AIMS Agriculture and Food, 11(4): 847–866.
DOI: 10.3934/agrfood.2026042
Received: 30 March 2026
Revised: 14 September 2026
Accepted: 15 September 2026
Published: 10 October 2026

https://www.aimspress.com/journal/agriculture

Research article

Agronomic performance evaluation and selection of doubled haploid rice lines in a lowland saline-prone area

Bambang Sapta Purwoko[1,*], Hayu Widi Yuana[2], Zendi Alhamami[2], Nono Carsono[3], Muhammad Fuad Anshori[4], Iswari Saraswati Dewi[5] and Willy Bayuardi Suwarno[1]

[1] Department of Agronomy and Horticulture, Faculty of Agriculture, IPB University, Bogor 16680, Indonesia
[2] Study Program of Plant Breeding and Biotechnology, Department of Agronomy and Horticulture, Faculty of Agriculture, IPB University, Bogor 16680, Indonesia
[3] Department of Crop Science, Faculty of Agriculture, Padjadjaran University, Sumedang 45363, Indonesia
[4] Department of Agronomy, Faculty of Agriculture, Hasanuddin University, Makassar 90245, Indonesia
[5] Research Center of Food Crops, National Research and Innovation Agency (BRIN), Cibinong, Indonesia

* **Correspondence:** Email: bspurwoko@apps.ipb.ac.id; Tel: +622518629353; Fax: 622518629353.

Abstract: Salinity stress is a major abiotic stress limiting rice productivity. The development of high-yielding and salinity-tolerant rice varieties is a key strategy for achieving global food security. Evaluation under contrasting saline field conditions is needed to validate salinity-tolerant rice genotypes. This study aimed to evaluate agronomic performance and select superior doubled haploid (DH) rice lines in yield trials in lowland saline-prone areas. The research was conducted during the 2025 dry season in two coastal areas in Indonesia—Subang (strongly saline: 1.61 dS/m) and Sidoarjo (saline: 0.62 dS/m)—using a randomized complete block design with one factor (genotypes) and three replications in Sidoarjo and two replications in Subang. The genetic materials consisted of 25 DH rice lines and three check varieties (Inpari 18, Inpari 30 Ciherang *Sub1*, Inpari 34 Salin Agritan). Observations were conducted on agronomic characters, including growth, phenological, yield components, and grain yield. The results showed that all observed traits were significantly influenced by genotype × environment interactions (p-values <0.01 and <0.05), indicating differential genotype responses across two environments. DH rice lines exhibited higher grain yield than the check varieties in Sidoarjo and

comparable performance in Subang. Among them, GN12, GN18, and GN21 consistently outperformed the salinity-tolerant check variety, Inpari 34 Salin Agritan, across both locations. A weighted selection index enabled the identification of 14 DH lines with desirable agronomic performance in two lowland saline-prone environments, including a high number of productive tillers (23.8 tillers), a low number of unfilled grains (22.8 grains/panicle), and a high mean grain yield (6.96 t/ha) exceeding that of the check varieties. Those selected DH lines are promising candidates for salinity-tolerant rice breeding and should be further evaluated in multi-location yield trials for their yield stability and adaptability.

Keywords: abiotic stress; agronomic characters; index selection; salinity rice breeding

1. Introduction

Rice is one of the most important cereal crops, providing a primary source of energy for approximately half of the world's population [1]. The global population is projected to reach 9.7 billion by 2050, necessitating a substantial increase in food production to meet future demand [2]. Salinity stress is a major abiotic constraint that profoundly affects rice production worldwide, particularly in coastal and irrigated lowland areas that are highly vulnerable to salt intrusion [3]. According to the Global Map of Salt-Affected Soils (GSASmap), approximately 424 million hectares of topsoil and 833 million hectares of subsoil worldwide are affected by salinity [4]. Salinity acts as a primary limiting factor for crop productivity by inducing ionic imbalance and disrupting essential metabolic processes in plants. In rice, the most critical stages affected by salinity are the seedling and reproductive phases, during which exposure to salt stress can reduce growth and cause significant declines in yield components [5]. Salinity tolerance in rice is a multilevel trait integrating ion and ROS homeostasis, tissue tolerance, and whole-plant physiology [6].

The development of high-yielding and salinity-tolerant rice varieties is a key strategy for achieving global food security by 2050 [7,8]. The increasingly dynamic nature of climate change necessitates the rapid development of improved varieties within a relatively short timeline. Conventional breeding methods typically require approximately 4–5 years to produce homozygous lines through successive selfing generations [9]. Doubled haploid (DH) technology through anther culture offers a powerful alternative by significantly shortening the breeding cycle and enabling the rapid production of fully homozygous lines in one generation [10]. This approach is highly valuable for accelerating the development of high-yielding and salinity-tolerant rice varieties. The application of DH lines derived from anther culture in rice breeding programs has successfully generated DH lines with tolerance to salinity stress in controlled environments [11].

Studies on the development of salinity-tolerant rice genotypes have primarily focused on testing in controlled environments. Multi-environmental trials are needed to address the complexity of abiotic stress and validate the potential of stress-tolerant genotypes [12]. Subang is the third-largest rice producer in West Java, with higher rice production along the northern coast of Subang [13]. Sidoarjo is one of the rice production centers in East Java, with a topography influenced by fluvio-marine sediments and alluvial material, indicating potential vulnerability to seawater intrusion and soil salinization [14]. As major rice-producing regions affected by seawater intrusion, Subang and Sidoarjo provide representative agroecosystems for evaluating the performance of salt-tolerant rice genotypes under saline conditions.

Grain yield is the primary trait in rice and constitutes a key requirement for the official release of national rice varieties, particularly in Indonesia [15]. Therefore, the development of salinity-tolerant varieties must also ensure the maintenance of high yield potential. Grain yield is a complex quantitative trait influenced by multiple environmental factors, and its expression is strongly affected by genotype × environment interactions [16]. Evaluation under contrasting salinity conditions is essential to distinguish the responses of salt-sensitive and salt-tolerant rice genotypes, as salt-sensitive genotypes exhibit greater reductions in grain yield under saline environments [17]. Accordingly, evaluating yield performance under saline field conditions is a critical step in validating the potential of newly developed lines for varietal release and large-scale cultivation in salt-affected areas. This study aimed to evaluate the agronomic performance and select superior doubled haploid rice lines through yield trials conducted in lowland saline-prone area. The results will contribute to a better understanding of the agronomic responses of rice genotypes to salinity stress and provide valuable genetic resources for salt-tolerant rice breeding programs.

2. Materials and methods

2.1. Plant material and experimental design

The research was conducted during the same dry season in 2025 at two saline-prone field locations in Indonesia: Subang, West Java (6°15'07.6"S 107°55'03.2"E), where the field trial was conducted from August to November, and Sidoarjo, East Java (7°33'12.6"S 112°45'09.7"E), where the field trial was conducted from June to September. Both sites have an alluvial soil type but differ in salinity level, with Subang being classified as strongly saline (EC = 1.61 dS/m) and Sidoarjo as saline (EC = 0.62 dS/m). The genetic material consisted of DH lines selected by Yuana et al. [18], previously developed by Gunarsih [19] through anther culture derived from parental cross combinations possessing abiotic stress tolerance traits. Twenty-five DH rice lines and three check varieties (Inpari 18, Inpari 30 Ciherang *Sub1*, Inpari 34 Salin Agritan) were used; these populations included CGH1 (GN01-GN14) = HS4-11-1-2/B13926E-KA-23; CGH2 (GN17-GN32) = HS4-11-1-2/CG8-93-1-1; CGH4 (GN39-GN50) = DR5-83-1-3/B13926E-KA-23; CGH5 (GN52-GN60) = FL478/B13926E-KA-23; CGH7 (GN69-GN74) = IR64 Dro1/IR86384-46-3-1-B; and CGH8 (GN79-GN90) = IR64 Dro1/HS4-11-1-2. The experimental design used was a randomized complete block design with one factor, i.e., genotype, which included 25 DH rice lines and three check varieties, which were evaluated with three replications in Sidoarjo and two replications in Subang, resulting in 84 experimental units in Sidoarjo and 56 in Subang. Each experimental unit was a plot of 3 m × 3 m.

