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Research Article

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Posted Date: January 24th, 2026

DOI: https://doi.org/10.21203/rs.3.rs-8445346/v1

Additional Declarations: No competing interests reported.

Multi-Trait Selection Index for the Improvement of Agronomic and Yield Traits in Rice (*Oryza sativa* L.)

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Abstract

Despite the critical role of rice (*Oryza sativa* L.) as a staple food in Ghana, national demand far exceeds local production. This low production is partly attributed to the limited availability of improved varieties, highlighting the urgent need for varietal enhancement. This field study evaluated 295 diverse rice genotypes from multiple Ghanaian sources for variation in 14 agro-morphological and yield-related traits using advanced multivariate analyses and the Multi-Trait Genotype-Ideotype Distance Index (MGIDI) to identify superior genotypes for breeding. Significant variation ($p < 0.001$) was observed across all traits. Moderate to high broad-sense heritability (76.9–86.3%) and strong positive phenotypic and genotypic correlations ($r \geq 0.85$) were found among key yield traits, including grain yield, hundred-grain weight, panicle number, and tiller number, underscoring their importance in yield improvement. Conversely, days to heading and maturity were highly positively correlated (phenotypic $r = 0.96$; genotypic $r = 0.98$) but strongly negatively correlated with all yield and morphological traits (phenotypic $r = –0.84$ to $–0.98$; genotypic $r = –0.94$ to $–0.99$), highlighting the trade-off between early phenology and yield performance. Principal component and hierarchical cluster analyses revealed distinct trait groupings and genotype clusters, providing valuable insight into trait associations and germplasm diversity. Notably,

accessions from KUMASI-CRI tended to associate with yield and yield-related traits, including grain yield, hundred-grain weight, panicle number, tiller number, and grain thickness. The MGIDI identified 44 promising genotypes combining desirable trait profiles (e.g., SA2-SARI, Togo Marsha, SA51-SARI, KBR 12, NERICA-L 41, JKE56-30, CRI-AMANKWATIA, AGRA-CRI-LOL-1-21, AGRA-CRI-LOL-2-29) that enable simultaneous improvement of yield, phenology, and plant architecture while overcoming limitations of traditional indices. These genotypes represent valuable breeding material for enhancing rice production and food security in Ghana. Future multi-environment testing and stress screening are recommended to confirm stability and adaptability. This study demonstrates the effectiveness of multi-trait selection indices in accelerating genetic gains in rice breeding programs toward developing climate-resilient, high-yielding cultivars.

Keywords

Oryza sativa L.; Ghanaian rice germplasm; Agro-morphological diversity; Genetic variability; Multi-trait Genotype-Ideotype Distance Index; Yield improvement; Rice breeding.

Introduction

Rice (*Oryza sativa* L.) is a vital staple crop worldwide, supplying about 20% of global dietary energy [1] and serving as a cornerstone of food security, economic development, and social stability [2]. In Ghana, it is the fastest-growing staple and a priority crop, supporting the livelihoods of over 500,000 smallholder farmers [3,4]. National consumption has more than doubled in recent years, rising from 32.0 kg per person in 2008 to over 45 kg in 2023 [3,5] with total demand now exceeding 1.48 million metric tonnes [5,6]. This makes rice central not only to nutrition but also to Ghana's economic resilience and agricultural development.

Unfortunately, over 950,000 MT accounting for 60% of Ghana's rice demand is met through imports, costing the nation approximately US$1 billion annually [3,7]. This heavy reliance on imports stems from a persistent domestic production deficit. In 2023, although local rice production reached a high of about 771,000 MT (milled equivalent), this covered only about 40–45% of national demand [5]. Key contributing factors to

this deficit include low yields and high susceptibility to climate stress. For example, the average national yield of 3.33 MT/ha remains significantly below the potential yield of over 6 MT/ha creating a deficit of about 2.7MT/ha [5]. Furthermore, erratic rainfall patterns and recurring droughts continue to undermine both the quantity and quality of rice produced in the country. These challenges are exacerbated by Ghana's over-reliance on a limited number of jasmine-type rice varieties with a narrow genetic background [8]. Although the country possesses a wealth of rice genetic resources, only a few germplasms are utilised in breeding programmes, partly because many of them remain poorly characterised. Proper characterisation of rice genetic materials will enable breeders to select the most suitable parents for developing superior, high-yielding and climate-resilient varieties.

Agro-morphological characteristics, which are observable traits related to plant growth, development, and yield, have traditionally been used to assess genetic diversity in rice. Although advances in molecular biology have introduced more sophisticated tools for evaluating diversity, agro-morphological traits remain a valuable and cost-effective method, especially in the early stages of germplasm characterisation. Generally, the selection of superior genotypes has relied on single-trait approaches, often overlooking the complex interactions among multiple traits that influence overall performance. Such an approach is considered inadequate, as it does not ensure genetic gains in other important traits [9]. Consequently, experienced breeders often aim to combine multiple desirable traits within a single, high-performing genotype [10]. This ideal genotype is known as an ideotype*,* a concept first introduced by [11].

While several selection indices have been proposed for selecting superior genotypes based on the defined selection criteria [12], a widely used selection index is the Smith-Hazel (SH) index, which relies on phenotypic and genotypic variance and covariance matrices [13, 14]. However, this index has several limitations, such as multicollinearity when assessing multiple traits, which compromises the accuracy of genetic gain estimation [15]. Additionally, assigning economic weights to different traits poses challenges for breeders when computing the SH index [15, 16]. To address these issues, [10] introduced a novel multivariate selection approach known as the Multi-Trait Genotype-Ideotype Distance Index (MGIDI). This index effectively accounts for

multicollinearity and enables the favorable selection of all traits under consideration, resulting in significant genetic gain [10]. MGIDI not only resolves multicollinearity concerns but also alleviates the difficulty breeders face in assigning genetic weights to traits [17]. The MGIDI has been successfully employed by several researchers to select superior genotypes across diverse crops, including rice [18-23], barley [24], oats [25] sesame [26] and maize [27].

Therefore, the objectives of this study were to: (i) quantify the variation in agro-morphological and yield traits among rice accessions in Ghana; (ii) identify key variables contributing most significantly to the observed variability; and (iii) apply an index selection method to identify desirable rice genotypes/ideotypes based on the agro-morphological and yield traits for future genetic improvement.

Materials and Methods

Site description

A field study was conducted from June to October 2020 at the rice research field of the Council for Scientific and Industrial Research–Crop Research Institute (CSIR-CRI) in Fumesua (latitude 6°42′51″N, longitude 1°31′53″W). The area lies within the Forest agro-ecological zone of Ghana, at an altitude of 228 m above sea level. Daily temperature and relative humidity were recorded using a data logger (WS-520 indoor/outdoor thermometer and hygrometer, Denver Electronics A/S). Temperatures ranged from 17.5 °C to 31.0 °C, with a mean of 23.1 °C, while relative humidity varied between 70% and 100%, averaging 94.69%. Fumesua experiences a bimodal rainfall pattern, with the major rainy season occurring from March to July and the minor rainy season from September to December [28]. Cumulative rainfall during the experimental year totalled 1,254.5 mm, with 801.5 mm recorded over the crop growth period. The soils at Fumesua are classified as Ferric Acrisols of the Asuansi series [29]. At the CSIR-CRI rice field, the topsoil is predominantly sandy loam, extending to a depth of approximately 20 cm. This layer is gritty in texture, dark brown in color, and tends to dry out quickly, often forming a crust when moisture is lost. Beneath the topsoil, at a depth of 25–30 cm, the soil is heavier in texture and exhibits a higher moisture retention capacity, capable of holding up to 115 mm/m of water [30]. The pH ranges between 6.0 - 7.5 [28].

