length; FGN = filled grain number; TGN = total grain number; FGP = filled grain percentage. FA1, FA2, FA3= factor related to the variable; X_0= mean value of the variable before selection. X_s= mean value of the variable after selection (selected genotypes); Sense= desired direction of change.

negative direct effect on yield (–0.40), which appears inconsistent with its positive correlation with yield observed in Figure 1. However, in path analysis, the overall contribution of a trait is determined by the balance between its direct and indirect effects rather than the direct coefficient alone.

The decomposition of effects showed that FGN exerted substantial indirect influences on yield through other yield components, particularly via total grain number (TGN) and filled grain percentage (FGP). The total indirect effect of FGN was positive (+0.465), which offset the negative direct effect and resulted in a small but positive total effect (+0.065). This indicates that FGN contributes to yield formation primarily through its interaction with other yield-related traits rather than acting as an independent determinant.

Biologically, FGN remains an essential component of yield formation because it is closely associated with grain number per panicle and reproductive success, which directly determine final yield. Therefore, despite its negative direct coefficient, FGN should not be interpreted as a detrimental trait. Instead, it should be considered a complementary selection trait, particularly in combination with TGN and FGP, which mediate its contribution to yield.

FGP, which showed a weak correlation with yield, exhibited notable direct and indirect effects in the path analysis, indicating that its role may be masked by interactions with other traits but still relevant for selection. In contrast, traits such as VTN, PTN, PH, and W1000 showed minimal total effects and are therefore less recommended as primary selection criteria for yield improvement.

The selection index was constructed based on three principal components with eigenvalues greater than one, which together explained 89.2% of the total variation. Subsequent factor analysis with varimax rotation grouped the traits into three latent factors (FAs) as shown in Table 3. FA1 represents the early maturity trait, expected to decrease in value, as well as the yield, which is projected to increase. FA2 groups yield components, including panicle length (PL, -0.86), number of filled grains (FGN, -0.92), and total number of grains (TGN, -0.85), representing traits that can be improved through selection. The percentage of filled grain percentage (FGP) was included in FA3 with a high loading value of -0.96. The high average communality value for all traits (average = 0.89) indicates that the formed factor structure can retain important trait information relevant for genotype evaluation.

Selection traits showed improvement based on differential selection analysis. Based on the results, yield increased from 8.64 to 10.15 tha^{-1} (+17.5%), panicle length (PL) improved by 0.99 cm (+3.99%), filled grain (FGN) rose by 40.5 grains (+29.8%), total grain (TGN) improved by 39.9 grains (+23.8%), and filled grain percentage (FGP) increased by 3.11% (+3.81%). Days to flowering (DTF) and days to harvest (DTH) increased slightly after selection, although both traits were targeted to decrease in the MGIDI analysis. However, this change did not reduce the agronomic value of the selected genotypes because all remained within the early-maturing category and were still earlier than or comparable to the check varieties

(Table 2). This pattern indicates a trade-off between maturity duration and other agronomic traits during the multi-trait selection process; therefore, the slight increase in DTF and DTH mean value of selected genotype should be interpreted as an acceptable adjustment within the MGIDI framework rather than a deviation from the breeding objective.

Based on MGIDI values (Figure 3a), four DH lines were identified as closest to the ideotype, namely M9, M11, M7, and M14 (Figure 3a). FA3 had the largest contribution in MGIDI selection of lines M9, M11, and M14, as indicated by the polygon angle closest to the internal edge, indicating that these two lines had a high percentage of filled grain percentage (FGP) compared to other test genotypes. Meanwhile, FA2 had the largest contribution in MGIDI selection of line M7, indicating that this line had the best combination of PL, TGN, and FGN traits (Figure 3b).

Information regarding the strengths and weaknesses of each selected MGIDI line is shown in Figure 3b. M14 line demonstrated strength in DTF, DTH, and Yield traits, as indicated by FA1 angle closest to the genotype point. However, considering the ideotype objective for DTF and DTH traits was to decrease while yield was expected to increase, M14 did not fully meet the selection goal for DTF and DTH, despite being classified as early maturing. M7 line was distinct due to the strong contribution to FA1, as shown by the polygon angle, which exceeds MGIDI theoretical value (dashed line). With high Yield and a lower combination of DTF and DTH, M7 is well consistent with the selection objective. In addition, it also showed a strong contribution to FA3, indicated by a high percentage of filled grains (FGP).

Blast resistance evaluation and genotypic clustering

Blast resistance was evaluated separately against four races of *Pyricularia oryzae* (033, 073, 133, and 173). The resistant check, Situ Patenggang, consistently exhibited low disease scores, whereas Kencana Bali showed high susceptibility across races, confirming the reliability of the screening system. Several DH lines displayed diverse resistance responses. Such differential responses are consistent with the gene-for-gene interaction governing the rice–blast pathosystem, in which specific resistance (R) genes recognize corresponding avirulence (AVR) genes in *Pyricularia oryzae*, resulting in race-specific resistance patterns (Younas *et al.*, 2024; Valent, 2025). The presence of lines resistant to multiple races suggests

