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Research article

Multi-trait selection of doubled haploid green super rice lines for good agronomic performance and brown planthopper resistance using MGIDI

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Abstract: Rice is a staple food for Asian people. Green super rice (GSR) features improved quantity and yield quality, resistance to major pests and diseases, and adaptability to planting in less favorable conditions. This study aimed to assess the agronomic performance of doubled haploid (DH) lines in advanced yield trials, select the best lines for multi-location yield trials, and evaluate resistance to brown planthopper (BPH) using the multi-trait genotype-ideotype distance index (MGIDI). The advanced yield trials were conducted at three locations in Indonesia—Indramayu (West Java), Bogor (West Java), and Malang (East Java)—from August 2022 to January 2023. Evaluation of the DH lines to brown planthopper was conducted in the greenhouse of the Center for Standard Instruments Testing of Rice, West Java, Indonesia, from October 2023 to January 2024. The materials used were 27 DH GSR lines and 3 check varieties (Inpari IR Nutri Zinc, Inpari 42 Agritan GSR, and Inpari 18) for advanced yield trials, and 20 DH GSR lines, two check varieties (Inpari 42 Agritan GSR and Inpari 18), two resistant checks (PTB33 and IR74), and a susceptible check (TN1) for evaluation of BPH

resistance. The experiment used a randomized complete block design with three replications. The results showed that the genotype × environment interaction had a significant effect on all agronomic traits. Nine DH lines (SN11, 14, 32, 40, 51, 57, 58, 59, and 60) had high yield, and among those, six (SN 40, 51, 57, 58, 59, and 60) had better resistance to BPH based on MGIDI selection. SN11 has a yield of 5.04 ton·ha^{-1} and is moderately resistant to BPH biotype 1. Lines SN57, 58, 59, and 60 have yields ranging from 5.29 to 5.67 ton·ha^{-1} and are resistant to all tested BPH. SN51 has a yield of 5.07 ton·ha^{-1} and is moderately resistant to all tested BPH. Those six lines are stable according to Kang's method and can be further evaluated to determine their adaptations across multiple environments.

Keywords: brown planthopper; doubled haploid; MGIDI; rice breeding

1. Introduction

Rice is one of the main food sources, being consumed by more than half of the world's population [1]. World rice production has experienced an increasing trend over the past decade, from 736 million tons in 2013 to 776 million tons in 2022 [2]. Workers in the agricultural sector in the last 20 years have experienced a significant decline from 40% (in 2000) to 27% (in 2021) of the total world population [3], while the need for consumption is increasing as the population grows each year. The number of hungry people in the world has increased from around 724 million in 2020 to 770 million in 2021 [3].

Breeders face various challenges in breeding new varieties, including an increasing population [4] and shifting consumer preferences regarding the importance of safe and environmentally friendly grain quality [5]. Moreover, global climate change has impacts such as droughts, high temperatures, and unpredictable weather [4], resulting in significant inputs of pesticides and synthetic fertilizers [3,6]. Apart from that, biotic factors that affect yield, such as pests and diseases, have also increased. The brown planthopper (BPH) is one of the main pests of rice plants [7], posing a significant threat due to its adaptability [8]. BPH, as a vector for multiple plant viruses, can quickly adjust to environmental conditions. It harms rice plants by extracting sap from their stems, causing them to wither and dry out [8]. The virulence of pests continues to change from previous populations [9]. Breeding of BPH-resistant varieties is an effective way to control damage [10].

Green Super Rice (GSR) is one potential solution to existing challenges. GSR has the characteristics of high yield with good grain quality, resistance to major pests and diseases, high nutrient efficiency, and drought tolerance, so it promises to significantly reduce inputs in the form of pesticides, synthetic fertilizers, and water [11]. Testing of GSR lines has been carried out in various countries. The GSR Huanghuazhan (HHZ) lines generally present higher yields than check varieties. The HHZ10-DT7-Y1 line has better morphological performance in terms of yield, 1000-grain weight, and biomass than the Hardinath-3, a drought-resistant check variety [12]. IR83142-B-20-B, WTR1, 08Fan2, and 926 were not significantly different from the Ciherang and Inpari 13 check varieties from 18 GSR lines [13]. The HHZ5-Y7-Y2-SUB1 line had a short posture with higher yields than Ciherang [13].

New varieties are expected to meet market demand regarding quantity and quality. Plant breeding can be done in several stages, such as determining goals, selecting, evaluating, and releasing varieties [14]. This cycle requires resources, including time, funding, and effort. The success of

developing food crops depends on the availability of genetic variability in the tested populations [15].

Variability can be created by crossing pure lines; the initial generation will segregate, requiring time for the loci to become homozygous to form inbred rice varieties. The large number of characters handled by breeders presents a challenge for effective genotype selection [16]. Normally, plants require 8 selfing cycles to obtain a homozygous line [17]. Doubled haploid technology through anther culture offers an alternative for accelerating the development of pure lines to breed superior rice varieties. There are many advantages to using anther culture, including accelerating the locus to become homozygous in a short time [18,19] or just one generation [17], allowing recessive genes to be expressed, and increasing genetic variability [20]. This technique reduces the plant breeding cycle to make the selection process more efficient [20].

Multi-character selection has been used to select potential lines, as it is better than using single-character selection [16]. The multi-trait genotype-ideotype distance index (MGIDI) is a relatively new statistical tool that can be used to select ideal genotypes by effectively selecting all variables in the evaluation process [21]. MGIDI is easy to handle and interpret, and it considers the inherent correlations among traits [21–23]. Therefore, in this research, the selection of superior DH lines and BPH-resistant genotypes was analyzed using the MGIDI approach.

This research material includes anther culture-derived DH lines of F1s from crosses involving several parents, such as Inpari 42 Agritan GSR, Inpari 46 GSR TDH, Inpari IR Nutri Zinc, B-22-1, and BioNil-6-1 varieties. The derivatives of these lines were selected from a preliminary yield trial [24]. The lines have been tested for bacterial leaf blight (BLB) resistance [25]. Then, a follow-up advanced yield trial was carried out to evaluate the agronomic performance of the selected lines. This research aims to select promising DH rice lines for good agronomic performance and their resistance to brown planthopper using the multi-trait genotype-ideotype distance index (MGIDI).

2. Materials and methods

2.1. Advanced yield trials

2.1.1. Description and study area

The research was conducted in three locations, Indramayu (West Java), Bogor (West Java), and Malang (East Java), from August 2022 to January 2023. Indramayu lies at an altitude of 34 m above sea level (asl), with an average temperature of 27.7 ℃, humidity of 82%, and rainfall of 603 mm·month^{-1} [26]. Bogor Regency has an altitude of 192 m asl, an average temperature of 21.3 ℃, humidity of 87.7%, and rainfall of 352 mm·month^{-1} [27]. Malang Regency has an altitude of 336 m asl, an average temperature of 23.8 ℃, an average humidity of 80.4%, and rainfall of 284 mm·month^{-1} [28].

2.1.2. Materials

The research material used consisted of 30 genotypes: 27 genotypes of DH2 generation originating from 5 combinations of biparental crosses (SN2: Inpari 42 Agritan GSR × B22-1; SN3–SN5: B-22-1 × Inpari 42 Agritan GSR; SN9–SN20: Inpari 42 Agritan GSR × Inpari 46 GSR TDH; SN25–SN52: Inpari 42 Agritan GSR × Inpari IR Nutri Zinc; SN57–SN60: Inpari 42 Agritan GSR ×

BioNil 6-1) and three check varieties (Inpari 42 Agritan GSR, Inpari IR Nutri Zinc, and Inpari 18) [24]. Fertilizers used were urea (46% N), SP-36 (36% P_2O_5), and KCl (60% K_2O) with dosages of 300, 100, and 100 kg·ha^{-1}, respectively.