Genetic materials

A total of 295 rice accessions were used in this study, sourced from AfricaRice, the Korea-Africa Food and Agriculture Cooperation Initiative (KAFACI), the Council for Scientific and Industrial Research–Savannah Agricultural Research Institute (CSIR-SARI), and CSIR-CRI. Of these, 75 accessions originated from AfricaRice, 97 from KAFACI, 65 from CSIR-CRI, and 58 from CSIR-SARI. A complete list of the rice accessions and their sources are provided in Table S1. CRI-AgraRice was used as the national check, while CRI-Enapa served as the local check.

Experimental design, field establishment and management

The experiment was arranged in an alpha lattice design with 295 rice genotypes evaluated across 3 replications. Each replication consisted of 59 incomplete blocks, with 5 genotypes per block. A total of 885 plots were assessed, ensuring efficient control of field heterogeneity and improved precision of genotype evaluation.

After slashing the field with a cutlass and removing the vegetation, the land was rotovated and subsequently levelled. Seeds were sown directly by manual dibbling, with two seeds per hill, later thinned to one seedling per hill. Each entry consisted of a single row of five plants, spaced 20 cm apart within rows and 30 cm between rows. A pre-emergent herbicide (ButaForce EC) Butachlor 500 g/L was applied for initial weed control, and the field was kept weed-free through hand and spot weeding to prevent weed growth and alternate host infestation. Fertilization followed the recommended rate in Ghana (90 kg N: 60 kg P: 60 kg K per hectare). A basal application of NPK (15-15-15) was applied 10 days after planting, supplying all the required phosphorus and potassium, along with 40% of the total nitrogen. Urea (46-0-0) was top-dressed in two split applications: 40% at maximum tillering and the remaining 20% at panicle initiation. Supplementary irrigation was provided as needed. Water levels were maintained at 3–5 cm from 14 days after seedling emergence until panicle initiation, except during nitrogen applications when the field was temporarily drained. During flowering (heading) until maturity, water was maintained and then drained 10 days before harvest. Insect pests and birds were managed using Sunpyrifos 48 EC and nets, respectively. No disease symptoms were observed throughout the crop growth period.

Data collection

A total of fourteen quantitative traits were measured: heading days/days to 50% heading (HD), maturity days (MD), plant height (PH), panicle length (PL), culm length (CL), panicle number (PN), sterile lemma length (SLEMMAL), grain length (GL), grain width (GW), grain thickness (GT), tiller number (TN), hundred-grain weight (HGW), grain length-to-width ratio (GLWR), and grain yield (GY).

Phenological traits

Days to 50% heading was recorded as the number of days from the effective sowing date to the date on which 50% of the plants had headed. Maturity date was recorded as the number of days from sowing to physiological maturity, defined as when 80–85% of the grains on the panicles were fully ripened.

Structural traits

Culm length was measured from ground level to the base of the panicle using five plants per plot, with measurements recorded to the nearest centimeter. The tiller number was recorded as the total number of grain-bearing and non-bearing tillers on five plants, assessed after ripening (80–85% maturity). Panicle number was recorded as the number of panicles per plant. Sterile lemma length, grain length, grain width, and grain thickness were measured using a digital caliper. Sterile lemma length was measured from the neck of the panicle to its tip. For grain length, measurements were taken on random samples of ten representative whole grains, from the pointed end (apiculus) to the base, excluding the awn for awned genotypes.

Yield and yield related parameters

The tiller number was recorded as the total number of grain-bearing and non-bearing tillers on five plants, assessed after ripening (80–85% maturity). Panicle number was recorded as the number of panicles per plant. Grain width was measured as the maximum distance across the fertile lemma and palea using the same ten representative grains. For hundred-grain weight, a random sample of 100 well-developed, whole grains was selected, dried to approximately 14% moisture content, and weighed using a precision electronic balance. The grain length-to-width ratio was calculated as the quotient of grain length and grain width from the ten representative grain samples. Grain yield per plant was calculated from five plants by harvesting

panicles, threshing, winnowing, and drying the grains to a constant moisture content of 14%. The grain yield per plant and grain yield per hectare were computed as follows:

$$Grain\ yield\ per\ plant\ \left({}^{g}/_{plant}\right) = \frac{Total\ grain\ weight\ from\ 5\ plants\ (g)}{5} \quad \text{Equ (1)}$$

$$Grain\ yield\ per\ hectare\ \left({}^{kg}/_{ha}\right) = \frac{Grain\ yield\ per\ plant\ (g) \times plants\ per\ hectare}{1000} \quad \text{Equ (2)}$$

$$Grain\ yield\ \left({}^{t}/_{ha}\right) = \frac{Grain\ yield\ \left({}^{kg}/_{ha}\right)}{1000} \quad \text{Equ (3)}$$

Statistical analysis

Descriptive statistics, including the mean, coefficient of variation (CoV), range, and standard deviation (SD) were first calculated for each measured trait using a combination of base R functions (R Core Team, 2024 version 4.3.3) and the dplyr [31] and tidyr [32] packages. The CV was categorised as high (≥60%), intermediate (30% to 59%), and low (< 30%) [33]. An analysis of variance (ANOVA) was performed using the PBIB.test function from the agricolae package [34] (Equ 4), and significant differences between means were determined using Tukey's Honestly Significant Difference (HSD) test. To estimate genetic parameters, the traits were further analysed with a mixed-effects model implemented via the gamem() function of the metan package [35]. The model was fitted within the Restricted Maximum Likelihood/Best Linear Unbiased Prediction (REML/BLUP) framework. In the model specification, rice genotype and block nested within replication were treated as random effects, while replication was included as a fixed effect (Equ 5). From the mixed effects model, summary statistics including observed means and trait specific ranges (minimum, maximum, and genotypic extremes) and genetic parameters, such as genotypic, phenotypic, and residual variances, were estimated. Based on these variance components, the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and broad sense heritability on an entry mean basis (H^2) were calculated following Equ (6), Equ (7) [36] and Equ (8) [35] respectively. According to the classification criteria proposed by [37], GCV and PCV values were categorised as low (<10.00%), moderate (10.00–20.00%), or high (>20.00%). This categorization is widely applied in contemporary germplasm studies [38-42]. Similarly, heritability (H^2) was classified as low (<30%), moderate (30–60%), or high (>60%) following [43]. This classification remains common in recent empirical studies [34, 43].

$$Y_{ijk} = \mu + g_i + r_j + b_{k(j)} + \varepsilon_{ijk} \qquad Equ\ (4)$$

where Y_{ijk} is the observed value for genotype *i*, in block *k* within replication *j*; μ is the overall mean; g_i is the fixed effect of the i^{th} genotype; r_j is the random effect of the j^{th} replication; $b_{k(j)}$ is the random effect of the k^{th} block nested within the j^{th} replication; and ε_{ijk} is the experimental error.