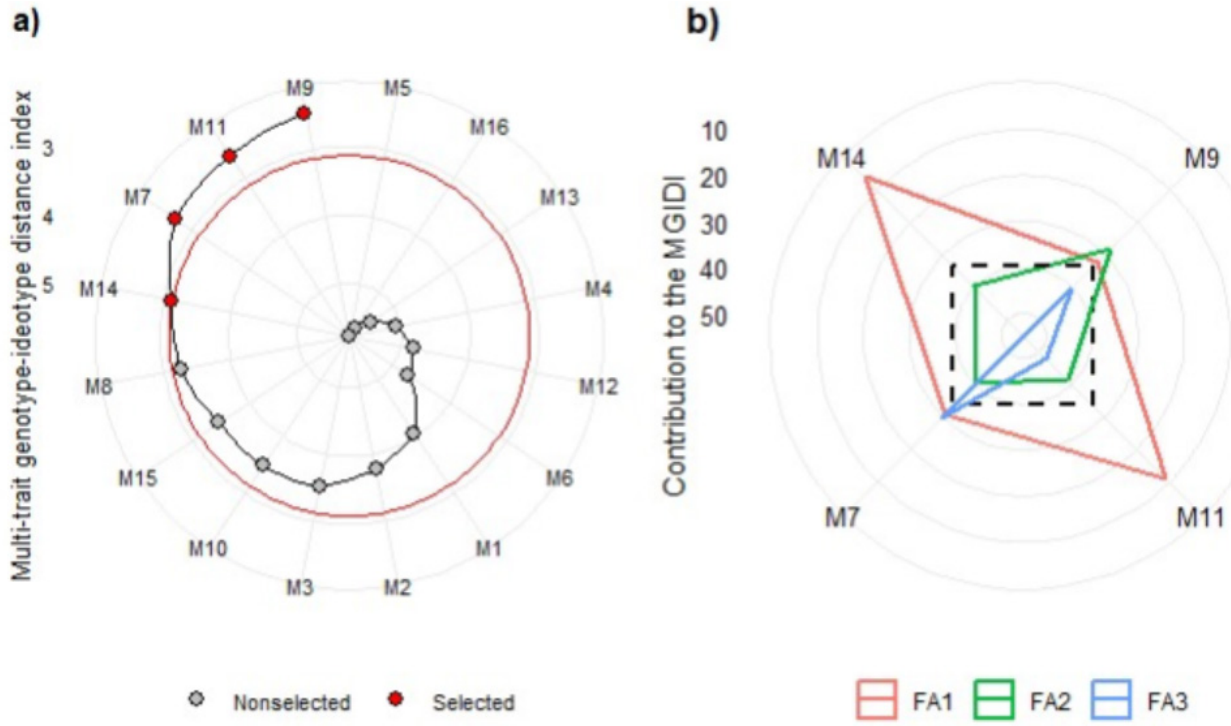

Figure 3: *(a) Selected genotypes based on Multi-Trait Genotype-Ideotype Distance Index (MGIDI). Genotypes located closer to the origin represent those with a smaller distance to the ideotype and thus higher overall desirability based on multiple traits. (b) Contribution of each factor to MGIDI values of selected genotypes.*

FA= Factor analysis, FA1 is primarily associated with days to flowering (DTF), days to harvest (DTH), and grain yield (Yield), FA2 related to panicle length (PL), filled grain number (FGN), and total grain number (TGN), FA3 is related to filled grain percentage (FGP).