2.2. Experimental procedure and observations

Twenty-one-day-old seedlings were transplanted into 3 m × 3 m plots with plant spacing of 25 cm × 25 cm. Fertilization was carried out with urea at 350 kg/ha, SP-36 at 100 kg/ha, and KCl at 100 kg/ha. SP-36 and KCl were applied as a single basal application at 1 week after transplanting (WAT). Urea was split into three equal applications at 1, 4, and 7 WAT, with one-third of the total rate applied at each time. Maintenance in the form of weeding was done manually at 3 and 6 WAT. Pest and disease control was adjusted to the level of attack. Harvesting was done when the rice was fully ripe, which is characterized by 90% of the grain turning yellow and hard.

Observations were conducted on plant height (PH), number of vegetative tillers (NVT), number of productive tillers (NPT), days to 50% flowering (DTF), days to harvesting (DTH), number of filled grains (NFG), number of unfilled grains (NUG), total grains per panicle (TG), panicle length (PL), 1000-grain weight (GW), and grain yield (GY).

2.3. Environmental characterization of trial sites

Monthly rainfall at each experimental site was obtained from the nearest meteorological station and classified into four categories: low (0–100 mm/month), moderate (100–300 mm/month), high (300–500 mm/month), and very high (>500 mm/month), according to [20]. Based on this classification, Subang has moderate monthly rainfall, while Sidoarjo has low monthly rainfall (Table 1). Temperature, relative humidity, sunshine duration, soil type, and elevation were comparable between the two trial sites.

Table 1. Climatic parameters of two trial sites.

Sidoarjo Month	Temperature (℃)	Relative humidity (%)	Rainfall (mm)	Sunshine duration (hours)	Soil type	Elevation (m above sea level)
June	28.30	76.10	62.70	6.95		
July	27.30	72.70	11.40	7.36		
August	27.80	71.20	36.20	7.70	Aluvial	1
September	29.10	68.20	2.50	7.56		
Average	**28.13**	**72.05**	**28.20**	**7.39**		
Subang Month	Temperature (℃)	Relative humidity (%)	Rainfall (mm)	Sunshine duration (hours)	Soil type	Elevation (m above sea level)
August	27.84	75.93	103.75	8		
September	28.86	73.43	26.70	8		
October	29.07	76.29	58.42	8	Aluvial	3
November	27.71	83.46	341.46	8		
Average	**28.37**	**77.28**	**132.58**	**8**		

*Note: Source: Indonesian Agency for Meteorology, Climatology, and Geophysic, 2025.

Soil samples were collected before transplanting and were analyzed for electrical conductivity (EC), pH, available P, and exchangeable cations (Mg, K, Ca, and Na). Soil salinity was classified based on EC measured using the 1:5 soil/water extract method as follows: non-saline (0.0–0.25 dS/m), slightly saline (0.25–0.5 dS/m), saline (0.5–1.0 dS/m), strongly saline (1.0–2.0 dS/m), and extremely saline (>2.0–3.0 dS/m) [21]. Soil analysis revealed differences between the two environmental conditions, particularly in EC, pH, available P, and exchangeable cations (Mg, K, Ca, and Na), which may contribute to variations in plant performance (Table 2).

Table 2. Soil characterization of trial sites.

Parameter	Subang	Sidoarjo
EC (dS/m)[#]	1.61	0.62
pH	7.24	7.87
Organic content (%)	2.10	2.59
Total N (%)	0.39	0.37
Available P (ppm P_2O_5)	31.4	68.1
CEC (cmol/kg)	32.7	35.9
Exch. Mg (cmol Mg/kg)	17.8	15.2
Exch. Ca (cmol Ca/kg)	10.1	19.1
Exch. K (cmol K/kg)	2.55	1.64
Exch. Na (cmol Na/kg)	18.00	6.50
Texture		
Sand (%)	11.95	11.06
Silt (%)	43.08	41.79
Clay (%)	44.97	47.15

*Notes: #1:5 soil/water extract (EC 1:5).

2.4. Data analysis

Data were analyzed using a linear mixed model. When significant effects were detected, mean comparisons were performed using the least significant difference (LSD) test at the 5% significance level. Variance components were estimated separately using restricted maximum likelihood (REML). The REML estimates of genotypic variance, genotype × location interaction variance, and residual variance were used to calculate phenotypic variance on an entry-mean basis and broad-sense heritability according to Fehr [22]. The genotypic and phenotypic coefficient of variation were calculated according to Singh and Chaudhary [23]. To examine relationships among observed traits and identify potential selection criteria, Pearson correlation analysis was conducted. A weighted selection index based on multiple traits was constructed using the method of Falconer [24], and genotypes were ranked in descending order by index value to identify the most promising lines. Prior to index calculation, phenotypic data were standardized using the formula proposed by Walpole [25]. All genetic parameter estimations, correlation analyses, and selection index calculations were performed using SAS OnDemand for Academics and Microsoft Excel.

(1) Estimation of phenotypic variance was calculated based on [22], as follows:

$$\sigma_P^2 = \frac{\sigma_e^2}{rl} + \frac{\sigma_{G\times E}^2}{l} + \sigma_G^2 \quad (1)$$

σ_G^2 is the genetic variance.
$\sigma_{G\times E}^2$ is the genotype-by-environment interaction variance.
σ_E^2 is the environmental variance.
σ_P^2 is the phenotypic variance.
r is the harmonic mean of replications across environments [r= 2 / (1/3 + 1/2) = 2.4] as an approximation, because the number of replications differed between environments [26].
l is the number of locations.

(2) The estimation of broad-sense heritability (h^2_{bs}) on an entry-mean basis was calculated based on [22] as follows:

$$h^2_{bs} = \frac{\sigma^2_G}{\frac{\sigma^2_e}{rl} + \frac{\sigma^2_{G\times E}}{l} + \sigma^2_G} \quad (2)$$

The estimates of h^2_{bs} were then categorized as high ($0.50 < h^2_{bs} < 1.00$), moderate ($0.20 < h^2_{bs} < 0.50$), and low ($h^2_{bs} < 0.20$).

(3) The genotypic coefficient of variation (GCV) was calculated based on [23], as follows:

$$GCV = \frac{\sqrt{\sigma^2_G}}{\bar{x}} \quad (3)$$

(4) The phenotypic coefficient of variation (PCV) was calculated based on [23], as follows:

$$PCV = \frac{\sqrt{\sigma^2_P}}{\bar{x}} \quad (4)$$

(5) The relative reduction from saline to strong saline was estimated based on [11], as follows:

$$\text{Relative reduction} = \frac{(x_0 - x_1)}{x_0} \quad (5)$$

x_0 is the genotype value under saline condition.
x_1 is the genotype value under strong saline condition.