$$Y_{ijk} = m + g_i + r_j + b_{k(j)} + \varepsilon_{ijk} \qquad Equ\ (5)$$

where m is the intercept; g_i is the random effect of the i^{th} genotype; r_j is the fixed effect of the j^{th} replication; Y_{ijk}, $b_{k(j)}$, and ε_{ijk} are as previously described in Equ 1.

$$GCV = \frac{\sqrt{\sigma_g^2}}{Grand\ mean} \times 100 \qquad Equ\ (6)$$

$$PCV\ \frac{\sqrt{\sigma_p^2}}{Grand\ mean} \times 100 \qquad Equ\ (7)$$

$$H^2 = \left(\frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_\varepsilon^2}{r}} \right) \qquad Equ\ (8)$$

where r is the number of replicates per genotype, and σ^2_g, σ^2_p, and σ_ε^2 are the genotypic, phenotypic and residual variance, respectively.

Phenotypic and genotypic correlation coefficients were computed using functions from base R (R Core Team, 2024 Version) and the metan package [35] to assess the relationships among traits. Principal component analysis (PCA) was conducted using the FactoMineR [44] and factoextra [45] packages to identify traits contributing most significantly to the observed variation in the dataset. The PCA was based on the correlation matrix, and only principal components (PCs) with eigenvalues greater than 1 were retained, following the Kaiser criterion [46,47]. Genotypic classification was carried out using Ward's hierarchical clustering method, applying the minimum variance algorithm with Euclidean distance as the dissimilarity measure [48]. The optimal number of clusters was determined using the "majority rule" implemented in

the NbClust package [49], and the resulting dendrogram was visualised using the dendextend package [50].

The theoretical foundation of the MGIDI index involves four key steps: (i) rescaling all trait values to a common range of 0 to 100; (ii) performing factor analysis to account for trait correlations and reduce data dimensionality; (iii) defining an ideotype based on pre-specified or desired trait values; and (iv) computing the distance of each genotype from the defined ideotype [10].

Step (i), the rescaling of traits was carried out according to Equ (9):

$$rX_{ij} = \frac{\eta_{nj} - \varphi_{nj}}{\eta_{oj} - \varphi_{oj}} \times \left(\theta_{ij} - \eta_{oj}\right) + \eta_{nj} \qquad Equ\ (9)$$

where η_{nj} and φ_{nj} represent the new maximum and minimum values, respectively, for trait j after rescaling; η_{oj} and φ_{oj} denote the original maximum and minimum values for trait j, respectively; and θ_{ij} is the original value of the *jth* trait for the *ith* genotype or treatment. The values for η_{nj} and φ_{nj} are determined as follows: for traits in which a decrease is desirable, $\eta_{nj} = 0$ and $\varphi_{nj} = 100$ are used; for traits in which an increase is desirable, $\eta_{nj} = 100$ and $\varphi_{nj} = 0$ are applied. In the rescaled two-way matrix *(rXij)*, each column spans a 0–100 range, reflecting the intended direction of selection (increase or decrease) while preserving the original correlation structure among variables.

Step (ii), the factor analysis involved an exploratory assessment of the rX_{ij} matrix to group correlated traits into distinct factors and to estimate the factor scores for each genotype according to Equ (10). The eigenvalues and eigenvectors were derived from the correlation matrix of rX_{ij}. Initial loadings were extracted by retaining only those factors with eigenvalues greater than one. Following varimax rotation [45] the final loadings were obtained and subsequently used to compute the genotype scores as shwon in Equ (11).

$$X = \mu + Lf + \varepsilon \qquad Equ\ (10)$$

where *X* is a *p×1* vector of rescaled observations; *μ* is a *p×1* vector of standardised means; L is a *p×f* matrix of factor loadings; *f* is a *p*×1 vector of common factors; and *ε* is a *p*×1 vector of residuals, with *p* and *f* denoting the number of traits and retained common factors, respectively.

$$F = Z(A^T R^{-1})^T \qquad Equ\ (11)$$

where *F* is a *g×f* matrix of factor scores; *Z* is a *g×p* matrix of rescaled standardised means; *A* is a *p×f* matrix of canonical loadings; and *R* is a *p×p* correlation matrix among the traits. Here, *g*, *f*, and *p* represent the number of genotypes, retained factors, and analysed traits, respectively.

Step (iii), The ideotype is conceptualised as the genotype exhibiting the maximum rescaled value (100) across all evaluated traits. Accordingly, the ideotype is defined as a *1* × *p* vector *I*, where *I* = [100, 100, …, 100].

Step (iv), the MGIDI is estimated according to Equ (12):

$$MGIDI_i = \left[\sum_{j=1}^{f} (\gamma_{ij} - \gamma_j)^2\right]^{0.5} \qquad Equ\ (12)$$

where $MGIDI_i$ denotes the multi-trait genotype–ideotype distance index for the i^{th} genotype; γ_{ij} is the value of the i^{th} genotype in the j^{th} factor (i = 1, 2,…., g; j = 1, 2,….,*f*), g and f are the number of genotypes and factors, respectively; γ_j is the j^{th} score of the ideotype. A genotype with the lowest MGIDI value is considered closest to the ideotype, indicating that it possesses more desirable values across all *p* traits.

The proportion of the MGIDI index for the *i*th genotype explained by the *j*th factor (ω_{ij}) is used to identify the strengths and weaknesses of the genotypes and is calculated as follows:

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=1}^{f} \sqrt{D_{ij}^2}} \qquad Equ\ (13)$$

D_{ij} is the distance between the i^{th} genotype or treatment and the ideotype for the j^{th} factor. A low contribution from a factor suggests that the traits associated with that factor are near the ideotype.

The predicted genetic gain (SG%) for each trait was calculated using the MGIDI index, considering the selection intensity percentage, as shown below:

$$SG\ (\%) = \frac{\left(\overline{X}_s - \overline{X}_o\right) \times H^2}{\overline{X}_o} \times 100 \qquad Equ\ (14)$$

where $\overline{X}_s$ is the mean of the selected genotypes, $\overline{X}_o$ is the mean of the original population, and H^2 is the heritability.

Results

Descriptive statistics and analysis of variance

The mean grain yield, hundred-grain weight, grain thickness, grain length, grain width, and grain length-to-width ratio were 30.4 t/ha, 3.3 g, 2.1 mm, 6.6 mm, 2.6 mm, and 2.6, respectively, with corresponding ranges of 39.2 t/ha, 3.4 g, 2.5 mm, 3.0 mm, 3.0 mm, and 2.9 (Table 1). Days to heading and days to maturity averaged 88.4 and 124.0 days, with ranges of 42.0 and 48.0 days, respectively. Plant height had a mean value of 102.5 cm and a range of 110.7 cm. The CoV across traits varied from 7.7 % for grain length to 18.8 % for panicle length. Descriptive statistics for all traits are presented in Table 1. The ANOVA results revealed highly significant differences ($p<0.001$) among the rice genotypes for all measured traits (Tabe 1).