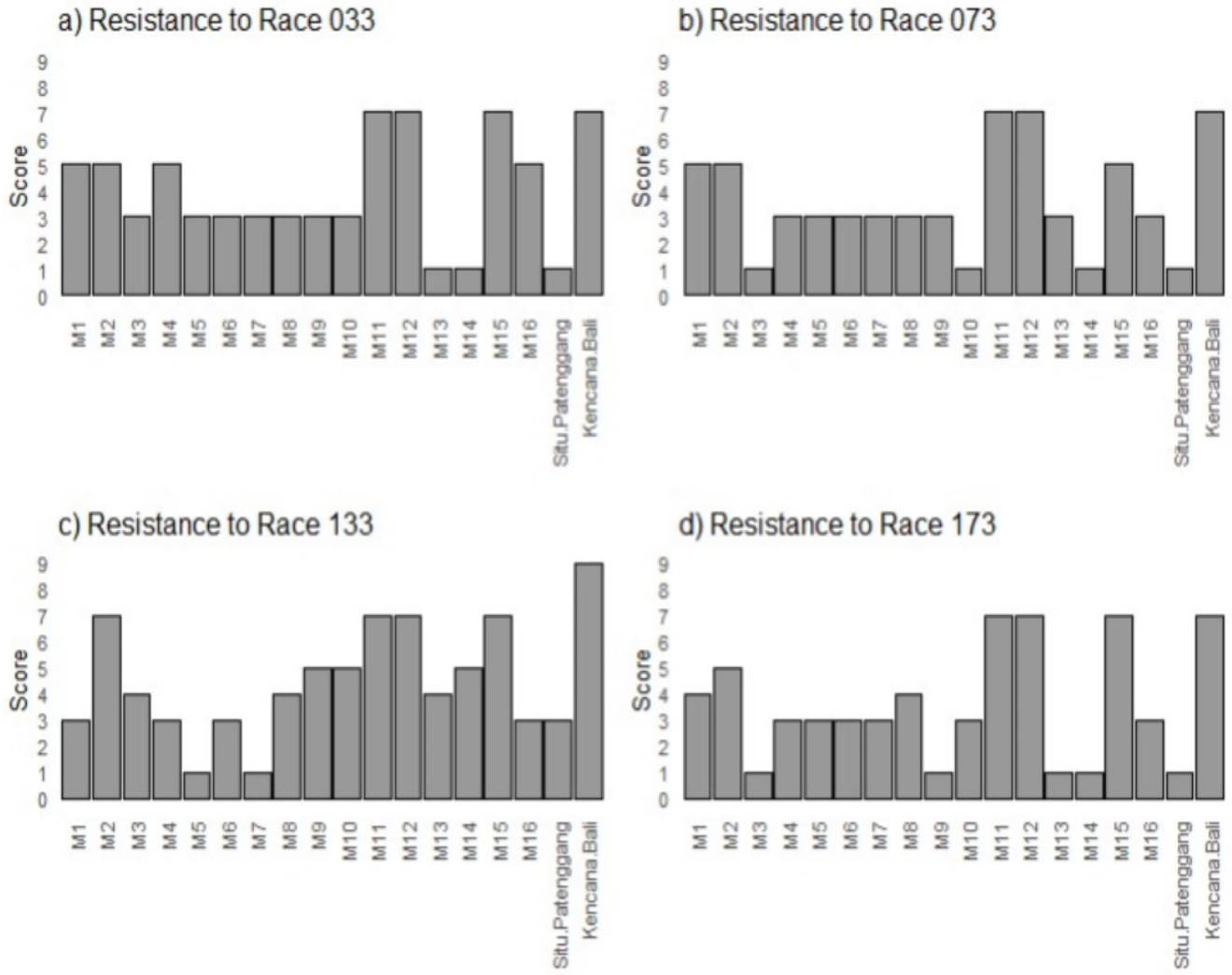

Figure 4: *Resistance scores of tested rice genotypes against four races of Pyricularia oryzae based on visual disease assessment a) Race 033, b) Race 073, c) Race 133, and d) Race 173. Scores are following the Standard Evaluation System (SES) by IRRI (2014) and Fukuta et al. (2009): 1 = resistant; 3 = moderately resistant; 5 = moderately susceptible; 7 = susceptible, and 9 = highly susceptible.*

the possible involvement of multiple resistance loci or quantitative resistance mechanisms that contribute to broader protection (Cheng *et al.*, 2024).

Several test genotypes demonstrated promising resistance, in some cases comparable to Situ Patenggang for specific races (Figure 4a). For race 033, M13 and M14 lines showed the lowest score (1), comparable to the resistant check. This was followed by M3, M5, M6, M7, M8, M9, and M10, which recorded a score of 3 (moderately resistant). For race 073, the highest level of resistance (score 1) was observed in M3, M10, and M14 lines, comparable to Situ Patenggang. Six DH lines, M5, M6, M7, M8, M9, and M13, showed moderate resistance (score 3) (Figure 4b). Lines M5 and M7 achieved the lowest score of 1 against race 133, surpassing Situ Patenggang, which scored 3. Two DH lines, M4 and M6, also demonstrated moderate resistance with a score of 3. Although the remaining genotypes showed higher scores, the ability of M5 and M7 lines to resist the particularly virulent race emphasizes the potential as key sources of resistance (Figuire 4c). For race 173, M3, M9, M13, and M14 lines scored 1, indicating high resistance similar to Situ Patenggang, while M4, M5, M6, M7, and M10 lines scored 3, suggesting moderate resistance (Figuire 4d).

For further interpretation, the resistance scores obtained from each race were then analyzed collectively to examine the overall response patterns of genotypes across races. Hierarchical clustering based on ordinal blast resistance scores separated the genotypes into two major groups (Figure 5). The optimal number of clusters was determined using silhouette analysis (Figure 6). The highest average silhouette width

was obtained at k = 2 (0.597), indicating the most appropriate grouping structure for the ordinal blast resistance data. Therefore, hierarchical clustering was interpreted based on two main clusters.

The first group was closely associated with the susceptible check, Kencana Bali, and included M2, M15, M11, and M12, indicating consistently high disease scores and susceptibility across races. The second group was positioned closer to the resistant check, Situ Patenggang, and comprised the remaining genotypes. Within this group, a subcluster consisting of M13 and M14 was located nearest to Situ Patenggang, indicating resistance responses relatively high similar to the resistant check. Their proximity to Situ Patenggang indicates relatively stable resistance across races, which is a desirable attribute in breeding programs targeting durable resistance (Sahu *et al*., 2022). Durable resistance is particularly important in blast management due to the high evolutionary potential and pathogenic variability of *P. oryzae* (Cheng *et al*., 2024). Other genotypes such as M3, M9, M10, M5, M7, M6, M8, M1, M4, and M16 formed adjacent branches.

The selection of superior genotypes based on MGIDI identified four promising candidates, M9, M11, M7, and M14, as presented previously in Figure 3a. These tested genotypes demonstrated the closest proximity to the ideotype, indicating the most favorable combination of agronomic and yield traits. Further refinement of recommendations is possible when these selections are examined in the context of blast resistance. Among the four DH lines, M14 and M9 demonstrated high levels of resistance (score 1) to races 033 and 173, and moderate resistance (score 3) to race 073, displaying response patterns similar to the resistant check, Situ Patenggang. M7 DH line showed exceptional resistance to race 133, with a score of 1, surpassing the resistant check (score 3), and also maintained moderate resistance (score 3) to races 033, 073, as well as 173. In contrast, M11 showed higher scores across all races (7–9), indicating a different response pattern compared with the resistant reference.