(6) The standardized phenotype mean of each genotype was calculated based on [25], as follows:

$$p_i = \frac{(x_i - \bar{x})}{s} \quad (6)$$

p_i is the standardized phenotypic mean of genotype-i.
x_i is the original phenotypic mean of genotype-i.
$\bar{x}$ is the mean of the variable.
s is the standard deviation of the variable.

(7) The selection index formula is based on [24]:

$$I = b_1X_1 + b_2X_2 + \cdots + b_nX_n \quad (7)$$

I is the selection index.
b_n is the weight of the selection variable-n.
X_n is the selection variable-n.

3. Results and discussion

3.1. Environmental characterization of trial sites

Based on monthly rainfall classification [20], Subang had moderate rainfall, whereas Sidoarjo had low rainfall (Table 1). Rainfall is a critical environmental factor influencing soil salinity dynamics. Soil salinity tends to increase under conditions of low rainfall combined with elevated air temperatures [27]. Kawser et al. [28] also reported a strong correlation among rainfall, air temperature, and soil salinity levels. Soil analysis showed clear differences between the two environmental conditions, particularly

in EC, pH, available P, and exchangeable cations (Mg, K, Ca, and Na), which may contribute to variations in plant performance (Table 2). Electrical conductivity (EC) is a key variable for quantifying soil salinity and estimating total dissolved salts [29]. Subang had an EC of 1.61 dS/m and was classified as strongly saline, whereas Sidoarjo had an EC of 0.62 dS/m and was classified as saline based on the EC measured using the 1:5 soil/water extract method [21].

Two experimental sites exhibited soil pH values ranging from neutral to slightly alkaline (Table 2). Soil pH plays an important role in regulating cation exchange capacity (CEC) and the availability of exchangeable cations (Mg, Ca, K, and Na). Cation exchange capacity influences nutrient availability by enhancing cation retention and maintaining a balanced exchangeable cation, which affect nutrient uptake efficiency [30]. Salt accumulation is associated with increases in EC and exchangeable Na, accompanied by decreases in exchangeable Ca [31]. Subang showed higher EC and exchangeable Na values than Sidoarjo (Table 2). High ionic strength, due to the electrolyte concentration in saline soil, can reduce P availability [32]. Soil analysis results also show that Subang (strongly saline) has lower available P than Sidoarjo (saline) (Table 2). Based on the soil analysis results and the supporting literature, the soils at Subang and Sidoarjo met the criteria for conducting field evaluations under saline conditions.

3.2. Combined analysis of variance

The combined analysis of variance generally showed significant effects of genotype (G), environment (E), and G × E interaction on agronomic performance (Table 3). The significant effect of genotype on all observed agronomic traits indicates that genotypes differ in these characters. This is useful for improving selection effectiveness [33]. Genotypic performance is not determined solely by genetic factors but is also shaped by the interaction between genetic constitution and environmental conditions [34]. Therefore, differences in climatic conditions (Table 1) and soil characteristics (Table 2) between the two experimental sites contributed to differential responses across environments and among the tested genotypes. Experimental variability, measured as the coefficient of variation (CV), ranged from 1.87% to 15.52% (Table 3). In agronomic field experiments, CV values below 20% are generally considered acceptable [35]. The CV values in this experiment reflected the precision of the experimental data; low CV values indicate greater experimental reliability.

Variance components for agronomic and yield-related traits decomposed into genetic variance (σ_G^2), genotype × environment interaction variance ($\sigma_{G\times E}^2$), environmental variance (σ_e^2), and phenotypic variance (σ_P^2). These components provide a basis for evaluating the relative contribution of each source of variation, which is useful for determining breeding strategies [36]. These components can be used to estimate heritability values and determine the extent to which observed trait variation is caused by genetic factors [37]. The heritability estimates were high for plant height, phenological traits, number of grains, and 1000-grain weight; moderate for number of tillers; and low for panicle length. The zero genetic variance of grain yield resulted from the negative estimate of genetic variance (MS Genotype < MS G×E) and was therefore constrained to zero. Consequently, the heritability estimate for grain yield was not available (Table 4). Grain yield is a quantitative trait that is responsive to environmental changes. Differences in stress intensity lead to inconsistent genotype performance, therefore reducing the proportion of grain yield variation explained by genetics and potentially leading to negative estimates of genetic variance [38,39].

Table 3. Combined analysis of variance.

Characters	MS genotype	MS environment	MS G×E	MS residuals	CV (%)
Plant height (cm)	368.43**	4838.88**	93.07**	14.50	3.35
Number of vegetative tillers	48.20**	5772.91**	26.90**	5.20	7.81
Number of productive tillers	9.89**	4828.80**	5.77*	3.25	7.41
Days to flowering (DAS)	73.43**	3810.14**	33.61**	5.77	2.77
Days to harvest (DAS)	57.03**	9956.74**	25.58**	4.53	1.87
Panicle length (cm)	15.43**	194.11**	12.47**	0.73	3.12
Number of filled grains	4103.81**	101029.32**	667.99**	89.96	5.91
Number of unfilled grains	510.96**	0.07ns	226.83**	17.98	15.52
Total number of grains	4914.13**	100862.69**	625.85**	88.49	5.01
1000-grain weight (g)	14.28**	0.16ns	3.87**	0.71	3.13
Grain yield (t/ha)	1.81**	724.38**	1.92**	0.25	7.12

*Notes: ** significant at α 0.01; * significant at α 0.05; ns = not significant at α 0.05; MS = mean square; CV = coefficient of variation; and DAS = days after sowing.

Table 4. Variance components of agronomic and yield traits of rice genotypes.

Traits	σ^2_G	$\sigma^2_{G\times E}$	σ^2_e	σ^2_P	h^2_{bs}	GCV (%)	PCV (%)
PH	57.08	32.20	14.64	76.23	0.75	6.72	7.76
NVT	4.38	8.89	5.22	9.92	0.44	7.51	11.29
NPT	0.92	1.25	3.18	2.21	0.42	4.14	6.42
DTF	8.22	11.45	5.79	15.15	0.54	3.26	4.43
DTH	6.43	8.56	4.56	11.66	0.55	2.19	2.95
PL	0.62	4.94	0.73	3.25	0.19	2.91	6.64
NFG	721.10	243.03	89.74	861.31	0.84	17.32	18.93
NUG	61.13	85.31	17.93	107.52	0.57	28.62	37.95
TG	900.78	226.80	86.72	1032.25	0.87	16.46	17.62
GW	2.17	1.27	0.71	2.95	0.74	5.48	6.39
GY	0.00	0.68	0.25	0.39	NA	0.00	9.51

*Notes: σ^2_G = genetic variance; $\sigma^2_{G\times E}$ = genotype ×environment interaction variance; σ^2_P = phenotypic variance; σ^2_e = environmental variance; GCV = genotypic coefficient of variation; PCV = phenotypic coefficient of variation; h^2_{bs} = heritability; PH= plant height (cm); NVT = number of vegetative tillers (tillers); NPT = number of productive tillers (tillers); DTF = days to 50% flowering (days after sowing); DTH = days to harvesting (days after sowing); NFG = number of filled grains (grains); NUG = number of unfilled grains (grains); TG = total grains per panicle (grains/panicle); PL = panicle length (cm); GW = 1000-grain weight (g); GY = grain yield (t/ha); NA = the heritability estimate is not available because the estimated genetic variance was negative (MS G < MS G×E) and was therefore constrained to zero.