Significant variation in measured traits among rice genotypes

The top five genotypes for grain yield were KBR 2 (41.47 t/ha), SA38-SARI (39.97 t/ha), AgKE99-56 (39.73 t/ha), JKE56-30 (39.07 t/ha), and SR34053(#5-52)-1-4-2-10-1-2 (39.00 t/ha) (Table S2). SA38-SARI exhibited the highest hundred-grain weight (4.6 g), representing an approximate 1.9-fold difference compared with the lowest value recorded for WAIQ1-SARI (2.43 g). Grain thickness (2.8 mm) and grain width (3.38 mm) were greatest in KBR 2, showing ~44% and ~73% differences, respectively, from the lowest values recorded for WAB 2085-TGR2-WAT4-1-1 (1.79 mm and 1.57 mm). The top ten genotypes for grain length recorded values ranging from 7.31 mm in CRI-Emopa to 7.62 mm in AgKE99-56. ART75-14-1-2-B-B produced the highest tiller number (16.78), representing an ~84% difference from the lowest recorded for WAIQ1-SARI (6.89). Similarly, panicle number showed an approximate 60% difference between SA38-SARI (13.78) with the best performance and WAIQ1-SARI (7.39) with the least value. The earliest heading and maturity were observed in SA38-SARI (71.33 days) and KBR 2 (111.33 days), respectively. Other genotypes with early heading included AgKE99-56 (74.67 days), SR34053(#5-52)-1-4-2-10-1-2, and KBR 2 (75.67 days each). For maturity, SR34053(#5-52)-1-4-2-10-1-2, SA38-SARI, AGRA-CRI-LOL-1-11, CRI-Kantinka, AGRA-CRI-LOL-2-7, and CRI-Mpuntuo matured at 112.00 days. Among the top ten genotypes, plant height ranged from 125.38 cm in Gigante-SARI to 136.54 cm in AgKE99-56, whereas the bottom ten genotypes ranged from 6.48 cm in ART75-57-1-1-B-B to 80.68 cm in SAHEL 177. Complete genotypic differences across all traits are presented in Table S2. BLUP values were extracted for each trait (Table S3) and found to be highly consistent with the observed mean values.

Fig 1: (a) Variation in paddy grains, with each grain representing a unique rice genotype.

Table 1: Descriptive statistics, ANOVA, variance components and broad-sense heritability estimate for the rice genotypes evaluated.

Trait	Unit	Descriptive statistics				ANOVA	Variance Components (%)		H^2 (%)
		Mean	Range	SD	CoV (%)	F-prob Geno	GCV	PCV	
Grain yield	t/ha	30.4	39.2	5.5	18.1	p<0.001	14.2	17.2	86.3
Hundred grain weight	G	3.3	3.4	0.4	13.2	p<0.001	9.8	12.5	82.3
Grain thickness	Mm	2.1	2.5	0.2	9.8	p<0.001	4.2	9.5	42.4
Grain length	Mm	6.6	3	0.5	7.7	p<0.001	5.2	7	78.9
Grain width	Mm	2.6	3	0.3	13	p<0.001	10	12.3	85.1
Grain length-to-width ratio	–	2.6	2.9	0.2	8.9	p<0.001	4.1	8.4	47.9
Tiller number	–	11.7	21.3	1.4	11.9	p<0.001	8.2	11.3	76.9
Panicle number	–	11.2	10	1.1	10.1	p<0.001	7.9	9.6	86.1
Panicle length	Cm	25.2	37	4.7	18.8	p<0.001	12.6	17	78.4
Heading days	Days	88.4	42	7	7.9	p<0.001	6.1	7.5	85.3
Maturity days	Days	124	48	8.4	6.8	p<0.001	5.4	6.5	87.8
Culm length	Cm	77.3	95.3	14.6	19	p<0.001	12.7	17.2	78.1
Sterile lemma length	Mm	2.6	9.1	0.4	15.2	p<0.001	6.1	14.3	40
Plant height	Cm	102.5	110.7	16	15.6	p<0.001	10.2	14.1	76.7

Genotypic and phenotypic coefficients of variation, and broad-sense heritability

Both the GCV and PCV ranged from low (<10%) to moderate (10–20%) across all measured traits (Table 1). Moderate GCV and PCV values were observed for traits such as grain yield (14.2% and 17.2%), grain width (10.0% and 12.3%), plant height (10.2% and 14.1%), and culm length (12.7% and 17.2%). In contrast, low GCV and PCV values were recorded for panicle number (7.9% and 9.6%), days to heading (6.1% and 7.5%), days to maturity (5.4% and 6.5%), and grain thickness (4.2% and 9.5%) (Table 1). Except for grain thickness, sterile lemma length, and grain length-to-width ratio, which exhibited moderate broad-sense heritability (42.2%, 40.0%, and 47.7%, respectively), broad-sense heritability was high (>60%) for all other traits (Table 1).

Phenotypic and genotypic correlations coefficients of measured traits

Correlation analysis revealed highly significant associations ($p < 0.001$) among many traits at both the phenotypic and genotypic levels (Fig 2; Table S4A and S4B). Grain yield exhibited strong positive correlations with yield-related traits such as hundred-grain weight ($r = 0.96$ and 0.98 for phenotypic and genotypic correlations, respectively), panicle number ($r = 0.93$; 0.97), and tiller number ($r = 0.85$; 0.96). Similarly, panicle number was strongly associated with grain width ($r = 0.94$; 0.99), tiller number ($r = 0.93$; 0.98), and hundred-grain weight ($r = 0.91$; 0.96). Morphological traits also showed close associations: panicle length was highly correlated with plant height ($r = 0.99$; 0.99), grain length ($r = 0.99$; 0.99), and culm length ($r = 0.97$; 0.98). In contrast, days to heading and days to maturity were positively correlated with each other ($r = 0.96$; 0.98) but negatively associated with all yield and morphological traits, with correlation values ranging from –0.84 to –0.98 phenotypically and –0.94 to –0.99 genotypically. The complete correlation matrices are presented in Fig 2.

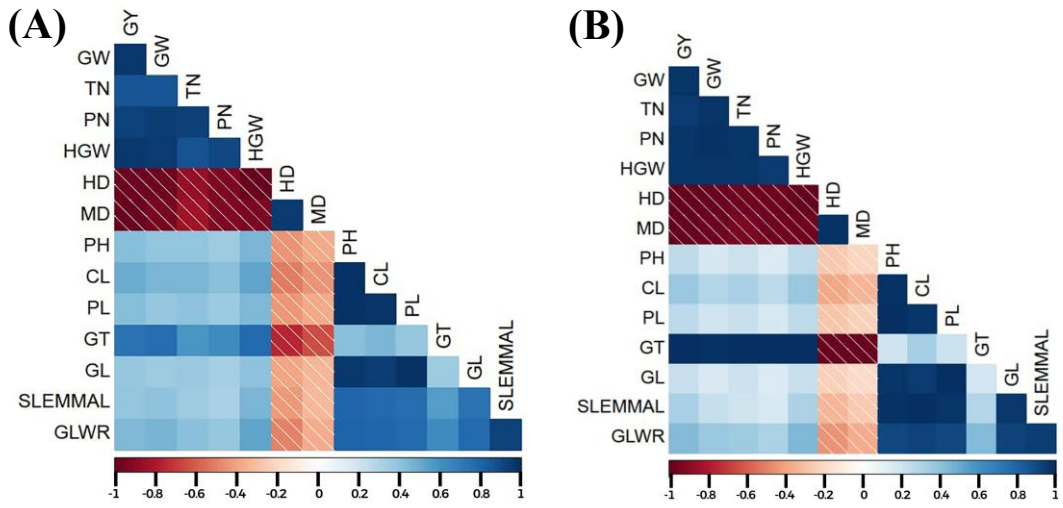


Fig 2: Correlation coefficients among the fourteen quantitative traits. (A) Phenotypic; (B) Genotypic. The scale is shown in the bar at the bottom of each matrix.