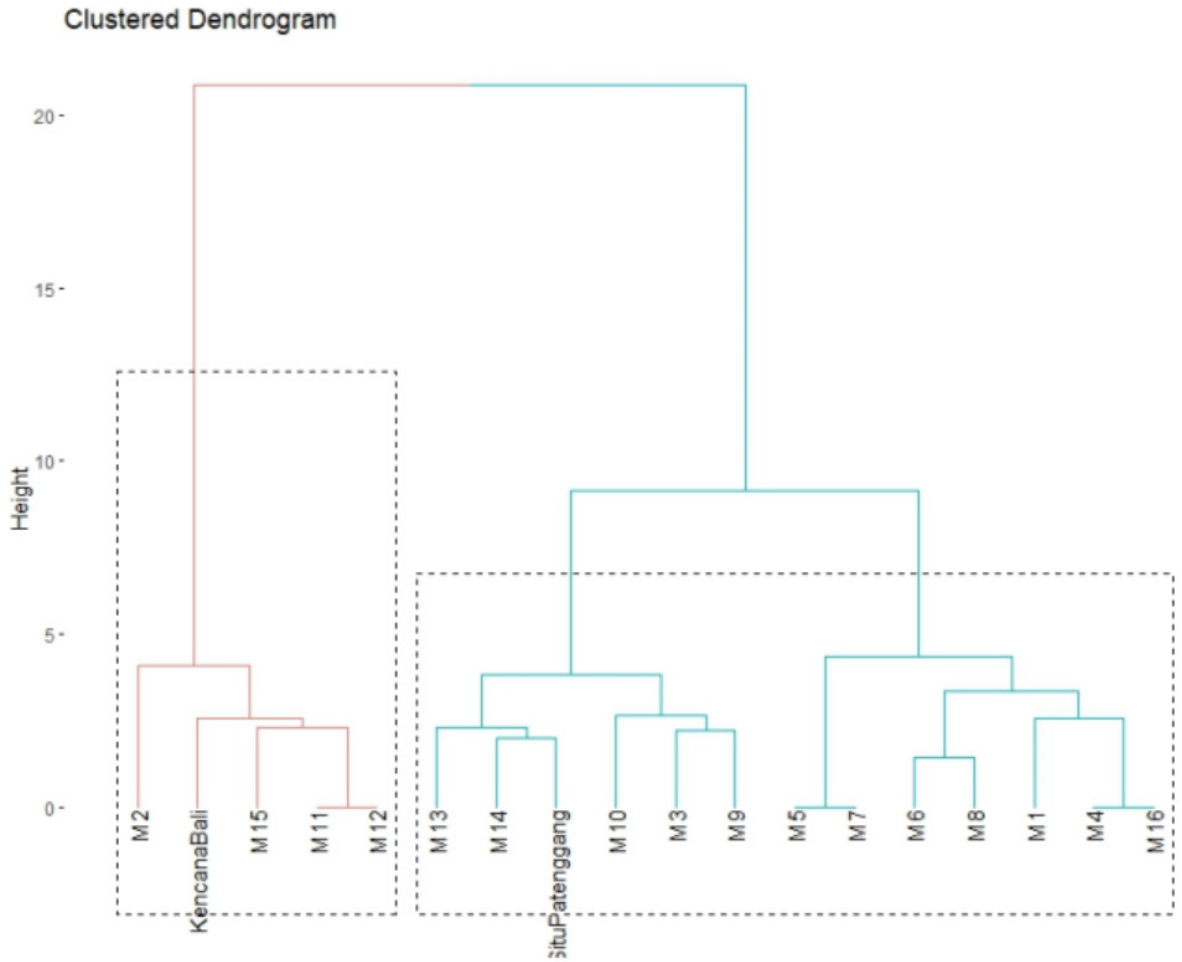

Figure 5: *Average silhouette width for different numbers of clusters (k = 2–6) based on ordinal blast resistance scores. The highest silhouette value at k = 2 indicates the optimal clustering structure for the dataset.*

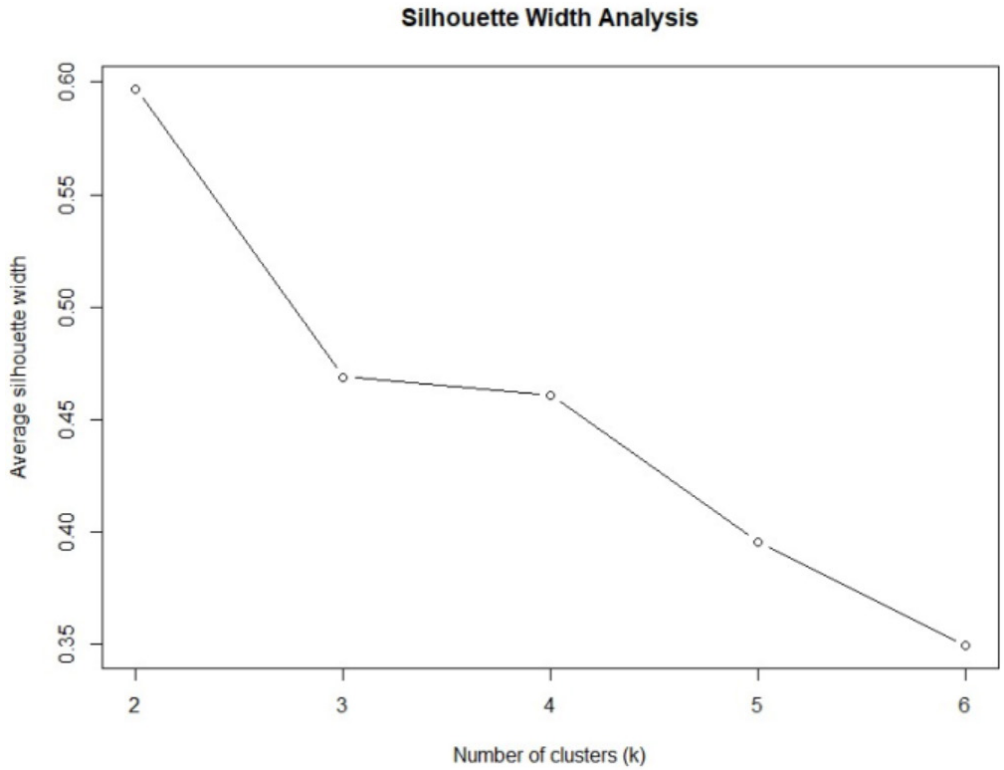

Figure 6: *Hierarchical clustering dendrogram of rice genotypes based on blast disease scores across four races (033, 073, 133, and 173).*