Phenotypic response can be further examined using the genotypic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV), which are used to assess the relative magnitude of

trait variability [40]. For all observed traits, PCV values were higher than GCV values. This indicates that phenotypic expression is influenced not only by genetic factors but also by environmental conditions [41]. This interpretation is supported by the influence of the environment and the G×E interaction variance, as shown in Table 4. Low estimates of PCV and GCV (< 10%) were observed for the traits PH, NPT, DTH, DTF, PL, GW, and GY. Moderate GCV and PCV values (10%–20%) were observed for the traits NFG and TG. High GCV and PCV values (> 20%) were observed for NUG. High GCV values indicate greater genetic variability, while high PCV values reflect greater phenotypic variability. Conversely, low GCV and PCV values indicate limited genetic and phenotypic variability, respectively [42]. In this study, PCV values were consistently higher than GCV values for all traits (Table 4), suggesting that environmental factors, together with G×E interaction, contributed to the observed phenotypic variation [43].

3.3. Agronomic performance

The average agronomic performance of the tested DH rice lines and check varieties in two lowland saline-prone areas is shown in Table 5. In general, DH rice lines exhibit agronomic performance comparable to that of check varieties. Inpari 34 Salin Agritan is one of the check varieties with a claimed tolerance to salinity at the seedling stage [44]. Plant height for the DH rice lines ranged from 97.9 to 128.42 cm, which is classified as short to medium plant height [45] and is lower than that of Inpari 34 Salin Agritan (Table 5). Soil salinity is known to be one of the environmental factors that can suppress plant height [46]. An optimal rice plant height of 100–120 cm was crucial for sustaining high yields under both normal and salt-stress conditions [47]. This indicates that DH rice lines exhibit optimal plant height under the evaluated saline field conditions.

The number of tillers is an important trait, closely associated with increased crop productivity [48]. The tillering performance of DH rice lines ranged from 20.9 to 25.6 productive tillers, categorized as high (20–25 tillers) to very high (>25 tillers) according to the SES IRRI classification [45]. DH rice lines showed similar performance to Inpari 34 Salin Agritan, which falls into the high tillering category (Table 5). Days to flowering and harvesting showed longer growth periods in the DH lines than in the check varieties. Yield components such as panicle length, number of grains, and grain weight showed that the DH rice lines had values that were as good as, and in some cases better than, those of the check varieties, particularly Inpari 34 Salin Agritan (Table 5). The observed agronomic performance results showed relatively low CV and standard error of the mean values, indicating relatively low experimental variation and good precision of the estimates [35]. All observed traits showed significant G×E effects; thus, although DH rice lines generally performed as well as the check varieties, the response of each genotype across test environments still needs to be studied to identify interaction patterns and better understand the G×E effect.

The agronomic performance of DH rice lines and check varieties in two lowland saline-prone area was lower in Subang (strongly saline) than in Sidoarjo (moderate salinity). A reduction in agronomic performance is a common plant response to salt stress [17], although other climatic and edaphic factors may also contribute to the observed responses. The relative reduction in agronomic performance from the saline to the strongly saline environment is presented in Table 6. Agronomic traits related to vegetative growth, such as plant height and the number of vegetative tillers, showed that the DH lines exhibited a relatively smaller reduction than the check varieties. This indicates that DH rice lines maintain good vegetative growth and have the potential for salinity tolerance during the vegetative phase. Xu et al. [17] reported that salt-tolerant genotypes exhibit smaller reductions in plant height and tiller number than salt-sensitive genotypes, supported by strong antioxidant capacity and

osmotic adjustment.

Table 5. Mean performance of DH rice lines across two saline soils.

Genotype	PH	NVT	NPT	DTF	DTH	PL	NFG	NUG	TG	GW
GN01	116.25	30.1	23.2	86.7	116.7	30.18	135.1	35.9	171.1	29.20
GN04	128.08	32.0	23.7	84.3	113.8	28.35	152.3	28.3	180.6	30.37
GN12	111.41	25.9	22.7	88.0	116.1	25.78	159.5	19.2	178.8	28.04
GN14	106.70	30.9	22.2	93.4	120.2	25.95	132.4	28.4	160.8	29.20
GN17	97.90	27.8	25.2	82.2	110.8	24.15	130.9	14.1	145.0	25.94
GN18	104.38	32.8	25.2	91.8	117.5	25.37	142.2	21.7	163.9	28.11
GN21	103.80	31.7	25.3	86.8	115.0	25.13	138.2	35.5	173.7	25.91
GN31	105.50	28.3	22.0	84.7	115.1	26.28	173.2	17.0	190.2	25.78
GN32	109.76	29.3	25.1	87.3	114.8	29.83	174.6	26.5	201.0	23.72
GN39	115.97	26.0	21.7	84.3	110.8	26.78	150.9	25.3	176.1	25.62
GN46	111.58	27.0	23.0	86.5	113.8	26.50	188.1	27.2	215.3	24.78
GN50	123.80	25.5	23.9	94.3	120.3	28.98	136.3	42.4	178.7	26.25
GN52	109.37	28.4	23.0	84.6	111.5	26.45	152.1	24.3	176.3	27.67
GN56	113.65	24.3	23.3	91.2	118.1	26.88	186.9	44.5	231.3	26.13
GN57	120.10	25.9	21.6	88.3	116.4	27.92	244.3	32.0	276.3	23.97
GN58	120.53	24.6	23.4	87.2	113.9	26.35	224.8	25.6	250.4	23.88
GN60	114.07	24.3	22.5	92.1	117.9	24.35	151.7	16.7	168.4	27.86
GN69	103.15	32.1	25.6	89.1	119.3	27.37	146.4	16.8	163.2	26.99
GN70	99.48	30.3	23.4	83.9	112.6	25.17	125.2	17.6	142.8	27.66
GN73	109.65	28.6	23.6	91.8	120.0	25.58	124.2	11.4	135.6	25.96
GN74	128.42	29.8	21.4	94.8	121.6	28.97	137.8	54.3	192.0	29.48
GN79	121.10	27.4	22.1	91.6	120.0	27.23	183.5	33.5	217.0	25.67
GN83	116.18	32.5	24.8	87.3	114.7	29.07	114.4	33.6	148.0	28.08
GN85	103.97	22.9	20.9	80.8	110.0	25.55	140.4	25.4	165.8	27.36
GN90	109.53	25.8	22.2	90.8	117.1	28.70	151.0	42.3	193.3	27.37
Mean of DH	**112.17**	**28.2**	**23.2**	**88.1**	**115.9**	**26.92**	**155.9**	**28.0**	**183.8**	**26.84**
Inpari 18	102.78	23.6	21.2	82.1	110.2	28.45	149.4	17.2	166.6	28.83
Inpari 30[(1)]	112.28	31.4	24.8	91.2	120.1	27.73	145.5	18.5	164.0	26.74
Inpari 34[(2)]	129.98	22.0	21.0	83.8	113.1	30.98	148.8	30.1	178.9	26.71
Mean of check	**115.02**	**25.6**	**22.3**	**85.7**	**114.4**	**29.06**	**147.9**	**21.9**	**169.8**	**27.42**
Grand mean	**112.48**	**27.9**	**23.1**	**87.9**	**115.8**	**27.14**	**155.0**	**27.3**	**182.3**	**26.90**
SEm	1.74	1.04	0.82	1.10	0.97	0.39	4.33	1.94	4.29	0.38
CV (%)	3.35	7.81	7.41	2.77	1.87	3.12	5.91	15.52	5.01	3.13
F-value G×E	6.42**	5.17**	1.78*	5.82**	5.65**	17.05**	7.43**	12.62**	7.07**	5.46**

*Notes: PH = plant height (cm); NVT = number of vegetative tillers (tillers); NPT = number of productive tillers (tillers); DTF = days to 50% flowering (days after sowing); DTH = days to harvesting (days after sowing); NFG = number of filled grains (grains); NUG = number of unfilled grains (grains); TG = total grains per panicle (grains/panicle); PL = panicle length (cm); GW = 1000-grain weight (g); (1) = Inpari 30 Ciherang *Sub1*; (2) = Inpari 34 Salin Agritan; SEm = standard error of the mean; CV = coefficient of variation; ** significant at α 0.01.