Principal components analysis of evaluated traits

The first two principal components (PCs) had eigenvalues greater than 1.0 and were therefore considered significant, together explaining 91.77% of the total variation in the dataset (Table 2). PC1 accounted for 62.47% of the variation, with major contributors including heading days, hundred-grain weight, grain yield, grain width, and tiller number (Fig S1a). PC2 explained 29.3% of the variation, with grain length, plant height, panicle length, culm length, and the grain length-to-width ratio contributing most strongly (Figure S1B). Several traits, such as heading days, grain width, grain yield, hundred-grain weight, and maturity days, contributed above average to the combined PC1 and PC2 (Fig 3a).

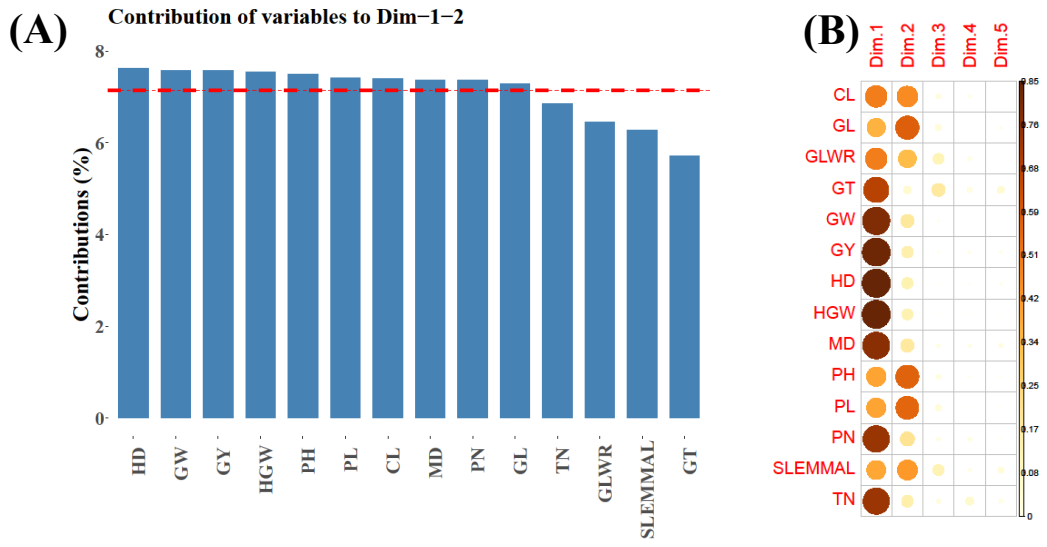
Most traits were well represented on PC1 (Table S5; Figure 3b). Heading days, hundred-grain weight, grain yield, grain width, maturity days, panicle number, and tiller number had high $\cos^2$ values (0.73–0.85). In contrast, only grain length, plant height, and panicle length were moderately represented on PC2, with $\cos^2$ values of 0.58, 0.57, and 0.56, respectively, while the remaining traits were poorly represented. The levels of correlation among the traits are presented on the PCA biplot of variables and genotype origins, which indicated three main groups of correlated traits (Figure 3c). The first group included plant height, grain length, and panicle length, which showed positive associations. The second group comprised yield and yield-related traits,

including grain yield, hundred-grain weight, and panicle number. Both groups were negatively correlated with the third group, consisting of the phenological traits, heading days and maturity days. The biplot also revealed partial overlap among genotypes from different sources (Figure 3c). Accessions from KUMASI-CRI tended to associate with yield and yield-related traits, including grain yield, hundred-grain weight, panicle number, tiller number, and grain thickness, whereas KAFACI accessions aligned more closely with phenological traits such as heading days and maturity days. In contrast, AFRICARICE and NYANKPALA-SARI accessions were more widely dispersed, showing no strong alignment with specific trait groups.

The biplot of variables and individual genotypes revealed distinct groupings (Figure S1c). Plant height, grain length, culm length, and panicle length resolved in the first quadrant and were associated with genotypes such as AgKE99-56, SA38-SARI, AGRA-CRI-LOL-1-11, AGRA-CRI-LOL-2-7, and CRI-Mpuntuo. Heading days and maturity days resolved in the second quadrant alongside genotypes including WAB 2085-TGR2-WAT4-1-1, SA52-SARI, SA14-SARI, WAIQ1-SARI, and SR33705F2-61-1-3-HV-1-1 Yield and yield-related traits resolved in the fourth quadrant and were associated with genotypes such as KBR 2, SA38-SARI, AgKE99-56, JKE56-30, SR34053(#5-52)-1-4-2-10-1-2, and AGRA-CRI-LOL-1-11

Table 2: Variable coordinates, eigenvalues, percent variance and cumulative variance for all traits evaluated traits.

Variables	PC1	PC2	PC3
GY	0.91	-0.38	-0.05
GW	0.89	-0.43	0.00
TN	0.86	-0.38	-0.14
PN	0.86	-0.46	-0.12
HGW	0.92	-0.36	0.02
HD	-0.92	0.37	0.02
MD	-0.88	0.43	0.11
PH	0.63	0.75	-0.15
CL	0.70	0.68	-0.16
PL	0.63	0.75	-0.20
GT	0.82	-0.24	0.42
GL	0.60	0.76	-0.19
SLEMMAL	0.62	0.65	0.36
GLWR	0.70	0.58	0.35
Eigenvalues	**8.75**	**4.10**	**0.60**
Variance (%)	**62.47**	**29.3**	**4.30**
Cumulative variance (%)	**62.47**	**91.77**	**96.07**