2.1.3. Experimental design and cultural practices

The experiment was conducted at three locations using a randomized complete block design (RCBD) with genotype as a single factor and replicated three times. Each experimental unit was a plot size of 3 m × 3 m. Seeds of 30 genotypes were sown in a nursery and grown for 21 days. Three seedlings were transplanted per hole with a spacing of 25 cm × 25 cm.

Rice cultivation was carried out using the Standard Operating Procedure for Food Crop Varieties Release in Indonesia, including seeding, planting, maintenance, and harvesting [29]. Fertilization was applied three times. One week after planting (WAP), urea, SP-36, and KCl fertilizers were administered at 100 kg·ha^{-1}. The second and third applications involved only urea fertilizer, administered at 4 and 8 WAP at a rate of 100 kg·ha^{-1}.

Observed characters included plant height (cm), measured from ground level to the highest tip; the number of productive tillers, counted by those producing panicles; days to flowering (days after sowing, DAS), recorded when 50% of the plot had flowered; days to harvesting (DAS), determined when 90% of the rice grains turned yellow; panicle length (cm), measured from the panicle base to the tip; the weight of 1000 grains (g), obtained by weighing all grains; number of total grains, calculated by summing the number of filled and unfilled grains; the percentage of filled grains per panicle (%), calculated by comparing the number of filled grains to the total grain number; and productivity (ton·ha^{-1}), measured by converting plot yields at a 14% moisture content.

2.1.4. Data analysis

Data were analyzed using a combined analysis of variance using environment and genotype as fixed effects and replication within the environment as a random effect, with the following model:

$$Y_{ijk} = \mu + E_i + R_{ji} + G_k + (GE)_{ki} + \varepsilon_{ijk}, \quad (1)$$

where Y is the response variable, μ is the overall mean, E is the effect of environment, R is the effect of replication within the environment, G is the effect of genotype, GE is the effect of genotype by environment interaction, and ε is the experimental error.

Broad-sense heritability, following [30], was assessed by the following formula:

$$H^2_{bs} = \frac{\sigma^2_g}{\sigma^2_p} \times 100\%, \quad (2)$$

where H^2_{bs} is the broad-sense heritability, σ^2_g is the genotypic variance, and σ^2_p is the phenotypic variance. The broad-sense heritability can be classified as low (0%–20%), moderate (20%–50%), and high (> 20%).

The genotypic coefficient of variation (GCV), following [31], was calculated using the formula:

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100\%, \quad (3)$$

where $\bar{x}$ is the mean of each character. The GCV is classified as low (<20%), moderate (10%–20%), and high (> 20%).

Stability analysis using Kang's yield and stability index (YSi) method [32] utilizes the genotype mean yield across environments and Shukla's stability measure. The sum of each genotype's adjusted yield rank (Y) and Shukla's stability rating (S) determines the YSi statistic. Selected genotypes are those with YSi values > average YSi.

The MGIDI were computed by calculating the Euclidean distance between treatment scores and the ideal treatment/genotype following Olivoto and Nardino [22], as follows:

$$MGIDI_i = \left[\sum_{j=1}^{f} (\gamma_{ij} - \gamma_j)^2\right]^{0,5}, \quad (4)$$

where $MGIDI_i$ is the multi-trait genotype-ideotype distance index for the *i*th genotype/treatment; γ_{ij} is the score of the *i*th genotype per treatment in the *j*th factor (i = 1, 2, 3, ..., g; j = 1, 2, ..., f), being g and f the number of genotypes and factors, respectively; and γ_j is the *j*th score of the ideal genotype. The treatment with the lowest MGIDI is then closer to the ideal genotype and therefore presents desired values for all the p traits.

The strengths and weaknesses were estimated using Olivoto and Nardino [22], as follows:

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=1}^{f}\sqrt{D_{ij}^2}}, \quad (5)$$

Where ω_{ij} is the proportion of the MGIDI of the *i*th treatment explained by the *j*th factor, and D_{ij} is the distance between the *i*th treatment and the ideal genotype for the *j*th factor. Low contributions of a factor suggest that the traits within such a factor are close to the ideal genotype.

The best genotype is selected by considering heritability, Pearson correlation, principal component analysis, and economic weight using the MGIDI index [22]. The yield is given a weight of +5, while other traits are given a weight of +1. Each trait is multiplied by the PC1+PC2 weights for each main contributor in the PCA analysis.

Data analyses were performed using R with packages *factoextra* and *metan*, Meta R (data.cimmyt.org), and PBSTAT-GE 3.0.3 (pbstat.com).

2.2. Screening of brown planthopper resistance using bioassay in greenhouse

2.2.1. Study area and plant materials

The experiment was conducted from October 2023 to January 2024 in the greenhouse of the Center for Standard Instruments Testing of Rice (BBPSI Padi), Sukamandi, West Java, Indonesia. The BPH resistance test used 20 lines of DH3 generations selected from the advanced yield trials, PTB33 and IR72 as resistant checks, and TN1 as a susceptible check. BPH consists of four biotypes (biotypes 1, 2, 3, and the Cilacap population). The three selected BPH biotypes (biotypes 1, 2, and 3) were

collected from any areas in rice production centers, and the Cilacap population was collected from Cilacap, one of the rice production centers in Central Java, Indonesia. The three biotypes were from the BBPSI Padi collection and have been tested for their virulence against differential varieties. The screening tank measured 2 m × 0.8 m × 0.25 m. The tools used included an aspirator for helping in imago suction, wire mesh, Millar plastic, and a Millar plastic cover cloth for air ventilation.

2.2.2. Preparation of planting materials and infestation of BPH imago on rice seedlings

One-month-old rice plants were transferred into buckets to serve as a food source for BPH. Each bucket was covered with Millar plastic and cloth to contain the insects. A total of 25 pairs of male and female BPH adults (imago) were placed into each bucket to allow oviposition over a period of 2–3 nights. The resulting eggs were maintained until they developed into 2–3 instar nymphs.

Rice seeds were planted in a screening box of 20 seeds per line with a spacing of 2 cm and replicated 3 times randomly. The seeds were maintained until 6 DAS. Furthermore, 2–3 instar nymphs were infested evenly with as many as 8 individuals per plant on rice seedlings using the tapping method [33].

2.2.3. Evaluation of BPH resistance

Injury-caused insect calculations were carried out 5–6 days after infestation, at the same time as indicated by the TN1 experiencing > 50% death or all dead, with a score of 7–9 [34]. Scoring determination used a mode of 3 replications. Scoring and resistance criteria are presented in Table 1.

Table 1. Scores and resistance criteria for brown planthopper resistance in the greenhouse [34].