Table 6. Relative reduction of DH rice lines and check varieties across two saline soil environments.

Traits	Sidoarjo (saline)		Subang (strong saline)		Relative reduction (%)	
	DH	Check	DH	Check	DH	Check
Plant height (cm)	117.48	127.00	106.86	103.03	9.0	18.9
Number of vegetative tillers (tillers)	34.7	32.4	21.6	18.9	37.6	41.8
Number of productive tillers (tillers)	29.4	27.1	17.1	17.6	41.8	35.0
Days to flowering (DAS)	82.3	84.6	94.0	86.8	-14.2	-2.6
Days to harvest (DAS)	106.9	108.9	124.9	120.0	-16.8	-10.2
Panicle length (cm)	27.83	32.64	26.00	25.47	6.6	22.0
Number of filled grains (grains)	183.5	173.5	128.2	122.3	30.1	29.5
Number of unfilled grains (grains)	27.7	23.6	28.2	20.3	-1.8	14.0
Total grains/panicle (grains/panicle)	211.2	197.1	156.4	142.6	25.9	27.7
1000-grain weight (g)	26.79	27.52	26.89	27.33	-0.4	0.7
Grain yield (t/ha)	8.99	8.20	4.25	4.29	52.7	47.7

*Notes: DAS = days after sowing.

During the reproductive phase, DH rice lines showed greater relative reductions than the check varieties in NPT, DTF, and DTH. Delayed flowering and harvesting were consistent with the higher vegetative growth of the DH rice lines compared to the check varieties. Salinity can reduce photosynthetic efficiency, thereby limiting the accumulation of assimilates required for the transition from the vegetative to the reproductive stage and for grain filling [49]. Therefore, reduced assimilate availability under saline conditions may contribute to changes in both flowering and maturity times. Flowering time might be delayed when plants are exposed to salinity stress during the vegetative stage. Osmotic and ionic stress could reduce growth rate and biomass accumulation, thereby slowing the transition from the vegetative to the reproductive phase [50]. This is consistent with the response of DH rice lines and check varieties across the two evaluated saline field conditions, where flowering and maturity time were delayed. The prolonged crop duration was accompanied by an extended grain-filling period. However, the longer grain-filling period under salinity stress reflects delayed grain maturation rather than enhanced assimilate accumulation [51].

The yield components indicate that DH rice lines exhibit a lower relative reduction in panicle length, total grains, and 1000-grain weight. DH rice lines showed a relatively small decrease in panicle length (6.6%) and a 25.9% decrease in total grains per panicle, but maintained 1000-grain weight with a 0.4% increase under two evaluated saline field conditions. DH rice lines maintained 1000-grain weight under two evaluated saline field conditions, presumably because they adjusted sink number in response to the limited amount of assimilates available for translocation. Rusliani et al. [52] stated that balanced source-sink relationships are critical for grain filling, whereas abiotic stresses disrupt this balance by reducing assimilate production and resulting in a decline in grain weight.

Grain yield is the primary goal of rice breeding programs. Grain yield is a complex quantitative trait controlled by multiple genes and strongly influenced by environmental conditions [16]. Grain yield exhibited a greater relative reduction in DH rice lines than in the check varieties. Although DH rice lines showed smaller relative reductions in several agronomic traits, the check varieties showed smaller reductions in productive tiller number and longer grain-filling duration, along with greater reduction in unfilled grains (Table 6). These responses may have contributed to the lower reduction in

grain yield observed in the check varieties. Nevertheless, despite the greater relative yield reduction, the mean grain yield of the DH rice lines did not differ significantly from that of the check varieties.

Table 7. Mean grain yield of DH rice lines and check varieties across two saline soil environments.

Genotypes	Grain yield (t/ha)		
	Subang	Sidoarjo	Combined mean
GN01	4.94A	7.93bC	6.43
GN04	5.11A	7.71abC	6.41
GN12	5.35AC	9.97AC	7.66
GN14	4.54Ab	8.78C	6.66
GN17	4.27Ab	8.63C	6.45
GN18	5.25AC	9.60AC	7.42
GN21	5.20AC	8.98C	7.09
GN31	4.54Ab	10.03AC	7.29
GN32	4.25Ab	9.21C	6.73
GN39	4.66Ab	8.26bC	6.46
GN46	3.57b	8.63C	6.10
GN50	2.73bc	9.59AC	6.16
GN52	5.59AC	6.84ab	6.21
GN56	3.12bc	8.75C	5.94
GN57	2.76bc	7.86abC	5.31
GN58	4.31Ab	9.48C	6.89
GN60	4.45Ab	9.90AC	7.17
GN69	4.11Ab	10.19AC	7.15
GN70	4.78A	8.86C	6.82
GN73	4.31Ab	9.47C	6.89
GN74	3.92Ab	9.21C	6.56
GN79	4.20Ab	9.91AC	7.05
GN83	3.47b	8.48bC	5.97
GN85	3.59b	9.64AC	6.62
GN90	3.35b	8.72C	6.04
Mean of DH	4.25	8.99	6.62
Inpari 18	2.93bc	8.71C	5.82
Inpari 30 Ciherang *Sub1*	5.74AC	9.39C	7.56
Inpari 34 Salin Agritan	4.19Ab	6.49ab	5.34
Mean of check	4.29	8.20	6.24

*Notes: A/a = significantly higher/lower than Inpari 18; B/b = significantly higher/lower than Inpari 30 Ciherang *Sub1*; C/c = significantly higher/lower than Inpari 34 Salin Agritan based on LSD 5%.

Grain yield was significantly affected by the G × E interaction, indicating that genotypes responded differently across environments. In Subang (high salinity), grain yield ranged from 2.73 to 5.74 t/ha, with both the DH lines and the check varieties showing a mean yield of 4.25 and 4.29 t/ha, respectively. In contrast, Sidoarjo (saline) DH lines generally exhibited higher grain yields, ranging

from 6.49 to 10.19 t/ha. The mean yield of the DH lines in Sidoarjo reached 8.99 t/ha, exceeding that of the check varieties (8.20 t/ha) (Table 7). Moreover, DH lines GN52 (5.59 t/ha) and GN69 (10.19 t/ha) were the highest yielding in Subang and Sidoarjo, respectively. The grain yield of the salinity-tolerant check variety, Inpari 34 Salin Agritan, was exceeded by four DH lines in Subang (GN52, GN12, GN18, and GN21) and by most DH lines in Sidoarjo. Notably, three DH lines (GN12, GN18, and GN21) consistently outperformed Inpari 34 Salin Agritan across both locations. These results indicate that the evaluated DH rice lines demonstrated yield performance comparable to or exceeding that of the commercial check variety used in the experiment, highlighting their potential for cultivation in saline-prone environments.