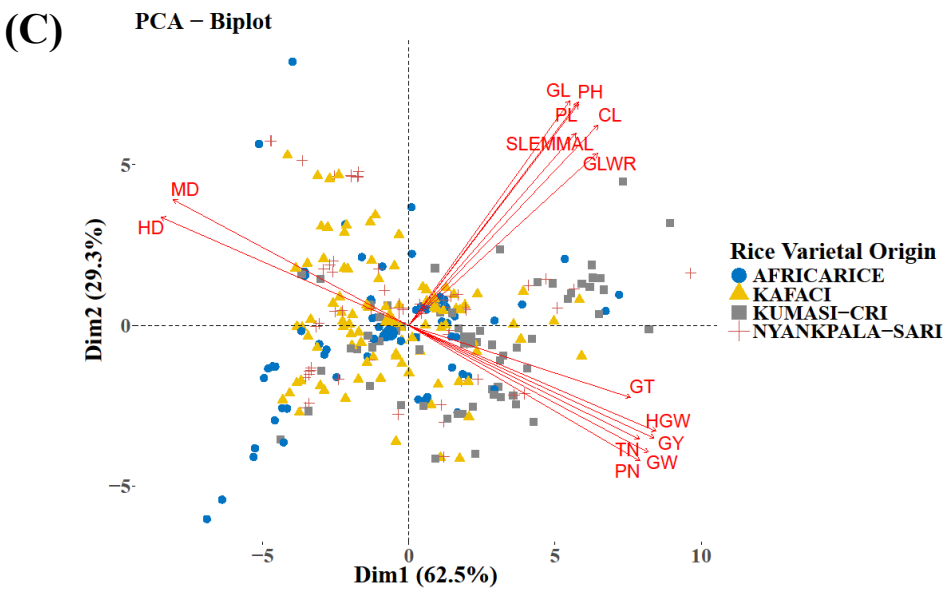
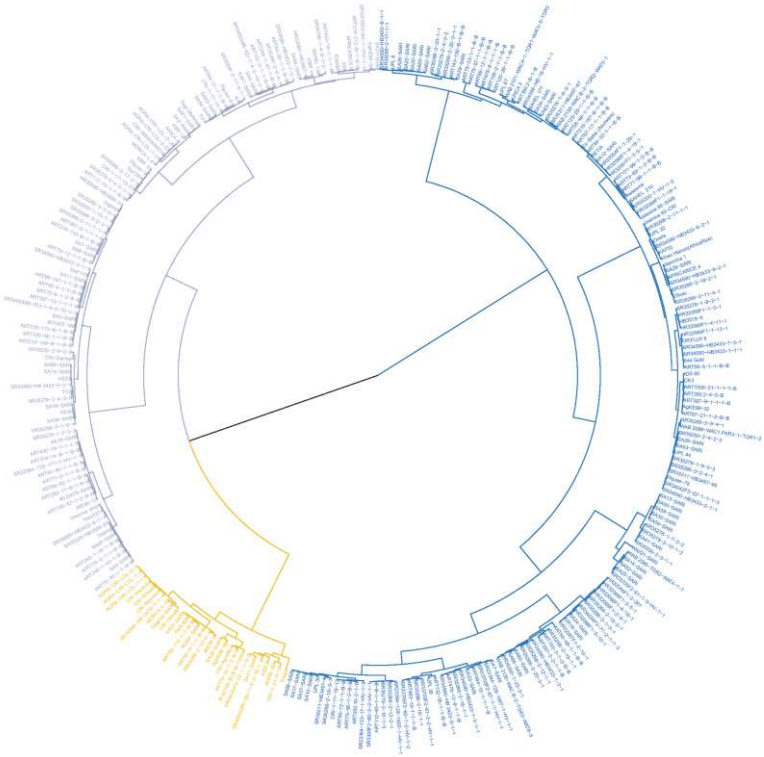


Fig 3: (a) Contribution of traits to the combined PC1 and PC2. The red dashed line is the expected average contribution; (B) Quality of representation of variables on the factor map for the first five PCs; (C) PCA biplot showing the relationships among quantitative variables and the distribution of rice genotypes according to their origins.

Hierarchical clustering

Hierarchical clustering grouped the rice genotypes into three clusters (Table S7; Figure 4a). There were 105 members in cluster 1, comprising genotypes such as 80 DAYS-SARI, AFRICARICE 6, ART216-149-B-1-B-B, CRI-1-11-15-21, SAHEL 134, SR35230-2-9-2-2, and Togo Marshall. Cluster 2 consisted of 161 genotypes, including AFRICARICE 4, ART125-26-1-1-B-B, BETIA, IDS 85, SR23364-128-1835-1-HV-1-1, and UPL 30. There were 29 genotypes in the third cluster, among which were AgKE99-56, ART90-9-1-1-B-B, Enapa, JKE56-30, Gigante-SARI, and SR35266-2-12-4-1. When superimposed on the PCA map, genotypes in clusters 1 and 3 showed predominantly positive associations with PC1, whereas those in cluster 2 were largely negative on PC1 (Fig 4b).

(A)



(B)

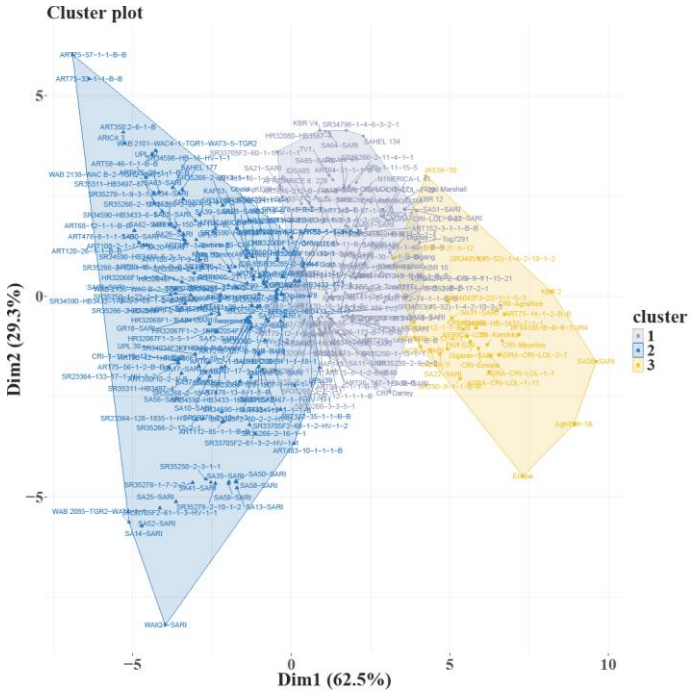


Fig 4: (a) Cluster analysis showing the grouping patterns of 295 rice genotypes based on 14 quantitative traits. Cluster 1 – grey, Cluster 2 – blue, and Cluster 3 – yellow; (B) Individual rice genotypes on the principal component map grouped and coloured according to their assigned group following cluster analysis.

Factor analysis, communality and genetic gain

The MGIDI analysis revealed that the first two factors (FA1 and FA2) captured the majority of trait variation (Table 3). Grain yield, hundred-grain weight, tiller number, panicle number, heading days, and maturity days loaded positively on FA1 (≥ 0.8), whereas grain width and grain thickness loaded negatively (≤ –0.8). Grain length, panicle length, and grain length-to-width ratio were strongly and positively associated with FA2 (~0.9), while plant height, culm length, and sterile lemma length showed strong negative correlations (≤ –0.8). Communality values were generally high (≤ 0.8) for most traits, including grain yield, hundred-grain weight, tiller number, and panicle number (Table 3). Genetic gain varied among traits, with grain yield recording 14.0%, hundred-grain weight 8.6%, grain width 8.3 %, panicle number 6.6%, and tiller number 5.2%. Negative values were observed for heading days (–5.7%) and maturity days (–5.8%). Other traits, including grain length (mm), grain width (mm), panicle length (cm), culm length (cm), and plant height (cm), exhibited relatively small changes (Table 3).