Score	Injuries caused by insects	Criteria of resistance
0	No injury	Highly resistant
1	Very slight injury	Resistant
3	First and second leaves of most plants are partially yellowing	Moderately resistant
5	Pronounced yellowing and stunting, or about 10%–25% of the plants wilting or dead, and the remaining plants severely stunted or dying	Moderately susceptible
7	More than half of the plants	Susceptible
9	All plants are dead	Highly susceptible

2.2.4. Data analysis

The assessment of brown planthopper resistance followed the Standard Evaluation System for Rice (SES) developed by IRRI [34]. The selection of genotypes with resistant traits was calculated using the multi-trait genotypes-ideotype distance index (MGIDI) following [23]. To each resistance score of all biotypes of BPH, a weight of +1 was assigned for each genotype. This was intended to accumulate GSR traits in selected lines with BPH resistance. The data were analyzed with the R package *metan* [35].

3. Results and discussion

3.1. Combined analysis of variance

The combined analysis of variance is presented in Table 2. Genotype (G) and environment (E) significantly affected most traits ($p < 0.01$), except for the genotype effect for the number of unfilled grains ($p < 0.05$). The G × E interaction significantly affected all traits ($p < 0.01$), except for panicle length ($p < 0.05$), due to differences in response patterns between genotypes across locations. This means that the variability between the tested genotypes and their rank performance may change due to changes in the environment. The large amount of genetic variability could be caused by various material sources (G) and environmental (E) influences that can influence plant phenotype [36]. The coefficient of variation (CV) for all traits ranged from 0.9% to 14.8%. A small coefficient of variation indicates that the experiment is reliable [37]. Experiments with a CV value of <15% are considered to have good accuracy; a CV close to 0 indicates a tendency for high precision of central data and low location variability [38].

Table 2. Combined analysis of variance on agronomic characteristics over three locations.

Traits	F-value			CV (%)
	G	E	G × E	
Plant height	17.05**	56.71**	1.62**	3.8
Number of productive tillers	1.81**	20.98**	1.42**	14.8
Days to flowering	4.58**	957.5**	14.59**	1.7
Days to harvesting	3.26**	1031.97**	18.77**	0.9
Panicle length	10.51**	5.32**	1.60*	3.4
Number of filled grains	6.39**	1.32**	1.99**	11.2
Number of unfilled grains#	1.98*	47.16**	3.19**	6.6
Number of total grains	8.33**	2.25**	2.09**	9.8
Percentage of filled grains	1.18**	21.86**	3.18**	6.3
Weight of 1000 grains	18.68**	45.18**	2.21**	3.5
Productivity	1.38**	42.99**	3.05**	12.5

Note: *, ** = significant at 0.05 and 0.01 levels, respectively. G = genotype. E: environment. G × E = genotype by environment interaction. CV = coefficient of variation. # = log-transformation was applied prior to ANOVA.

3.2. Performance of agronomic characters of DH GSR lines from anther culture

The agronomic characteristics of DH GSR lines derived from anther culture planted at three locations are presented in Table 3. The performance of the lines varied in agronomic characters, i.e., from lower to higher than the check variety, Inpari 42 Agritan GSR [34]. However, all the lines tested belong to the semidwarf category. Plant height is an important agronomic variable in rice that can influence biomass, yield, and the level of lodging [39,40]. The ideal rice plant height is around 90–100 cm to ease the maintenance and harvesting process in the field [41].

The number of productive tillers in the tested lines was high (20–25 tillers) [34]. Fourteen lines flowered and harvested faster than Inpari 42 Agritan GSR. The number of filled grains in 24 lines was

significantly lower, and three lines did not differ from Inpari 42 Agritan GSR.

Table 3. Average agronomic characteristics of DH GSR lines resulting from anther culture across three locations.

No.	Genotype	PH	NPT	DTF	DTH	PL	NFG	NUG	NTG	PFG	W1000
1	SN2	90.1[a]	19.4	84.7	122.6	23.9	166.9	44.6	211.5	79.1	23.46
2	SN3	90.9[a]	22.2	81.1[a]	121.0[a]	26.0[A]	135.6[a]	57.1[A]	192.8[a]	70.7[a]	23.32
3	SN5	90.4[a]	21.3	81.8[a]	121.6[a]	25.9[A]	131.3[a]	62.4[A]	193.7[a]	68.4[a]	22.79
4	SN9	95.3	23.9[A]	85.4	123.6	23.9	147.3[a]	58.4[A]	205.8	71.5[a]	22.83
5	SN10	92.9	21.9	84.4	124.1	23.2[a]	141.1[a]	45.3	186.4[a]	75.4	23.89[A]
6	SN11	92.0[a]	22.6	85.1	123.3	23.1[a]	141.8[a]	41.2	182.9[a]	77.6	23.58
7	SN12	92.8	22.6	84.6	123.9	22.9[a]	146.6	39.9	186.5[a]	78.7	23.58
8	SN13	89.7[a]	26.1[A]	82.2[a]	121.7[a]	23.9	140.2[a]	42.0	182.2[a]	76.8	23.00
9	SN14	92.5[a]	20.9	84.3	121.3[a]	22.6[a]	158.2	38.2[a]	196.3[a]	80.7	23.91[A]
10	SN15	91.7[a]	22.1	83.7[a]	121.1[a]	22.8[a]	143.6[a]	40.3	183.9[a]	78.2	24.08[A]
11	SN17	87.9[a]	21.4	85.0	123.9	22.4[a]	137.8[a]	46.6	184.4[a]	75.5	23.63
12	SN18	90.4[a]	22.4	83.7[a]	121.9[a]	22.5[a]	150.1[a]	43.3	193.4[a]	77.8	22.52
13	SN19	90.7[a]	22.4	83.0[a]	122.3[a]	22.2[a]	139.9[a]	42.2	182.1[a]	77.8	23.63
14	SN20	91.2[a]	21.2	84.1[a]	122.7	22.8[a]	140.3[a]	44.0	184.4[a]	76.7	23.60
15	SN25	88.4[a]	25.1[A]	82.4[a]	121.6[a]	24.2	109.4[a]	39.0[a]	148.4[a]	73.6[a]	22.39
16	SN27	80.7[a]	20.6	71.1[a]	113.4[a]	23.6[a]	91.3[a]	28.2[a]	119.5[a]	76.3	22.60
17	SN28	93.3	20.8	85.1	124.2	23.5[a]	145.7[a]	52.6	198.3[a]	73.9[a]	22.27[a]
18	SN32	80.7[a]	24.6[A]	81.8[a]	120.4[a]	23.9	130.2[a]	32.2[a]	162.4[a]	79.9	23.23
19	SN39	78.8[a]	23.1	80.3[a]	118.9[a]	21.6[a]	119.6[a]	28.4[a]	148.1[a]	80.8	25.03[A]
20	SN40	87.7[a]	24.0[A]	80.2[a]	120.3[a]	23.7[a]	113.5[a]	29.6[a]	143.0[a]	79.3	23.50
21	SN44	73.6[a]	25.2[A]	74.4[a]	114.6[a]	21.8[a]	105.3[a]	30.7[a]	136.1[a]	78.1	23.77[A]
22	SN51	76.8[a]	25.7[A]	78.3[a]	119.2[a]	22.3[a]	124.6[a]	34.3[a]	158.9[a]	78.4	21.73[a]
23	SN52	77.3[a]	23.9[A]	79.7[a]	119.7[a]	22.2[a]	121.4[a]	32.8[a]	154.2[a]	78.7	22.89
24	SN57	94.8	22.2	85.3	124.2	24.2	135.9[a]	39.2[a]	175.1[a]	77.4	25.10[A]
25	SN58	92.4[a]	22.2	84.2[a]	122.1[a]	23.9	136.4[a]	34.4[a]	170.9[a]	79.4	26.51[A]
26	SN59	94.4[a]	20.9	84.8	123.2	23.6[a]	122.0[a]	32.1[a]	154.1[a]	79.1	26.19[A]
27	SN60	91.0[a]	23.3[A]	85.1	122.9	23.5[a]	122.2[a]	32.8[a]	154.9[a]	78.9	25.54[A]
28	Inpari 42	95.4	20.6	85.3	123.4	24.4	167.1	47.1	214.2	77.8	23.02
29	Inpari NZ	91.8[a]	23.5[A]	81.4[a]	120.2[a]	25.3[A]	137.3[a]	33.1[a]	170.4[a]	81.1	23.57
30	Inpari 18	91.9[a]	19.1	73.1[a]	114.6[a]	22.9[a]	103.3[a]	41.1	144.4[a]	71.9[a]	31.30[A]
	Mean	88.9	22.5	82.2	121.3	23.4	133.5	40.4	174.0	76.9	23.88
	LSD 0.05	2.66	2.59	1.06	0.85	0.62	11.69	7.71	13.25	3.79	0.65
	CV (%)	3.83	14.8	1.66	0.90	3.40	11.23	6.63	9.77	6.31	3.49