Collectively, the three DH lines, namely M9, M7, and M14, were identified as promising lines due to the combination of agronomic excellence and blast resistance. M7, in particular, offers a balanced advantage of high-yielding performance and strong resistance to race 133, suggesting potential for varietal release or advanced breeding use. Integration of blast resistance with MGIDI-based multi-trait selection enabled refinement of superior genotypes by simultaneously considering yield and resistance performance. The incorporation of multiple agronomic and adaptive traits into multi-trait indices has been shown to improve selection efficiency and facilitate the identification of elite breeding materials with balanced trait performance (Chaity *et al*., 2026; Habib *et al*., 2024). Although M11 is agronomically competitive, it may require additional resistance breeding or deployment in blast-non-endemic areas.

Conclusions and Recommendations

In conclusion, this study identified several traits considered primary contributors to grain yield based on correlation and path analysis, including days to flowering, days to harvest, panicle length, and grain traits. Several DH lines demonstrated superior agronomic performance selected by multivariate analysis using MGIDI, namely M7, M9, M11, and M14, with significant improvements observed in grain yield (+17.5%) and other key traits. In addition, blast resistance screening across four races of *Pyricularia oryzae* followed by hierarchical clustering analysis grouped genotypes according to similarity in resistance responses. Genotypes such as M13 and M14 were positioned closest to the resistant check, while M3, M9, M10, M5, M7, M6, M8, M1, M4, and M16 formed adjacent branches with similar response patterns.. Collectively, these findings underscore the potential of M7, M9, and M14 as elite breeding materials that combine high agronomic performance with broad-spectrum blast resistance. These results also indicate that DH lines with both high productivity and broad-spectrum blast resistance, particularly M7, M9, and M14 may be considered for future variety release.

Acknowledgements

The authors are grateful for funding support 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. The authors are also grateful to the Installation for Testing and Development

of Agricultural Instrument Standards (IP2SIP) at Muara, Bogor, for the assistance in blast disease testing.

Novelty Statement

This study combines agronomic performance evaluation and blast resistance screening across four pathogen races to identify doubled haploid rice lines with simultaneous high yield and broad-spectrum blast resistance. The identification of superior lines such as M7, M9, and M14 provides novel candidates with potential for future variety release.

Authors' Contribution

Bambang Sapta Purwoko: Conducted the conceptualization, validation, investigation, resources management, data curation, original draft writing, review and editing, supervision, project administration, and funding acquisition.
Iswari Saraswati Dewi: Contributed to the conceptualization, methodology, validation, investigation, resources management, data curation, review and editing, visualization, supervision, project administration, and funding acquisition.
Ratna Kartika Putri: Performed the validation, formal analysis, investigation, data curation, original draft writing, review and editing, and visualization.
Iskandar Lubis: Contributed to the conceptualization, resources management, review and editing, and funding acquisition. All authors read and approved the final manuscript.

Generative AI and AI-assisted technology statement
The authors declare that no generative AI and AI assisted technology was used in the creation of this manuscript.

Conflict of interest
The authors declare that there are no conflicts of interest related to this article. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, or in the decision to publish the results.

References

Agbowuro, G.O., M.S. Afolabi , E.F. Olamiriki and S.O. Awoyemi. 2020. Rice blast disease (*Magnaporthe oryzae*): A menace to rice production and humanity. Int. J. Pathog. Res., 4(3): 32–39 https://doi.org/10.9734/ijpr/2020/v4i330114

Akbar, M.R., B.S. Purwoko, I.S. Dewi and W.B. Suwarno. 2018. Agronomic and drought tolerance evaluation of doubled haploid rice breeding lines derived from anther culture. Sabrao J. Breed. Genet., 50(2): 115-128

Akbar, M.R., B.S. Purwoko, I.S. Dewi, W.B. Suwarno and Sugiyanta. 2019. Selection of doubled haploid lines of rainfed lowland rice in preliminary yield trial. Biodivers. J. Biol. Divers., 20(10): 2796-2801 https://doi.org/10.13057/biodiv/d201003

Akbar, M.R., B.S. Purwoko, I.S. Dewi, W.B. Suwarno, Sugiyanta and M.F. Anshori. 2021. Agronomic and yield selection of doubled haploid lines of rainfed lowland rice in advanced yield trials. Biodivers. J. Biol. Divers., 22(7): 3006-3012 https://doi.org/10.13057/biodiv/d220754

Anand, G. and K.C. Rajeshkumar. 2022. Challenges and threats posed by plant pathogenic fungi on agricultural productivity and economy. In: Rajpal, V.R., I. Singhand S.S. Navi (eds), Fungal biology. Springer Nature, SG. https://doi.org/10.1007/978-981-16-8877-5_23