Table 3: Factorial loadings after varimax rotation, communalities, and selection gains for agro-morphological traits in rice genotypes. (Bold values represent traits with high contribution to each factor).

Variables	FA1	FA2	Communality	Xo	Xs	SDperc	SGperc	Sense	Goal
GY	**0.9**	0.2	0.8	30.4	35.4	16.2	14	increase	100
HGW	**0.9**	0.2	0.9	3.3	3.7	10.5	8.6	increase	100
GT	**-0.8**	-0.2	0.7	25.2	25.1	-0.4	-0.3	increase	0
GL	0.1	**0.9**	0.9	6.6	6.6	-0.6	-0.4	increase	0
GW	**-0.9**	-0.1	0.9	2.6	2.8	9.8	8.3	decrease	0
GLWR	0.3	**0.9**	0.8	2.6	2.6	-0.1	-0.1	increase	0
TN	**0.9**	0.1	0.9	11.7	12.5	6.8	5.2	increase	100
PN	**0.9**	0.1	0.9	11.2	12.1	7.6	6.6	increase	100
PL	0.1	**0.9**	0.8	77.3	78.5	1.6	1.3	decrease	0
HD	**0.8**	0.2	0.9	88.4	82.5	-6.7	-5.7	decrease	100

MD	**0.8**	0.1	0.9	124	115.8	-6.6	-5.8	decrease	100
CL	-0.2	**-0.9**	0.9	102.5	101.9	-0.6	-0.4	decrease	100
SLEMMAL	-0.2	**-0.9**	0.8	2.6	2.6	-0.3	-0.1	decrease	100
PH	-0.1	**-0.8**	0.7	2.1	2.1	2.2	0.9	decrease	0

Genotype selection using multi-trait genotype-ideotype distance index

Based on the MGIDI index, 44 rice genotypes were identified from the 295 evaluated as possessing the most desirable combination of traits (Fig 5; Table S8). The strength and weakness view (Fig 6) indicated that genotypes such as Sahel 134, SR34053(#5-52)-1-4-2-10-1-2, Togo Marshall, CRI-1-11-15-21, SR35276-2-4-3-1-1, and Tog7291 resolved on FA1, and had strengths for traits such as grain yield, hundred grain-weight, panicle number, and grain width that recorded high contributions on FA1 (Table 2). Genotypes such as AGRA-CRI-LOL-1-21, SA51-SARI, ART152-3-1-1-B-B, SA61-SARI, KBR 12, and ART248-1-97-1-B-B resolved on FA2 and associated with traits such as grain length, grain length-to-width ratio, culm length, and plant height (Table 3).

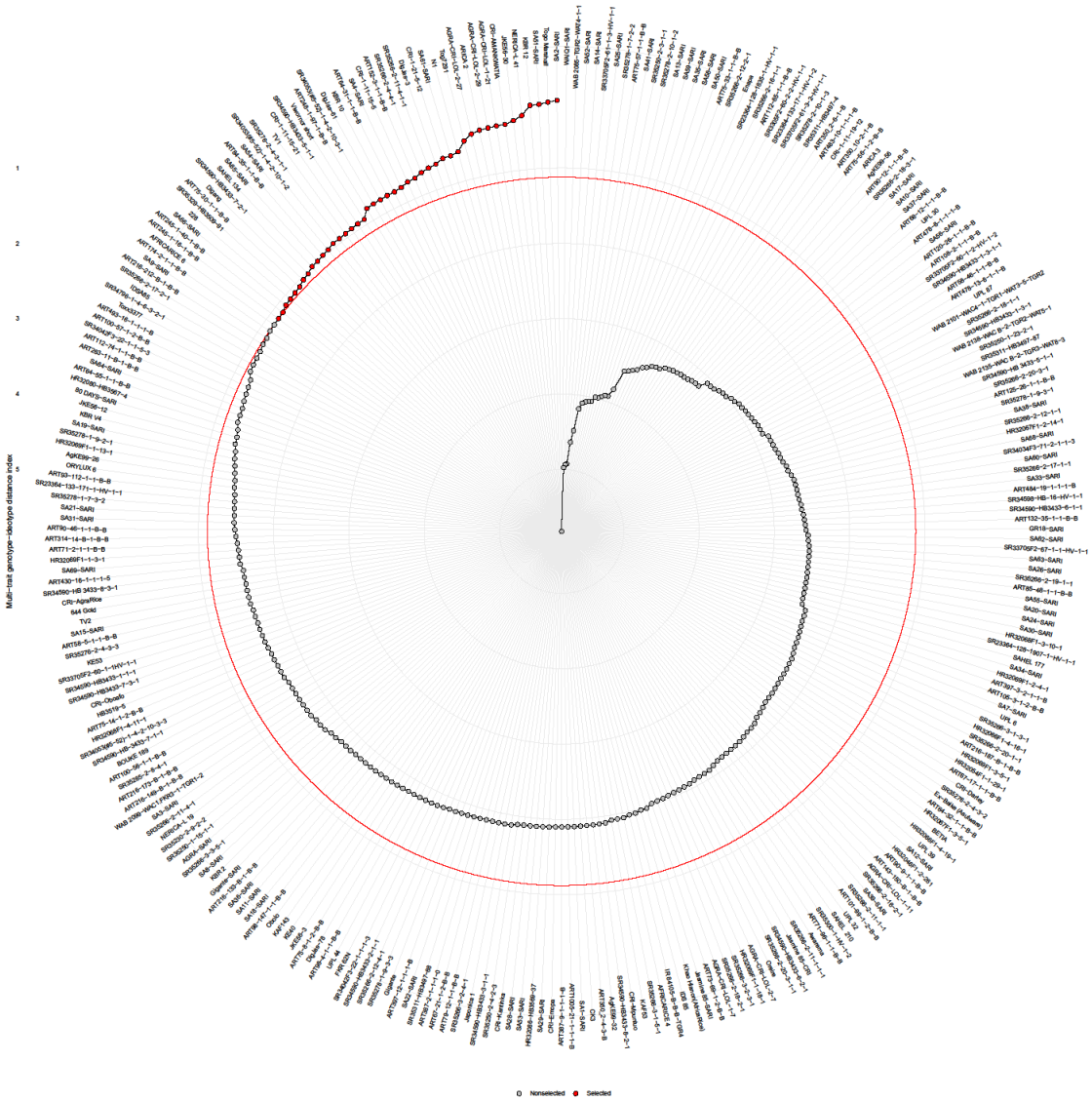


Fig 5: Rice genotypes rankings showing selected and non-selected genotypes using the multi-trait genotype ideotype index. The selected genotypes are shown as red dots, while the unselected genotypes are shown as black dots. The red circle represents the cut point according to 15% selection pressure.