3.4. Correlation analysis

Grain yield, as the primary trait, was strongly influenced by the G×E interaction (Table 4). Selection based solely on grain yield has low selection accuracy. Multi-trait selection can improve selection accuracy [53]. Correlation analysis can serve as a basis for considering secondary selection criteria in breeding programs [54,55]. Correlation analysis of all observed traits revealed that several characters were significantly associated with grain yield (Figure 1). NVT and NPT showed significant positive correlations ($p < 0.05$) with correlation coefficients of 0.42 and 0.40, respectively. The traits that had a significant negative effect on grain yield were PL ($r = -0.52$, $p < 0.01$) and NUG ($r = -0.42$, $p < 0.05$). Among these traits, NPT, PL, and NUG were selected as selection traits in index selection. NVT was not included as a selection trait because its effect was considered adequately represented by NPT, and its inclusion could introduce multicollinearity due to strong correlation among similar tillering-related traits.

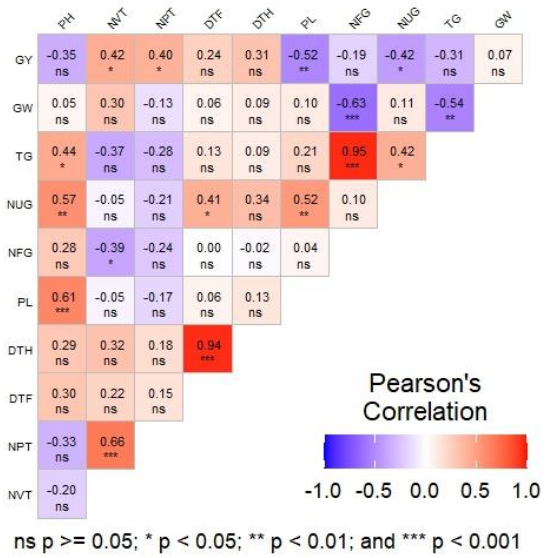


Figure 1. Pearson's correlation among the observed traits. *Notes: PH = plant height; NVT = number of vegetative tillers; NPT = number of productive tillers; DTF = days to 50% flowering; DTH = days to harvesting; NFG = number of filled grains; NUG = number of unfilled grains; TG = total grains per panicle; PL = panicle length; GW = 1000-grain weight; GY = grain yield.

3.5. Index selection

The traits included as selection criteria were determined based on the results of the correlation analysis and the targeted breeding objectives. NPT, PL, and NUG were included as selection traits in index selection. NPT exhibited moderate heritability with low GCV and PCV values, while PL showed low heritability as well as low GCV and PCV values, suggesting limited genetic variability for these traits. In contrast, NUG exhibited high heritability together with high GCV and PCV values, indicating substantial genetic variability and greater potential for effective selection. Although NPT and PL exhibited limited genetic variability (Table 4), they were retained as selection traits because they were significantly correlated with grain yield and can be measured rapidly, non-destructively, and at low cost in small experimental plots [56]. Moreover, integrating multiple traits into the selection strategy can provide more balanced genetic gains across target traits without substantial losses in grain yield, thereby improving overall selection efficiency [57].

For saline environments, the desired breeding direction in this study is to obtain genotypes with high NPT, high PL, low NUG, and high grain yield. The weights assigned in constructing the selection index were NPT (+1), PL (+1), NUG (−1), and grain yield (+3). These weights are determined by the economic value of a trait [24]. Panicle length has a negative correlation with grain yield, but the breeding direction of this study was to obtain a long panicle, so the PL index was constrained to positive values to prevent the selection of genotypes with short panicles. A reduction in panicle length is a common response to salt stress [58], and maintaining longer panicles under saline conditions has been widely considered an important trait in the development of salt-tolerant rice varieties [59,60]. Grain yield is assigned a weight three times higher than that of other traits because it represents the primary target trait in the breeding program, with the objective of identifying high-yielding genotypes [61].

The index selection identified 14 DH lines with a positive selection index (Table 8). The selection results indicated improvements in the mean values of the selected traits among these DH lines. The mean NPT of the population prior to selection was 23.2 tillers, which increased to 23.8 tillers after selection and exceeded the mean of the check varieties (22.3 tillers). The mean NUG before selection was 28.0 grains; after selection, it decreased to 22.8 grains, approaching the average number of unfilled grains of the check varieties (21.9 grains). Grain yield also improved from 6.62 t/ha before selection to 6.96 t/ha after selection, surpassing the mean yield of the check varieties (6.24 t/ha). The mean panicle length showed a slight decrease from 26.92 cm before selection to 26.51 cm after selection, with both values classified as medium panicle length [62]. The selected DH rice lines have the potential to be further developed into new varieties. The improved agronomic characters and high yield potential of the selected lines are expected to align with farmers' preferences. However, this study was limited to two environments; therefore, the selected lines should be further evaluated across broader multi-environment trials to assess their yield stability, adaptability, and salinity tolerance.

Table 8. Weighted selection index and means of the selection traits of 14 selected DH rice lines and three check varieties.

Genotypes	Weighted index	NPT	PL	NUG	GY
GN01	0.17	23.2	30.18	35.9	6.43
GN04	0.17	23.7	28.35	28.3	6.41
GN12	5.00	22.7	25.78	19.2	7.66
GN17	0.42	25.2	24.15	14.1	6.45
GN18	5.12	25.2	25.37	21.7	7.42
GN21	2.07	25.3	25.13	35.5	7.09
GN31	3.19	22.0	26.28	17.0	7.29
GN32	3.65	25.1	29.83	26.5	6.73
GN58	1.44	23.4	26.35	25.6	6.89
GN60	1.94	22.5	24.35	16.7	7.17
GN69	5.67	25.6	27.37	16.8	7.15
GN70	1.23	23.4	25.17	17.6	6.82
GN73	2.48	23.6	25.58	11.4	6.89
GN79	1.06	22.1	27.23	33.5	7.05
Inpari 18	-3.34	21.2	28.45	17.2	5.82
Inpari 30 Ciherang *Sub1*	7.18	24.8	27.73	18.5	7.56
Inpari 34 Salin Agritan	-5.68	21.0	30.98	30.1	5.34
Mean of all DH lines		23.2	26.92	28.0	6.62
Means of selected DH lines		23.8	26.51	22.8	6.96
Mean of the check varieties		22.3	29.06	21.9	6.24

*Notes: NPT = number of productive tillers (tillers); PL = panicle length (cm); NUG = number of unfilled grains (grains); GY = grain yield (t/ha).

4. Conclusions

Rice genotypes exhibited distinct agronomic responses under two evaluated saline-prone environments. DH rice lines exhibited higher grain yield than the check varieties in Sidoarjo and comparable performance in Subang. Among them, GN12, GN18, and GN21 consistently outperformed the salinity-tolerant check variety, Inpari 34 Salin Agritan, across both locations. A weighted selection index enabled the identification of 14 DH lines with desirable agronomic performance in two lowland saline-prone environments, including a high number of productive tillers (23.8 tillers), moderate panicle length (26.51 cm), a low number of unfilled grains (22.8 grains), and a high mean grain yield (6.96 t/ha) exceeding that of the check varieties. Those selected DH lines are promising candidates for salinity-tolerant rice breeding and should be further evaluated in multi-location yield trials for their yield stability and adaptability.

Use of AI tools declaration

The authors declare they have not used Artificial Intelligence (AI) tools in the creation of this article.

Acknowledgments

This research was funded by the IPB Community Fund through the Indonesian Collaboration Research scheme (Riset Kolaborasi Indonesia (RKI)) with contract number 14988/IT3.D10/PT.01.03/P/B/2025.

Conflict of interest

The authors declare that there are no conflicts of interest related to this article.