Note: SN1-SN60 = GSR lines. PH = plant height (cm). NPT = number of productive tillers (tillers). DTF = days to flowering (d). DTH = days to harvesting (d). PL = panicle length (cm). NFG = number of filled grains. NUG = number of unfilled grains. NTG = number of total grains. PFG = percentage of filled grains (%). W1000 = weight of 1000 grains (g). Prd = productivity (ton·ha^{-1}). Letters in the same column indicate significantly lower (a) or higher (A) values compared to the Inpari 42 Agritan GSR variety based on the LSD test at the 0.05 level.

The number of grains and filled grains per panicle and yield per plant are the main contributors to yield traits [42]. Weights of 1000 grains for SN10, 11, 14, 15, 39, 44, 57, 58, 59, and 60 ranged from 23.89 to 26.51 g, being significantly higher than Inpari 42 Agritan GSR (23.02 g). Previous research by Susanto and Rohaeni [43] reported that the weight of 1000 grains of the Inpari 42 Agritan GSR variety was 22.15 g, while formal descriptions of the varieties stated this value as being 24.1 g [44].

3.3. Variance components and heritability estimates

Heritability estimations are routine in plant breeding and genetic studies [45]. Heritability values can be useful in predicting the response to selection. Selection is influenced by the environment and genotype × environment interaction [46]. Heritability is calculated from the ratio of genotypic variance to phenotypic variance [15]. Broad-sense heritability is divided into three categories, i.e., low (< 20%), moderate (20%–50%), and high (> 50%) [30].

Table 4. Variance components and heritability of DH GSR lines resulting from anther culture across three locations.

Traits	σ_g^2	σ_{ge}^2	σ_e^2	GCV	GCV category	H^2_{bs} (%)	H^2_{bs} category
PH	33.6	2.4	11.6	6.52	Low	94.1	High
NPT	1.4	1.6	11.1	5.26	Low	44.8	Moderate
DF	1.1	0.1	0.6	4.47	Low	90.5	High
DH	10.8	8.4	1.9	4.00	Low	78.2	High
PL	5.6	7.0	1.2	6.17	Low	69.3	High
NFG	268.1	74.4	224.8	12.26	Moderate	84.3	High
NUG	43.3	73.3	97.7	16.27	Moderate	55.1	High
NTG	490.9	104.8	288.7	12.74	Moderate	88.0	High
PFG	1.5	17.1	23.6	1.59	Low	15.4	Low
W1000	3.0	0.3	0.7	7.25	Low	94.7	High
PRD	0.1	0.3	0.4	6.27	Low	27.7	Moderate

Note: σ^2_g = genotypic variance. σ^2_{ge} = genotype × environment variance. σ^2_e = environment variance. GCV = genotypic coefficient of variation. H^2_{bs} = broad-sense heritability. PH = plant height. NPT = number of productive tillers. DTF = days to flowering. DTH = days to harvesting. PL = panicle length. NFG = number of filled grains. NUG = number of unfilled grains. NTG = number of total grains. PFG = percentage of filled grains. W1000 = weight of 1000 grains. Prd = productivity.

The analysis of variance components is presented in Table 4. Almost all of the characters are categorized as having high heritability. The productivity and the number of productive tillers are in the moderate category of heritability, except for the percentage of filled grain, which is in the low category of heritability. These results are in line with those reported by Bhargavi et al. [15], who found that characters such as the flowering age, panicle length, harvest age, and the weight of 1000 grains had high heritability. The same results were also reported by Hasan-Ud-Daula and Sarker [47], who found that almost all the same agronomic characters had high heritability in the eight lines tested. Another study reported by Dhakal et al. [12] found that 1000-grain weight and yield characteristics had high

heritability in the GSR line. In contrast to that reported by Lakshmi et al. [48], harvest age and panicle length have low heritability, but other characters have moderate to high heritability. High heritability indicates low environmental influence. Traits with high heritability can be used for selection activities [49].

The analysis in Table 4 indicates that the genotypic coefficient of variation (GCV) value is in the low to moderate category, in line with research by Hasan-Ud-Daula and Sarker [47], who found that the flowering age, harvest age, and panicle length have low GCV values, but moderate GCV for the amount of filled grain. Many factors influence heritability, including the characteristics of the population used, the genotype sample being evaluated, the heritability calculation method used, the size of the genotype evaluation, linkage disequilibrium, and the conditions at the time of the research [50].

3.4. Correlation analysis of DH GSR lines in three locations

Correlation describes the closeness between variables and grain yield. Correlation analysis is associated with the interrelationships between independent and dependent traits in rice yield [51]. Based on the results of the correlation analysis (Table 5), the phenotypic correlations of productivity were significantly positive with days to flowering ($r = 0.52$, $p < 0.01$), days to harvesting ($r = 0.48$, $p < 0.01$), and panicle length ($r = 0.42$, $p < 0.05$). Similarly, significant, positive correlations were found between productivity and days to flowering ($r = 1.00$, $p < 0.01$), days to harvesting ($r = 1.00$, $p < 0.01$), panicle length ($r = 0.82$, $p < 0.01$), number of filled grains ($r = 0.45$, $p < 0.05$), and number of total grains ($r = 0.44$, $p < 0.05$).

Table 5. Genotypic correlations (lower diagonal) and phenotypic correlations (upper diagonal) for agronomic characters of DH GSR lines.