Anshori, M.F., Y. Musa, M. Farid, M. Jayadi, R. Padjung, K. Kaimuddin, Y.C. Huang, M. Casimero, I. Bogayong, W.B. Suwarno, *et al.* 2024. A comprehensive multivariate approach for G×E interaction analysis in early maturing rice varieties. Front. Plant Sci. 15:1462981 https://doi.org/10.3389/fpls.2024.1462981

Atique-ur-Rehman, N. Sarwar, S. Ahmad, M.A. Khan and M. Hasanuzzaman. 2022. World rice production: An overview. p. 3-12. In: Sarwar, N., Atique-ur-Rehman, Ahmad, S. and M. Hasanuzzaman. Modern techniques of rice crop production. Springer, Singapore. https://doi.org/10.1007/978-981-16-4955-4_1

Bhadouria, R., R. Singh, V.K. Singh, A. Borthakur, A. Ahmad, G. Kumar and P. Singh. 2019. Agriculture in the era of climate change: consequences and effects. In: Coudhary, K.K. and A. Kumar (eds), Climate change and agricultural ecosystems. 1st edition: current challenges and adaptation. Woodhead Publishing, India. https://doi.org/10.1016/B978-0-12-816483-9.00001-3

CABI. 2021. *Magnaporthe oryzae (rice blast disease)*.

CABI Plantwiseplus Knowledge Bank. https://doi/10.1079/PWKB.Species.46103

Chaity, S.S., M.R. Islam, M. Faruquee, J.U. Ahmed and A.A. Islam. 2026. Identification of elite rice lines with better breeding values using genomic prediction and multi-trait genotype ideotype distance index (MGIDI) for grain yield under irrigation cropping system. PLoS ONE., 21(2): e0340188 https://doi.org/10.1371/journal.pone.0340188

Cheng, X., G. Zhou, W. Chen, L. Tan, Q. Long, F. Cui, L. Tan, G. Zou and Y. Tan. 2024. Current status of molecular rice breeding for durable and broad-spectrum resistance to major diseases and insect pests. Theor. Appl. Genet., 137(10): 219 https://doi.org/10.1007/s00122-024-04729-3

Dean, R., J.A.L. Van Kan, Z.A. Pretorius, K.E. Hammond-Kosack, A. Di Pietro, P.D. Spanu, J.J. Rudd, M. Dickman, R. Kahmann, J. Ellis and G.D. Foster. 2012. The top 10 fungal pathogens in molecular plant pathology. Mol. Plant Pathol., 13(4): 414–430 https://doi.org/10.1111/j.1364-3703.2011.00783.x

de Mendiburu, F. 2023. Agricolae: Statistical procedures for agricultural research. Dataset. The R Foundation. https://cran.r-project.org/web/packages/agricolae/agricolae.pdf.

Dewi, I.S., B.S. Purwoko, R.K. Putri and I. Lubis. 2025. Brown plant hopper resistance in promising doubled haploid rice lines selected by MGIDI and FAI-BLUP Index. Pertanika J. Trop. Agric. Sci., 48(3): 1019-1040 https://doi.org/10.47836/pjtas.48.3.20

Fahad, S., M. Adnan, M. Noor, M.A. Alam, I.A. Khan, H. Ullah, F. Wahid, I.A. Mian and Y. Jamal, *et al*. 2019. Major constraints for global rice production. p. 1-21. in: Hasanuzzaman, M., M. Fujita, K. Nahar and J.K. Biswas (eds), Advances in rice research for abiotic stress tolerance. Woodhead Publishing, UK. https://doi.org/10.1016/B978-0-12-814332-2.00001-0

Fei, C., J. Yu, Z. Xu and Q. Xu. 2019. Erect panicle architecture contributes to increased rice production through the improvement of canopy structure. Mol. Breed., 39(9): 128 https://doi.org/10.1007/s11032-019-1037-9

Feizi, N., A. Sabouri, A. Bakhshipour and A. Abedi. 2025. Combinatorial approaches to image processing and MGIDI for the efficient selection of superior rice grain quality lines. Agric., 15: 615 https://doi.org/10.3390/agriculture15060615

Fitriah, N., U. Widyastuti, Suharsono, S. Nugroho, Suwarno and Miftahudin. 2019. Screening of markers and blast isolates for blast resistance selection on backcross-population from crossing Ciherang and IRBLta2-Re. Int. J. Agric. Biol., 22(3): 468–474 https://doi.org/10.17957/IJAB/15.1088

Galanakis, C. M. 2024. The future of food. Food., 13(4): 506. https://doi.org/10.3390/foods13040506

Habib, M.A., M.G. Azam, M.A. Haque, L. Hassan, M.S. Khatun, S. Nayak, H.M. Abdullah, R. Ullah, E.A. Ali, N. Hossain and S. Ercisli. 2024. Climate-smart rice (*Oryza sativa* L.) genotypes identification using stability analysis, multi-trait selection index, and genotype-environment interaction at different irrigation regimes with adaptation to universal warming. Sci. Rep., 14(1): 13836 https://doi.org/10.1038/s41598-024-64808-9

Hayashi, N., N. Kobayashi, C.M.V. Cruz and Y. Fukuta. 2009. Protocols for the sampling of diseased specimens and evaluation of blast disease in rice. Japan International Research Center for Agricultural Sciences, Japan.