Author contributions

Conceptualization: BSP, NC, MFA; Methodology: BSP, NC, MFA, ISD, WBA; Data curation: BSP, WBA, HWY, ZA; Formal analysis: BSP, WBA, ZA, HWY; Funding acquisition: BSP; Supervision: BSP, NC, MFA, ISD, WBA; Validation: BSP, NC, MFA, ISD, WBA; Writing–original draft: BSP, ISD, HWY, ZA; Writing review and editing: BSP, NC, MFA, ISD, WBA, HWY, ZA. All authors read and approved the final manuscript.

References

1. Fukagawa NK, Ziska LH (2019) Rice: importance for global nutrition. *J Nutr Sci Vitaminol* 65: S2–S3. https://doi.org/10.3177/jnsv.65.S2.
2. Rahman ANMRB, Zhang J (2022) Trends in rice research: 2030 and beyond. *Food Energy Secur* 12: 1–17. https://doi.org/10.1002/fes3.390.
3. Seck F, Covarrubias-Pazaran G, Gueye T, et al. (2023) Realized genetic gain in rice: achievements from breeding programs. *Rice* 16: 1–22. https://doi.org/10.1186/s12284-023-00677-6.
4. Food and Agriculture Organization (2021) Global map of salt-affected soils.
5. Krishnamurthy SL, Lokeshkumar BM, Rathor S, et al. (2022) *Development of salt-tolerant rice varieties to enhancing productivity in salt-affected environments*, The 2nd International Laayoune Forum on Biosaline Agriculture. 1–5.
6. Aycan M (2026) Salinity stress in rice: mechanisms and molecular approaches to mitigation. *Planta* 263: 1–18. https://doi.org/10.1007/s00425-026-04964-6.
7. Islam S (2025) Agriculture, food security, and sustainability: a review. *Explor Foods Foodomics* 3: 1–21. https://doi.org/10.37349/eff.2025.101082.
8. Oelviani R, Adiyoga W, Suhendrata T, et al. (2024) Effects of soil salinity on rice production and technical efficiency: Evidence from the northern coastal region of Central Java, Indonesia. *Case Stud Chem Environ Eng* 10: 1–11. https://doi.org/10.1016/j.cscee.2024.101010.
9. Tripathy SK (2018) Anther culture for double haploid breeding in rice-a way forward. *Rice Genomics Genet* 9: 1–6. https://doi.org/10.5376/rgg.2018.09.0001.
10. Chen X, Li S, Zha W, et al. (2025) Advances in anther culture-based rice breeding in China. *Plants* 14: 1–16. https://doi.org/10.3390/plants14111586.
11. Anshori MF, Purwoko BS, Dewi IS, et al. (2022) Salinity tolerance selection of doubled-haploid rice lines based on selection index and factor analysis. *AIMS Agric Food* 7: 520–535. https://doi.org/10.3934/agrfood.2022032.
12. Khan NA, Owens L, Nuñez MA, et al. (2025) Complexity of combined abiotic stresses to crop plants. *Plant Stress* 17: 1–19. https://doi.org/10.1016/j.stress.2025.100926.

13. Ramadhani SU, Rokhmatuloh R, Wibowo A (2022) The rice production of paddy field and relationship with elevation using sentinel-1a sar in Subang regency. *IOP Conf Ser: Earth Environ Sci* 1089: 1–9. https://doi.org/10.1088/1755-1315/1089/1/012029.
14. Putra AN, Martiana A, Alberth FS, et al. (2021) Response macronutrient content of saline-resistant paddy to the saline source distance. *J Trop Soils* 26: 63–74. https://doi.org/10.5400/jts.2021.v26i2.63-74.
15. Ministry of Agriculture of the Republic of Indonesia (2019) *Ministerial decree no. 681/HK.540/C/11/2019 on standard operating procedures for variety evaluation for release of food crop varieties*, In: Ministry of Agriculture of the Republic of Indonesia, Jakarta.
16. Li R, Li M, Ashraf U, et al. (2019) Exploring the relationships between yield and yield-related traits for rice varieties released in China from 1978 to 2017. *Front Plant Sci* 10: 1–12. https://doi.org/10.3389/fpls.2019.00543.
17. Xu Y, Bu W, Xu Y, et al. (2024) Effects of salt stress on physiological and agronomic traits of rice genotypes with contrasting salt tolerance. *Plants* 13: 1–18. https://doi.org/10.3390/plants13081157.
18. Yuana HW, Purwoko BS, Suwarno WB, et al. (2025) Yield trial of doubled-haploid rice lines with multiple abiotic stress tolerance. *Caraka Tani J Sustain Agric* 40: 390–403. https://doi.org/10.20961/carakatani.v40i3.94856.
19. Gunarsih C (2022) *Multiple tolerance to abiotic stress in doubled haploid rice lines derived from anther culture*, Bogor: IPB University.
20. Supriyati, Tjahjono B, Effendy S (2018) Analysis of rainfall pattern for lahar mitigation at sinabung volcano. *J Ilmu Tanam Lingkung* 20: 95–100. https://doi.org/10.29244/jitl.20.2.95-100.
21. Ismayilov AI, Mamedov AI, Fujimaki H, et al. (2021) Soil salinity type effects on the relationship between the electrical conductivity and salt content for 1: 5 soil-to-water extract. *Sustainability* 13: 1–11. https://doi.org/10.3390/su13063395.
22. Fehr WR, Fehr EL, Jessen HJ (1987) *Principles of cultivar development: Theory and technique*, Macmillan.
23. Singh RK, Chaudhary BD (1985) *Biometrical methods in quantitative genetics analysis*, Kalyani Publishers.
24. Falconer DS (1989) *Introduction to quantitative genetics*, Longman.
25. Walpole R (1982) *Introduction of statistics*, 3 Eds., New York: Macmillan Publishing Company, Inc.
26. Bakare MA, Kayondo SI, Aghogho CI, et al. (2022) Exploring genotype by environment interaction on cassava yield and yield related traits using classical statistical methods. *PLoS One* 17: 1–24. https://doi.org/10.1371/journal.pone.0268189.
27. Mondal KK, Akhter MAE, Mallik MAK (2025) Seasonal variability in soil salinity and its climatic drivers in Khulna, Bangladesh. *Forum Geogr* 39: 307–317. https://doi.org/10.23917/forgeo.v39i3.9038.
28. Kawser U, Nath B, Hoque A (2022) Observing the influences of climatic and environmental variability over soil salinity changes in the Noakhali Coastal Regions of Bangladesh using geospatial and statistical techniques. *Environ Chall* 6: 1–17. https://doi.org/10.1016/j.envc.2021.100429.
29. Corwin DL, Yemoto K (2020) Salinity: electrical conductivity and total dissolved solids. *Soil Sci Soc Am J* 2: 1442–1461. https://doi.org/10.1002/saj2.20154.