PC / GC	PH	NPT	DTF	DTH	PL	NFG	NUG	NTG	PFG	W	PRD
PH		-0.48	0.65	0.66	0.46	0.57	0.52	0.62	-0.23	0.23	0.27
NPT	-0.75		-0.09	-0.07	-0.12	-0.26	-0.29	-0.30	0.18	-0.41	0.14
DTF	0.81	-0.09		0.97	0.17	0.78	0.38	0.73	0.12	-0.20	0.52**
DTH	0.89	-0.11	1.00		0.22	0.73	0.45	0.72	0.01	-0.25	0.48**
PL	0.49	-0.23	0.21	0.27		0.14	0.47	0.28	-0.45	-0.11	0.42*
NFG	0.62	-0.33	1.00	1.00	0.11		0.51	0.95	0.12	-0.28	0.37
NUG	0.71	-0.62	0.60	0.76	0.60	0.83		0.76	-0.78	-0.21	0.09
NTG	0.67	-0.43	0.93	0.99	0.26	0.99	0.91		-0.20	-0.29	0.31
PFG	-0.62	0.96	0.39	0.06	-1.00	-0.19	-0.72	-0.36		0.00	0.19
W1000	0.26	-0.59	-0.25	-0.32	-0.11	-0.30	-0.28	-0.31	-0.02		-0.02
PRD	0.32	0.20	1.00**	1.00**	0.82**	0.45*	0.36	0.44*	0.06	-0.07	

Note: GC = genotypic correlation. PC = phenotypic correlation. PH = plant height. NPT = number of productive tillers. DTF = days to flowering. DTH = days to harvesting. PL = panicle length. NFG = number of filled grains. NUG = number of unfilled grains. NTG = number of total grains. PFG = percentage of filled grains. W1000 = weight of 1000 grains. PRD: productivity. *, ** = significant at $p < 0.05$ and $p < 0.01$ levels, respectively.

In line with the report by Adhikari et al. [52], a significant positive correlation also occurred between days to flowering and panicle length to yield. Another study by Saleh et al. [53] reported a significant positive correlation between yield and the panicle number per plant, number of filled grains per panicle, and weight of 1000 grains, with a significant negative correlation with days to flowering. This is slightly different from the report by Al-Daej [54] in which the grain yield was not only influenced by the filled grain per panicle, but there was also a contribution by the number of tillers per plant, the number of productive tillers, and plant height. A negative genotypic correlation between grain yield and plant height, unfilled grain, and flowering age occurred, but not for the number of productive tillers, panicle length, filled grains per panicle, and the weight of 1000 grains, which are significantly positively correlated with grain yield [55].

Several agromorphological characters significantly correlate with rice yield. However, environmental effects may influence such correlations [47,56]. Selection based on traits that are positively correlated with grain yield will determine the success of a breeding program [53]. Although there is a significant correlation between days to flowering and days to harvesting in this study, the days to harvesting the lines are still equivalent to the parent Inpari 42 Agritan GSR at around 120 DAS. Moreover, different environmental factors resulted in different harvest ages.

3.5. Principal component analysis of DH GSR lines across three locations

Based on principal component analysis (Table 6), the variability explained by the first principal component (PC1) was 44.4%, followed by 18.7% by PC2 and 10.9% by PC3. In PC1, plant height, days to flower, days to harvest, number of filled grains, and number of total grains significantly affected population variability. Moreover, PC2 showed high variability in the number of productive tillers, the percentage of filled grain, and productivity.

Table 6. Principal component analysis of agronomic characters of DH GSR lines from anther culture across three locations.

Traits	PC1	PC2	PC3	PC4	PC5
Plant height	0.36	0.16	0.30	-0.14	0.23
Number of productive tillers	-0.14	-0.35	-0.51	-0.16	0.47
Days to flowering	0.39	-0.28	0.09	0.00	0.32
Days to harvesting	0.39	-0.22	0.02	0.01	0.40
Panicle length	0.21	0.27	-0.25	-0.58	-0.31
Number of filled grains	0.39	-0.19	0.07	0.24	-0.33
Number of unfilled grains	0.34	0.37	-0.26	0.15	0.06
Number of total grains	0.42	-0.01	-0.04	0.24	-0.23
Percentage of filled grains	-0.11	-0.59	0.31	0.00	-0.31
Weight of 1000 grains	-0.09	0.23	0.64	-0.28	0.28
Productivity	0.20	-0.29	-0.03	-0.64	-0.19
Eigen value	4.88	2.05	1.52	1.19	0.57
Variability (%)	44.4	18.7	10.9	5.2	3.9
Accumulated variability (%)	44.4	63.0	76.8	87.7	92.9

In Figure 1, the two principal components (PC1 and PC2) provide an accumulated variability of

63% in the tested population. The lines show variability as shown by the distribution in each quadrant. Longer PCA arrows indicate a greater role of characters in grouping [57]. Principal components (PCs) with eigenvalues more than 1.00 were considered significant, and PC1 was the main contributor to the total variance [58]. Twelve lines (SN2, 11, 12, 13, 14, 15, 18, 19, 20, 57, 58, and 59) and Inpari IR Nutri Zinc were affected by days to harvesting (DTH), days to flowering (DTF), number of filled grains (NFG), and number of total grains (NTG). Seven lines (SN39, 40, 44, 51, 52, 32, and 60) were affected by the percentage of filled grains. Six lines (SN3, 5, 9, 10, 17, 28) and Inpari 42 Agritan GSR were affected by plant height and number of unfilled grains (NUG). Two lines, SN25 and SN27, and Inpari 18 were affected by the weight of 1000 grains.

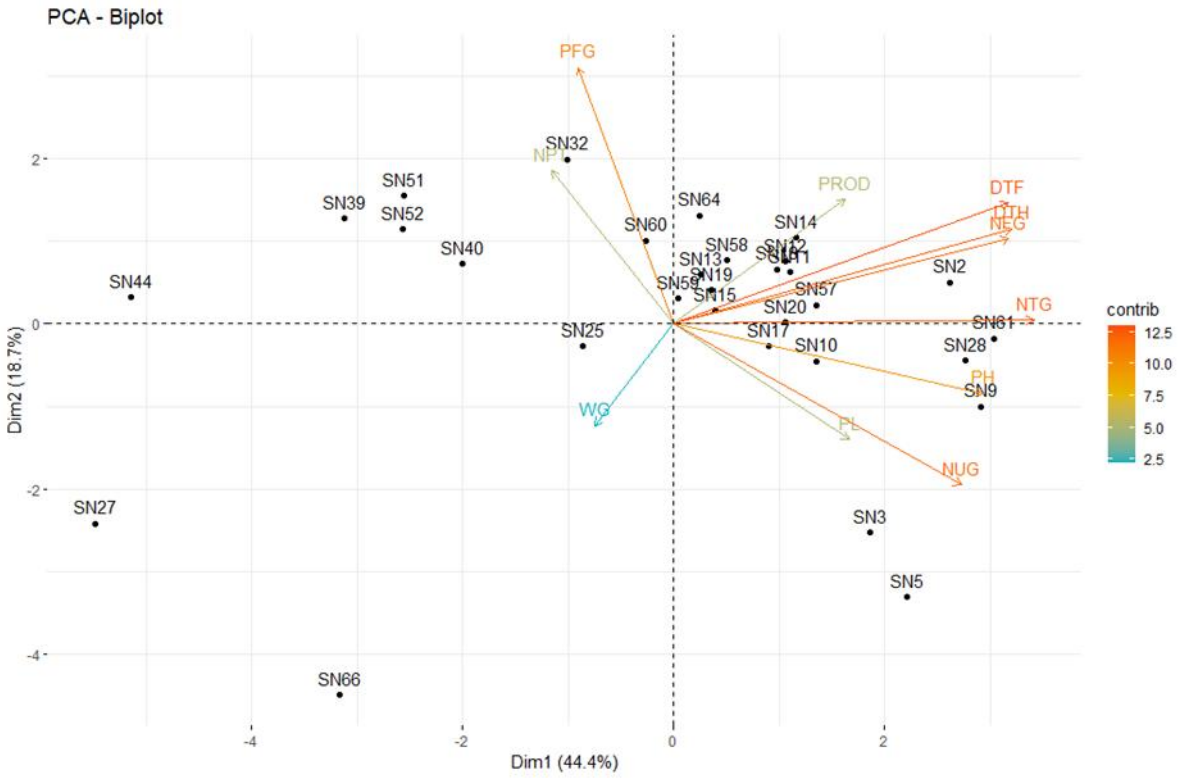

Figure 1. Biplot analysis of principal component analysis. SN1–60 = GSR lines. SN61 = Inpari 42 Agritan GSR. SN64 = Inpari IR Nutri Zinc. SN66 = Inpari 18. PH = plant height. NPT = number of productive tillers. DTF = days to flowering. DTH = days to harvesting. PL = panicle length. NFG = number of filled grains. NUG = number of unfilled grains. NTG = number of total grains. PFG = percentage of filled grains. W1000 = weight of 1000 grains. PRD: productivity.