Huang, M., T. Lei, J. Cao, Z. Tao, F. Cao, J. Chen, X. Yin and Y. Zou. 2022. Linking grain yield and lodging resistance with growth patterns in rice. Exp. Agric., 58: e24 https://doi.org/10.1017/S0014479722000230

Indonesian Centre for Plant Pest and Disease Forecasting. 2023. Performance report 2023 of Indonesian centre for plant pest and disease forecasting. Indonesian Centre for Plant Pest and Disease Forecasting, Ministry of Agriculture, Indonesia.

International Rice Research Institute. 2013. Standard evaluation system for rice (5th ed.). International Rice Research Institute, Phillipines.

Jena, B. K., S.R. Barik, A. Moharana, S.P. Mohanty, A. Sahoo, R. Tudu, P.C. Kole and S.K. Pradhan. 2023. Rice production and global climate change. Biomed J. Sci. Tech. Res., 48(1): 39075-39095. https://doi.org/10.26717/BJSTR.2023.48.007592

Kadeawi, S., A. Nasution, A. Hairmansis, M.J. Telebanco-Yanoria, M. Obara, N. Hayashi

and Y. Fukuta. 2021. Pathogenicity of isolates of the rice blast pathogen (*Pyricularia oryzae*) from Indonesia. Plant Dis., 105(3): 675–683 https://doi.org/10.1094/PDIS-05-20-0949-RE

Kakar, N., R. Bheemanahalli, S. Jumaa, E. Redoña, M.L. Warburton and K.R. Reddy. 2021. Assessment of agro-morphological, physiological and yield traits diversity among tropical rice. Peer J. 9:e11752 https://doi.org/10.7717/peerj.11752

Kalia, S. and R. Rathour. 2019. Current status on mapping of genes for resistance to leaf- and neck-blast disease in rice. Biotech., 9(6): 209 https://doi.org/10.1007/s13205-019-1738-0

Kassambara, A. and F. Mundt. 2016. Package 'factoextra'. Extract and visualize the results of multivariate data analyses. Dataset. (www.sthda.com/english/rpkgs/factoextra). https://doi.org/10.32614/CRAN.package.factoextra

Kim, J. and B. Vergara. 1991. Morpho-anatomical characteristics of different panicles in low and high tillering rices. Korean J. Crop Sci., 36(6): 568–575

Kirtphaiboon, S., U. Humphries, A. Khan and A. Yusuf. 2021. Model of rice blast disease under tropical climate conditions. Chaos, Solitons and Fract., 143: 110530 https://doi.org/10.1016/j.chaos.2020.110530

Lenné, J. and D. Wood. 2024. Crop diversity in agroecosystems for pest management and food production. Plant., 13(8): 1164 https://doi.org/10.3390/plants13081164

Li, R., M. Li, U. Ashraf, S. Liu and J. Zhang. 2019. Exploring the relationships between yield and yield-related traits for rice varieties released in China from 1978 to 2017. Front. Plant Sci., 10: 543 https://doi.org/10.3389/fpls.2019.00543

Liang, Z., J. Ruiz-Menjivar, L. Zhang, J. Zhang. and X. Shen. 2024. Examining the effects of adopting early maturing crop varieties on agricultural productivity, climate change adaptation, and mitigation. Int. J. Low-Carbon Tech., 19: 1256–1274 https://doi.org/10.1093/ijlct/ctad150

Meng, T., X. Chen, X. Zhang, J. Ge, G. Zhou, Q. Dai and H. Wei. 2021. Grain-filling characteristics in extra-large panicle type of early-maturing japonica/indica hybrids. Agric., 11(11): 1165 https://doi.org/10.3390/agriculture11111165

Ministry of Agriculture of the Republic of Indonesia. 2022. Minister of Agriculture Regulation Number 13 Year 2022 concerning the use of N, P, K fertilizer doses for rice, maize, and soybean on paddy fields. Ministry of Agriculture of the Republic of Indonesia, Indonesia,

Musa, Y., M. Farid, N. Nasaruddin, M.F. Anshori, A.F. Adzima, M.F. Maricar, A. Sulaiman, Y.C. Huang, H. Iswoyo, A.H. Bahrun and A. Adnan. 2023. Sustainability approach in cropping intensity (CI) 400 through optimizing the dosage of compost and chemical fertilizers to early-maturing rice varieties based on multivariate analysis. J. Agric. Food Res., 14: 100907 https://doi.org/10.1016/j.jafr.2023.100907

Mustikarini, E.D., T. Lestari, G.I. Prayoga, R. Santi and S. Dewi, 2020. Selection of red rice (*Oryza sativa* L.) resistant blast disease. IOP Conference Series: Earth and Env. Sci., 599(1): 012065 https://doi.org/10.1088/1755-1315/599/1/012065

Nasution, K.Y., N. Mustaqimah, P. Melati, A.K. Dewi, M.Y. Maryono, I. Dwimahyani and Sobrizal. 2025. Construction of near-isogenic lines for studying the resistance mechanism of durable blast resistant variety. IOP Conference Series: Earth and Env. Sci., 1478(1): 012001 https://doi.org/10.1088/1755-1315/1478/1/012001

Noviana, I., Y. Haryati, R. Sari and N. Sunandar. 2021. Adaptation to climate change by using drought tolerant and early maturing rice varieties in Majalengka Regency. IOP Conference Series: Earth Env. Sci., 648(1): 012118 https://doi.org/10.1088/1755-1315/648/1/012118

Nurhidayah, S., B.S. Purwoko, I.S. Dewi, W.B. Suwarno, I. Lubis and D. Efendi. 2025. Multi-trait selection of doubled haploid green super rice lines for good agronomic performance and brown planthopper resistance using MGIDI. AIMS Agric. Food., 10(4): 839–861 https://doi.org/10.3934/agrfood.2025044