30. Yang M, Zhou D, Hang H, et al. (2024) Effects of balancing exchangeable cations Ca, Mg, and K on the growth of tomato seedlings (*Solanum lycopersicum* L.) based on increased soil cation exchange capacity. *Agronomy* 14: 1–13. https://doi.org/10.3390/agronomy14030629.
31. Cucci G, Lacolla G (2013) Irrigation with saline-sodic water: effects on two clay soils. *Ital J Agron* 8: 94–101. https://doi.org/10.4081/ija.2013.e13.
32. Dey G, Banerjee P, Sharma RK, et al. (2021) Management of phosphorus in salinity-stressed agriculture for sustainable crop production by salt-tolerant phosphate-solubilizing bacteria—a review. *Agronomy* 11: 1–27. https://doi.org/10.3390/agronomy11081552.
33. Amanat MA, Naeem MK, Algwaiz HIM, et al. (2022) Evaluation of green super rice lines for agronomic and physiological traits under salinity stress. *Plants* 11: 1–19. https://doi.org/10.3390/plants11111461.
34. Crossa J (2012) From genotype × environment interaction to gene × environment interaction. *Curr Genomics* 13: 225–244. https://doi.org/10.2174/138920212800543066.
35. Gomez KA, Gomez AA (1984) *Statistical procedures for agricultural research*, New York: John Wiley & Sons.
36. Teressa T, Zigale S, Tamirat B (2021) Multi environments and genetic-environmental interaction (GxE) in plant breeding and its challenges: a review article. *Int J Res Stud Agric Sci* 7: 10–18. https://doi.org/10.20431/2454-6224.0704002.
37. Limbongan Y, Sjahril R, Pata'dungan AM, et al. (2024) Genetic performance, heritability, and correlation of traits in new plant type of rice lines for highland ecosystem. *Reprod Breed* 4: 203–211. https://doi.org/10.1016/j.repbre.2024.08.002.
38. Steinsaltz D, Dahl A, Wachter KW (2020) On negative heritability and negative estimates of heritability. *Genetics* 215: 343–357. https://doi.org/10.1534/genetics.120.303161.
39. Khanna A, Anumalla M, Ramos J, et al. (2024) Genetic gains in IRRI's rice salinity breeding and elite panel development as a future breeding resource. *Theor Appl Genet* 137: 1–14. https://doi.org/10.1007/s00122-024-04545-9.
40. Simmonds NW (1979) *Principles of crop improvement*, London: Longman.
41. Chacko A, Jayalekshmy V, Shahiba A (2023) Studies on pcv, gcv, heritability, and genetic advance in rice genotypes for yield and yield components. *Int J Plant Soil Sci* 35: 324–330. https://doi.org/10.9734/ijpss/2023/v35i163266.
42. Modarresi M (2026) Genetic variability, heritability and genetic advance in Iranian local rice genotypes for yield, and some agronomic traits. *Reprod Breed* 6: 9–20. https://doi.org/10.1016/j.repbre.2025.12.003.
43. Tiwari U, Singh L, Kumar S, et al. (2025) Evaluation of genetic variability, gcv and pcv in F_1 and F_2 populations of pea (*Pisum sativum* L.). *J Sci Res Rep* 31: 310–320. https://doi.org/10.9734/jsrr/2025/v31i123777.
44. Anshori MF, Purwoko BS, Dewi IS, et al. (2019) Selection index based on multivariate analysis for selecting doubled-haploid rice lines in lowland saline prone area. *SABRAO J Breed Genet* 51: 161–174.
45. International Rice Research Institute (2013) *Standard evaluation system for rice*, Manila: International Rice Research Institute.
46. Puvanitha S, Mahendran S (2017) Effect of salinity on plant height, shoot and root dry weight of selected rice cultivars. *Sch J Agric Vet Sci* 4: 126–131. https://doi.org/10.36347/sjavs.2017.v04i04.001.

47. Quan R, Wang J, Qin H, et al. (2025) Improving grain yield and salt tolerance by optimizing plant height with beneficial haplotypes in rice (*Oryza sativa*). *J Adv Res* 76: 17–32. https://doi.org/10.1016/j.jare.2024.12.007.
48. Akbar MR, Purwoko BS, Dewi IS, et al. (2021) Agronomic and yield selection of doubled haploid lines of rainfed lowland rice in advanced yield trials. *Biodiversitas* 22: 3006–3012. https://doi.org/10.13057/biodiv/d220754.
49. Hussain S, Zhang JH, Zhong C, et al. (2017) Effects of salt stress on rice growth, development characteristics, and the regulating ways: A review. *J Integr Agric* 16: 2357–2374. https://doi.org/10.1016/s2095-3119(16)61608-8.
50. Radanielson AM, Gaydon DS, Khan MMR, et al. (2018) Varietal improvement options for higher rice productivity in salt affected areas using crop modelling. *Field Crops Res* 229: 27–36. https://doi.org/10.1016/j.fcr.2018.08.020.
51. Wei HH, Zhang X, Zhu W, et al. (2024) Effects of salinity stress on grain-filling characteristics and yield of rice. *Acta Agron Sin* 50: 734–746. https://doi.org/10.3724/sp.J.1006.2024.32021.
52. Rusliani A, Nasrudin, Ramadhan RAM, et al. (2026) Source-sink dynamics and grain yield formation of rice under single and dual salinity-drought stresses. *Curr Appl Sci Technol* e0269229: 1–18. https://doi.org/10.55003/cast.2026.269229.
53. Vieira RA, Nogueira APO, Fritsche-Neto R (2025) Optimizing the selection of quantitative traits in plant breeding using simulation. *Front Plant Sci* 16: 1–19. https://doi.org/10.3389/fpls.2025.1495662.
54. Anshori MF, Purwoko BS, Dewi IS, et al. (2023) Systematic selection to adaptive doubled haploid rice lines under different environments of submergence screening methods. *J Agric Food Res* 14: 1–9. https://doi.org/10.1016/j.jafr.2023.100775.
55. Mahmud A, Islam MN, Islam AKMA, et al. (2024) Evaluation of yield-attributing parameters in Aus rice for enhancing productivity. *Plant Genet Resour-C* 22: 368–377. https://doi.org/10.1017/s1479262124000364.
56. Blancon J, Buet C, Dubreuil P, et al. (2024) Maize green leaf area index dynamics: Genetic basis of a new secondary trait for grain yield in optimal and drought conditions. *Theor Appl Genet* 137: 1–20. https://doi.org/10.1007/s00122-024-04572-6.
57. Guimarães PHR, Melo PGS, Cordeiro ACC, et al. (2021) Index selection can improve the selection efficiency in a rice recurrent selection population. *Euphytica* 217: 1–16. https://doi.org/10.1007/s10681-021-02819-7.
58. Cobos F, Reyes W, Perez-Almeida I, et al. (2025) Response of advanced rice lines from inter and intraspecific backgrounds to saline stress conditions. *AGRIVITA J Agric Sci* 47: 199–213. https://doi.org/10.17503/agrivita.v47i2.4466.
59. Khatun T, Khatun SM, Naim J, et al. (2024) Advanced mutant line developed from fatemadhan shows salinity tolerance at both seedling and reproductive stages. *Plant Sci Today* 11: 316–328. https://doi.org/10.14719/pst.2917.
60. Zayed BA, Anis GB, Abdel-Fattah AFG, et al. (2025) Validation and detection of some new rice hybrids to salt stress using various statistical Analysis Methods. *Trends Appl Sci Res* 20: 1–13. https://doi.org/10.3923/tasr.2025.01.13.
61. Hadianto W, Purwoko BS, Dewi IS, et al. (2023) Agronomic performance, yield stability and selection of doubled haploid rice lines in advanced yield trials. *AIMS Agric Food* 8: 1010–1027. https://doi.org/10.3934/agrfood.2023054.

62. Biodiversity International, International Rice Research Institute, Africa Rice Center (2007) *Descriptors for wild and cultivated Rice (Oryza spp.)*, Rome: Bioversity International.



AIMS Press

© 2026 the Author(s), licensee AIMS Press. This is an open access article distributed under the terms of the Creative Commons Attribution License (https://creativecommons.org/licenses/by/4.0)