3.6. Selection of genotypes of DH GSR lines based on MGIDI

In the MGIDI index analysis (Table 7, Figure 2), the weights assigned were based on the economic value of productivity traits and the PCs (PC1 and PC2). Productivity was given a higher weight of +5, followed by PH, PFG, and NTG, each given a weight of +1, with the formula I = 5 * 0.2 PRD + 1 * 0.36 PH + 1 * 0.59 PFG + 1 * 0.42 NTG. NTG had a positive genotypic correlation with productivity. NTG, PH, and PFG contributed to variability in the PCA analysis (PC1 and PC2). Several studies in

DH lines produced by anther culture have selected potential lines using selection indices in accordance with heritability, correlation, and principal component analysis [59−61]. Selection index with correlation value and path analysis approaches reported by Saleh et al. [53]. Heritability, correlation, path analysis, and cluster analysis approaches were reported by Ata-Ul-Karim et al. [42].

Based on MGIDI, nine potential genotypes were selected, namely SN60, 59, 58, 32, 14, 40, 57, 51, and 11 (Figure 2a). These lines have a plant height of 76.8–94.8 cm, number of grains per panicle of 143–196.3, percentage of filled grains of 77.4%–80.7%, and a grain yield of 5.04–5.67 tons·ha^{-1}. Factor analysis 1 consists of the number of total grains (NTG) and plant height (PH), and factor analysis 2 consists of productivity and percentage of filled grains (PFG) (Table 7). SN11, 32, 40, 59, and 60 have FA 1 (NTG and PH) strengths but are weak in FA2 (productivity and PFG) (Figure 2b). SN14, 51, 57, and 58 have strengths in FA2 (productivity and PFG) but are weak in FA1 (NTG and PH) (Figure 2b).

Table 7. Factor communalities, uniqueness, and selection differential of four agronomic traits of DH GSR lines from MGIDI analysis across three locations.

Variation	Factor	Communality	Uniquenesses	Xo	Xs	SD %	Sense	Goals
NTG	FA1	0.77	0.23	174.00	-0.46	-4.29	I	0
PH	FA1	0.76	0.24	88.91	0.23	0.26	I	100
Productivity	FA2	0.75	0.25	5.04	0.26	5.23	I	100
PFG	FA2	0.78	0.22	76.99	2.00	2.60	I	100

Note: NTG = number of total grains. PH = plant height. PFG = percentage of filled grains. Xo = mean of original population. Xs = mean of selected genotypes. I = increased.

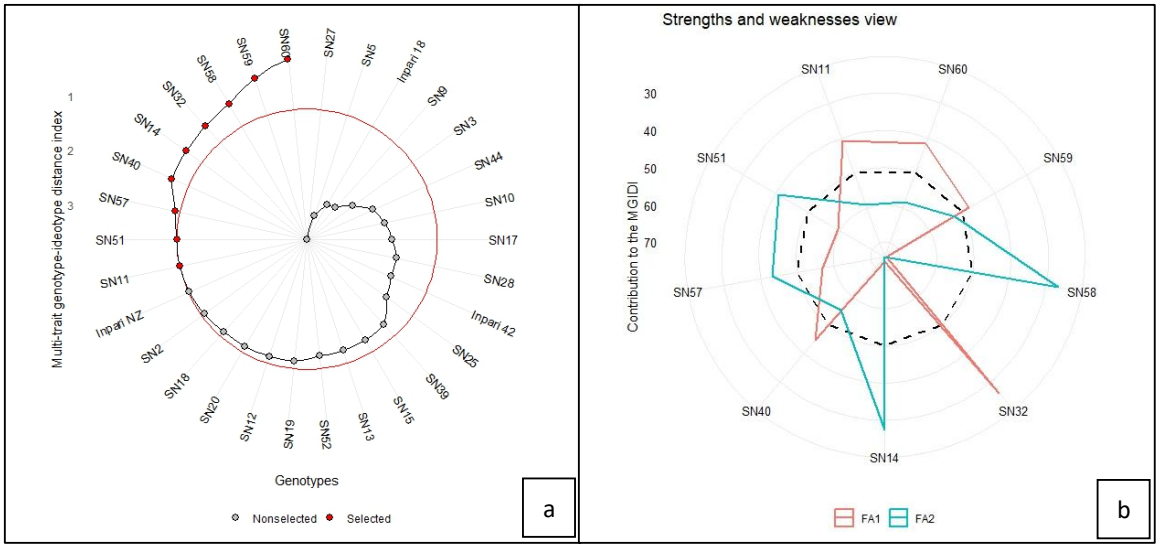

Figure 2. (a) Genotype ranking for productivity, PH, PFG, and NTG using the MGIDI index with a selection intensity of 30%. The selected genotypes are labeled with red dots, while the circle represents the cut point according to the selection pressure. (b) The strengths and weaknesses of the selected genotype are shown in the proportion of each factor in the computation. FA1 = NTG and PH. FA2 = Productivity and PFG.

Table 8. Mean productivity and yield-stability index (YSi) of DH GSR lines from anther culture evaluated in three locations.

No.	Genotype	Indramayu	Bogor	Malang	Mean	YSi
		(ton·ha^{-1} grain yield)				
1	SN2	5.30 [A]	4.80	6.53	5.54 [A]	29+
2	SN3	5.63 [A]	4.27	5.73	5.21	15+
3	SN5	5.00	4.07	6.27	5.11	21+
4	SN9	4.97	3.50 [a]	6.97 [A]	5.14	18+
5	SN10	4.80	3.83	5.37	4.67	3
6	SN11	4.87	4.20	6.07	5.04	16+
7	SN12	4.33	4.17	5.70	4.73	6
8	SN13	5.37 [A]	3.80	5.47	4.88	2
9	SN14	4.97	4.37	5.87	5.07	19+
10	SN15	4.57	4.17	5.30	4.68	2
11	SN17	4.80	4.33	4.73 [a]	4.62	-6
12	SN18	4.73	4.57	5.43	4.91	7.5
13	SN19	4.73	4.47	5.23	4.81	4
14	SN20	4.70	4.60	6.00	5.10	20+
15	SN25	4.70	3.93	6.57	5.07	17.5+
16	SN27	2.93 [a]	2.90 [a]	5.60	3.81 [a]	-2
17	SN28	4.53	4.53	7.50 [A]	5.52 [A]	23+
18	SN32	5.40 [A]	4.60	7.73 [A]	5.91 [A]	31+
19	SN39	3.83	4.80	5.70	4.78	-1
20	SN40	4.13	3.97	6.90 [A]	5.00	11
21	SN44	4.93	3.70	5.43	4.69	3
22	SN51	5.07	3.80	6.33	5.07	17.5+
23	SN52	4.73	3.43 [a]	6.57	4.91	11.5
24	SN57	4.23	4.47	7.23 [A]	5.31	21+
25	SN58	4.30	4.30	8.40 [A]	5.67 [A]	22+
26	SN59	4.33	3.90	7.63 [A]	5.29	16+
27	SN60	4.27	4.47	7.47 [A]	5.40 [A]	18+
28	Inpari 42 Agritan GSR	4.27	4.33	5.87	4.82	9
29	Inpari IR Nutri Zinc	5.00	4.93	7.93 [A]	5.96 [A]	28+
30	Inpari 18	4.23	3.73	5.73	4.57	1
	Mean	4.66	4.16	6.31	5.04	5.04
	LSD 0.05	0.97	0.79	0.81	0.49	
	CV (%)	15.33	13.94	9.36	12.52	

Note: The same lowercase or uppercase letters in the column indicate no significant differences. a = significantly lower than Inpari 42 Agritan GSR. A = significantly higher than Inpari 42 Agritan GSR based on the LSD test 5%. + = selected genotype with YSi higher than the mean YS.