Olivoto, T. and A.D. Lúcio. 2020. Metan: An R package for multi-environment trial analysis. Methods in Ecol. Evol., 11(6): 783–789 https://doi.org/10.1111/2041-210X.13384

Olivoto, T. and M. Nardino. 2021. MGIDI: Toward an effective multivariate selection in biological experiments. Bioinfo., 37(10): 1383–

1389 https://doi.org/10.1093/bioinformatics/btaa981

Parida, A.K., S. Sekhar, B.B. Panda, G. Sahu and B.P. Shaw. 2022. Effect of panicle morphology on grain filling and rice yield: Genetic control and molecular regulation. Front. Genet., 13: 876198. https://doi.org/10.3389/fgene.2022.876198

Sahu, P.K., R. Sao, D.K. Choudhary, A. Thada, V. Kumar, S. Mondal, B.K. Das, L. Jankuloski and D. Sharma. 2022. Advancement in the breeding, biotechnological and genomic tools towards development of durable genetic resistance against the rice blast disease. Plant., 11(18): 2386 https://doi.org/10.3390/plants11182386

Samantaray, S., J. Ali, K.L.C. Nicolas, J.L. Katara, R.L. Verma, C. Parameswaran, B.N. Devanna, A. Kumar, B. Dash and S.S. Bhuyan. 2021. Doubled haploids in rice improvement: Approaches, applications, and future prospects. p. 425-447. In: Ali, J. and S.H. Wani (eds), Rice improvement. Springer, Switzerland. https://doi.org/10.1007/978-3-030-66530-2_12

Saminadane, T., S. Geddam, P. Krishnaswamy, K. Jothiganapathy, A. Tamilselvan, B.R. Ramadoss, P. Sri Hari Reddy, U.S. Singh, R.K. Singh, J.D. Platten, G.B. Gregorio, N.K. Singh, D.S. Bisht, S. Kota, S. Ponnuvel and P. Guntupalli. 2024. Development of early maturing salt-tolerant rice variety KKL(R) 3 using a combination of conventional and molecular breeding approaches. Front. Genet., 14: 1332691 https://doi.org/10.3389/fgene.2023.1332691

Sao, R., P.K. Sahu, R.S. Patel, B.K. Das, L. Jankuloski and D.Sharma. 2022. Genetic improvement in plant architecture, maturity duration and agronomic traits of three traditional rice landraces through gamma ray-based induced mutagenesis. Plant., 11(24): 3448 https://doi.org/10.3390/plants11243448

Shanmugam, A., K. Manivelan, K. Deepika, G. Nithishkumar, V. Blessy, R.B. Monihasri, D. Nivetha, A. Roshini, P. Sathya, R. Pushpa, R. Manimaran, K. Subrahmaniyan, D. Sassikumar and R. Suresh. 2023. Unraveling the genetic potential of native rice (*Oryza sativa* L.) landraces for tolerance to early-stage submergence. Front. Plant Sci., 14: 1083177 https://doi.org/10.3389/fpls.2023.1083177

Simkhada, K. and R. Thapa. 2022. Rice blast, a major threat to the rice production and its various management techniques. Turkish J. Agric Food Sci. Tech., 10(2): 147–157 https://doi.org/10.24925/turjaf.v10i2.147-157.4548

Takai, T. 2024. Potential of rice tillering for sustainable food production. J. Exp. Bot., 75(3): 708–720 https://doi.org/10.1093/jxb/erad422

Valent, B. 2025. Dynamic gene-for-gene interactions undermine durable resistance. Mol. Plant-Microbe Interac., 38(2): 104-117 https://doi.org/10.1094/MPMI-02-25-0022-HH

Wang, F., Y. Liu, A. Zhang, D. Kong, J. Bi, G. Liu, X. Yu and L. Luo. 2022. Breeding an early maturing, blast resistance water-saving and drought-resistance rice (WDR) cultivar using marker-assisted selection coupled with rapid generation advance. Mol. Breed., 42(8): 46 https://doi.org/10.1007/s11032-022-01319-3

Wei, T., V. Simko, M. Levy, Y. Xie, Y. Jin and J. Zemla. 2017. Package 'corrplot', Dataset. (www.github.com/taiyun/corrplot).

Wickham, Chang, W. and M. Wickham. 2016. Package "ggplot2": An implementation of the Grammar of Graphics. Dataset. (www.github.com/hadley/ggplot2). https://doi.org/10.1007/978-3-319-24277-4

Younas, M.U., I. Ahmad, M. Qasim, Z. Ijaz, N. Rajput, S. Parveen Memon, W.U. Zaman, X. Jiang, Y. Zhang and S. Zuo. 2024. Progress in the management of rice blast disease: The role of avirulence and resistance genes through gene-for-gene interactions. Agron., 14(1): 163 https://doi.org/10.3390/agronomy14010163

Zhang, Y., C. Yu, J. Lin, J. Liu, B. Liu, J. Wang, A. Huang, H. Li and T. Zhao. 2017. (*OsMPH1*) regulates plant height and improves grain yield in rice. PLoS ONE., 12(7): e0180825 https://doi.org/10.1371/journal.pone.0180825

Zhu, D. and X. Pan. 1990. Rice (*Oryza sativa* L.): Guan 18-an improved variety through anther culture. p. 204-211. In: Bajaj, Y.P.S (ed), Haploids in crop improvement I. Springer-Verlag, Germany. https://doi.org/10.1007/978-3-642-61499-6_8