The selection determination is carried out so that the selection does not cause subjectivity, so it will not obscure the selection of the lines being tested [62]. Simultaneous selection through an

economic value approach, considering heritability and genetic or phenotypic correlation, has the potential for choosing the best genotype [62]. The productivity character is given a greater weight based on the principal component analysis result [60]. The heritability value and direct effect are also considered to improve the weight of secondary characters [60].

3.7. Yield stability analysis of DH GSR lines across three locations

Productivity varied within location (Table 8). Productivity at the Indramayu ranged from 2.93 to 5.63 tons·ha^{-1}, with an average of 4.66 tons·ha^{-1}. Grain yields in Bogor ranged from 2.9 to 4.93 tons·ha^{-1}, with an average of 4.16 tons·ha^{-1}, while in Malang, they ranged from 4.73 to 8.4 tons·ha^{-1}, with an average of 6.31 tons·ha^{-1}. The average productivity across the three locations was 5.04 tons·ha^{-1} (Table 8).

The Malang location had the highest yield of the other two. Differences in yield at planting locations seemed to be determined by soil fertility, altitude, temperature, and rainfall during the growing season. The Malang location has alluvial soil, which is more fertile than the latosol soil type in Bogor and Indramayu. Furthermore, Malang has a warmer temperature (23.8 ℃) than Bogor (21.3 ℃). The optimum temperature for rice plants is 25–35 ℃ [63]. SN2, 28, 32, 58, 60, and Inpari IR Nutri Zinc had significantly higher productivity than Inpari 42 Agritan GSR at three locations.

Kang's method [32] determines yield stability by the rank value of each genotype (YSi). The rank is calculated from the average genotypes corrected for the Shukla variance, then ranked again for each genotype. A line is considered stable if the line rank (YSi) is above the average of the total line ranks ($\overline{YS}$) or ($YSi > \overline{YS}$) (Table 8). DH lines of SN2 (5.54 tons·ha^{-1}), SN3 (5.21 tons·ha^{-1}), SN5 (5.11 tons·ha^{-1}), SN9 (5.14 tons·ha^{-1}), SN11 (5.04 tons·ha^{-1}), SN14 (5.07 tons·ha^{-1}), SN20 (5.10 tons·ha^{-1}), SN25 (5.07 tons·ha^{-1}), SN28 (5.52 tons·ha^{-1}), SN32 (5.91 tons·ha^{-1}), SN51 (5.07 tons·ha^{-1}), SN57 (5.31 tons·ha^{-1}), SN58 (5.67 tons·ha^{-1}), SN59 (5.29 tons·ha^{-1}), and SN60 (5.40 tons·ha^{-1}), and also variety Inpari IR Nutri Zinc (5.96 tons·ha^{-1}), are stable genotypes and have higher grain yields than Inpari 42 Agritan GSR (4.82 tons·ha^{-1}) and Inpari 18 (4.57 tons·ha^{-1}).

3.8. Evaluation of resistance to four biotypes of BPH using MGIDI

Based on Table 9, the tested lines exhibited varying responses, with resistance scores ranging from 1 to 7, being classified from resistant to susceptible. A total of 13 lines was moderately susceptible across all tested BPH. Two lines (SN40 and SN51) and a check variety IR74 demonstrated moderately resistant responses to all tested BPH. Meanwhile, four lines (SN57, 58, 59, and 60), along with the resistant check PTB33, exhibited good resistance, categorized as resistant to all tested BPH.

These results are consistent with the MGIDI analysis of agronomic traits when the lines were selected as the four top promising candidates. The lines must have BPH resistance because it is one of the mandatory requirements for releasing new rice varieties [29]. BPH populations are capable of adapting to the environment by altering their virulence and forming new biotypes [64]. Rainfall, evening humidity, and maximum temperature influence the development of BPH abundance [7]. In addition, high temperatures and rainfall during the dry season can increase BPH abundance [65].

Based on factor loading, all tested BPH were placed in one group, i.e., FA1 (Table 10). The contribution of genotypes to MGIDI indicates that all tested BPH had a strong relationship with factor analysis 1 (FA1), with values ranging from −0.97 to −0.99 (Table 10). FA value was closer to 1, indicating a strong relationship between the trait and FA. This is confirmed by the resulting

communality value (Table 10). The correlation between traits and factors is determined by the loading value of orthogonal rotation, ranging from −1 to +1 [22]. The selection differentials ranged from −55.8% (Biotype 1) to –60.6% (Biotype 3) (Table 10). The SD percentage value is desired for BPH resistance.

Table 9. Score and criteria for BPH resistance in DH GSR lines.

No.	Genotype	Biotype 1		Biotype 2		Biotype 3		Cilacap population	
		Score	Criteria	Score	Criteria	Score	Criteria	Score	Criteria
1	SN2	5	MS	5	MS	5	MS	5	MS
2	SN3	5	MS	5	MS	5	MS	5	MS
3	SN5	5	MS	5	MS	5	MS	5	MS
4	SN9	5	MS	5	MS	7	S	5	MS
5	SN11	3	MR	5	MS	5	MS	5	MS
6	SN12	5	MS	5	MS	5	MS	5	MS
7	SN13	5	MS	5	MS	5	MS	5	MS
8	SN14	5	MS	5	MS	5	MS	5	MS
9	SN15	5	MS	5	MS	7	S	5	MS
10	SN18	5	MS	5	MS	5	MS	5	MS
11	SN20	5	MS	5	MS	5	MS	5	MS
12	SN25	5	MS	5	MS	7	S	5	MS
13	SN28	5	MS	5	MS	7	S	5	MS
14	SN32	5	MS	5	MS	5	MS	5	MS
15	SN40	3	MR	3	MR	3	MR	3	MR
16	SN51	3	MR	3	MR	3	MR	3	MR
17	SN57	1	R	1	R	1	R	1	R
18	SN58	1	R	1	R	1	R	1	R
19	SN59	1	R	1	R	1	R	1	R
20	SN60	1	R	1	R	1	R	1	R
21	Inpari 42	5	MS	5	MS	5	MS	5	MS
22	Inpari 18	3	MR	5	MS	5	MS	5	MS
23	PTB33/RC	1	R	1	R	1	R	1	R
24	IR 74	3	MR	3	MR	3	MR	3	MR
25	TN 1/SC	9	HS	9	HS	9	HS	9	HS

Note: RC = resistant check. SC= susceptible check. R = resistant. MR = moderately resistant. MS = moderately susceptible. S = susceptible. HS = highly susceptible. RC = resistant check. SC = susceptible check.

Table 10. Factor loading after rotation, communalities, genetic value, and an indicator for BPH resistance.

Biotypes	FA1	Communality	Uniquenesses	Xo	Xs	SD %	Sense	Goals
1	−0.98	0.95	0.05	3.96	1.75	−55.8	D	100
2	−0.99	0.99	0.01	4.12	1.75	−57.5	D	100
3	−0.97	0.94	0.06	4.44	1.75	−60.6	D	100
Cilacap	−0.99	0.99	0.01	4.12	1.75	−57.5	D	100

Note: Xo = mean of original population. Xs = mean of selected genotypes. SD = selection differential. D = Decrease.

The MGIDI index in this study was carried out by weighting the four traits measured. Each trait was given a weight of +1. The lowest MGIDI indicates an ideal treatment with desired traits [22]. Loading resulting treatment rankings, when combined with strengths and weaknesses, can be used by researchers to recommend the best treatment [22].

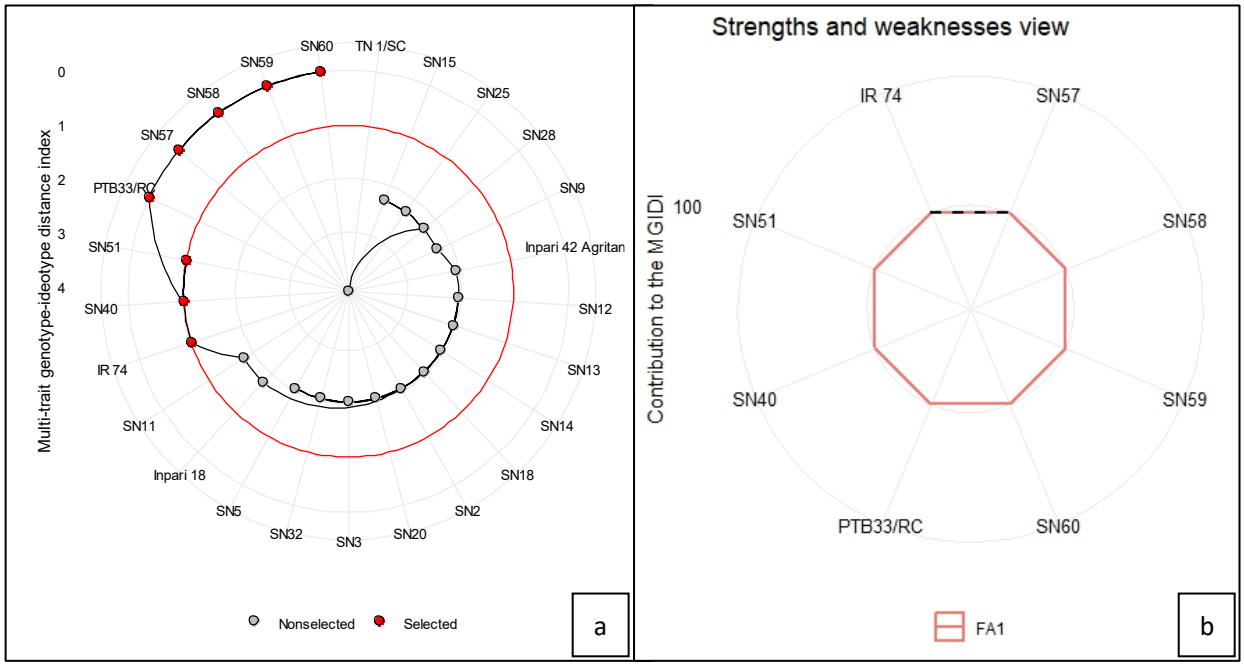

Figure 3. (a) Genotype ranking for resistance of biotypes of BPH using the MGIDI index with a selection intensity of 30%. The BPH resistance test used 20 lines of DH3 generations selected from the advanced yield trials. The selected genotypes are labeled with red dots, and the circle represents the cut point according to the selection pressure. (b) The strengths and weaknesses of the selected genotype were aligned with the proportion of each factor in the computation. FA1 = biotypes 1, 2, 3, and population Cilacap. SN2 to SN 60 = lines of DH3 generations. PTB33 and IR72 = resistant check. TN1 = susceptible check. Inpari 42 Agritan GSR and Inpari 18 are check varieties.

Meanwhile, the top six selected lines at 30% selection intensity were SN40, 51, 57, 58, 59, and 60, which had suitable index values based on resistance to all tested BPH (Figure 3a). MGIDI ranks all genotypes based on the value of the desired traits [66]. The distance of genotypes using MGIDI facilitates the selection process for breeders, highlighting characteristics that are easy to interpret and unique, avoiding multicollinearity issues, and that are free from weighting coefficients [22]. MGIDI can assist breeders in selecting ideal genotypes for developing new varieties [68].

Six lines (SN40, 51, 57, 58, 59, and 60) and a resistant check (PTB33 and IR 74) had the same strength to FA1 (Figure 3b). The dashed line shows the theoretical value if all the factors contributed equally [68].

The SN51 line is moderately resistant to all tested BPH. SN51 results from a cross between Inpari 42 Agritan GSR × Inpari IR Nutri Zinc. Inpari 42 GSR has resistance to BPH biotype 1, and Inpari IR Nutri Zinc is moderately resistant to biotypes 1 and 2 [44]. SN57, 58, 59, and 60 lines resist all tested

BPH. These lines result from a cross between Inpari 42 Agritan GSR × BioNL 6-1. BioNL 6-1 is a line derived from Ciherang × Swarnalata [69]. Having the *Bph*6 resistance gene, BioNL 6-1 showed resistance to biotype 1, biotype 2, biotype 3, Bekasi, and Klaten populations [69]. Inpari 42 resulted from the selection of the elite Huanghuazhan variety, which had the *bph*3, *Bph*6, and *Bph*9 genes [70].

4. Conclusions

The genotype × environment interaction significantly affected all observed characters, i.e., plant height, number of productive tillers, days to flowering, days to harvesting, panicle length, number of filled grains, number of unfilled grains, number of total grains, percentage of filled grains, weight of 1000 grains, and productivity. SN11 had a yield of 5.04 ton·ha^{-1}, showing moderate resistance to BPH biotype 1. Lines SN57, SN58, SN59, and SN60 had yields ranging from 5.29 to 5.67 ton·ha^{-1}, being resistant to all tested BPH. Line SN51 had a yield of 5.07 tons·ha^{-1}, being moderately resistant to all tested BPH. These six DH lines are stable according to Kang's method. Therefore, these DH lines will be subjected to further evaluation in a broader range of environments to determine their stability and adaptations and to fulfill the requirements for the release of a new rice variety.

Author contributions

Siti Nurhidayah, Bambang Sapta Purwoko, Iswari Saraswati Dewi, Willy Bayuardi Suwarno, Iskandar Lubis and Darda Efendi: Methodology, Writing – original draft, Writing – review & editing. All authors contributed equally to the manuscript. All authors have read and agreed to the published version of the manuscript.

Use of Generative-AI tools declaration

The authors declare that they have not used artificial intelligence tools in the creation of this article.

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Conflict of interest

The authors declare that there is no conflict of interest regarding the publication of this article.

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