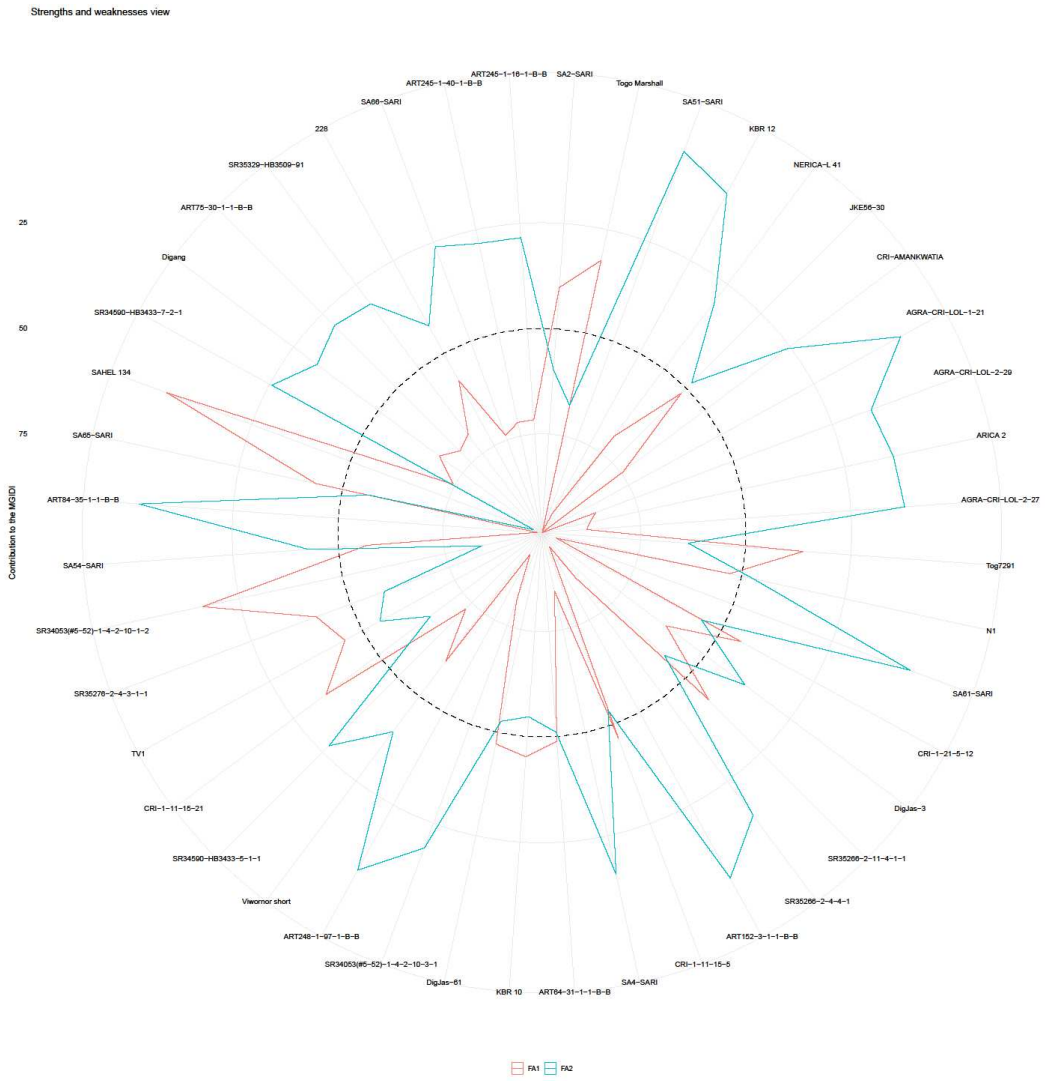


Fig 6: The strengths and weaknesses of the selected genotypes are shown as the proportion of each factor on the computed multi-trait genotype–ideotype index. The smaller the proportion explained by a factor (closer to the external edge), the closer the traits within that factor are to the ideotype. The black broken circle at the centre shows the theoretical value if all the factors contributed equally.

Discussion

Phenotypic diversity, genetic variability, and heritability estimate

In this study, fourteen quantitative traits were evaluated to assess variations among 295 rice genotypes collected from four research institutes in Ghana. The results revealed significant differences across all traits (Table 1), indicating substantial diversity within the collection. This variability, which may reflect both genetic factors and environmental influences, provides valuable opportunities for identifying genotypes with desirable trait combinations for further evaluation and selection. Traits

such as plant height, grain yield, and phenological parameters exhibited broad ranges, reflecting both adaptive responses and the influence of differing breeding backgrounds. These findings are consistent with previous studies on rice germplasm collections that have reported wide variability in yield, yield-related attributes, and phenological characteristics [19, 20, 38, 51-54] underscore the importance of characterising such variability to support targeted improvement programs. The phenotyping approach was robust, yielding low to moderate CoV across all assessed traits (Table 1). Low CoV values reflect high precision in trait estimation, whereas high CoV values are typically attributable to variability introduced by experimental conditions [19, 52, 55].

The extent of genetic variability and the magnitude of heritability are fundamental determinants of a population's potential response to selection in crop improvement programmes. In this study, the moderate and closely aligned GCV and PCV values (10–20%), coupled with high heritability (>60%) for grain yield, grain width, plant height, panicle length, and culm length (Table 1), indicate that variation in these traits is primarily controlled by genetic factors rather than environmental influences, rendering them highly amenable to direct phenotypic selection. Similar moderate GCV and PCV values have been reported for plant height [56], grain width [57] and panicle length [18] among rice genotypes, while [19] documented moderate GCV for grain yield in one hundred rice genotypes. High broad-sense heritability estimates for plant height [56], grain width [57], grain yield and panicle length [18] in rice further substantiate the present findings. In contrast, despite the low PCV and high heritability values for traits such as grain length, panicle number, heading days, and maturity days, the corresponding low GCV values recorded (Table 1) suggest a minimal genetic contribution to the observed phenotypic variation. Likewise, traits such as hundred grain weight and tiller number exhibited moderate PCV but low GCV (Table 1), indicating a predominance of environmental influence over genetic factors. Such traits, being relatively genetically uniform, are less responsive to direct phenotypic selection for substantial genetic improvement. Nevertheless, meaningful genetic gains can still be realised through selection approaches that minimise environmental influence, such as marker-assisted selection [56]. It is important to emphasise that narrow-sense heritability captures only the additive component of genetic variance, whereas the broad-sense heritability estimated in this study encompasses the total genetic

contribution to phenotypic expression, including additive, dominance, epistatic, and genotype-by-environment effects. Since only additive effects are consistently transmitted from parents to their offspring, further estimation of narrow-sense heritability is required to effectively partition additive variance from non-additive sources. Overall, the genetic parameter estimates provide compelling evidence of substantial trait differentiation among traits.

Strong correlations were observed between many traits

Deciphering the correlation structure among agronomic traits provides a strategic framework for enhancing selection efficiency and achieving sustained yield improvement in rice breeding. The strong positive associations of grain yield with key yield component traits, including hundred grain weight, panicle number, and tiller number, at both phenotypic and genotypic levels (Fig 2; Table S4A and S4B) indicate that these traits contribute directly and substantially to yield formation. Comparable significant positive relationships in these traits have been reported in rice germplasm by [58] and [56]. The consistently stronger genotypic correlations relative to phenotypic ones suggest these relationships are predominantly governed by genetic factors rather than environmental influences, underscoring the efficiency of indirect selection for yield improvement through these component traits. In contrast, days to heading and days to maturity were strongly positively correlated with each other, consistent with [59], yet exhibited marked negative correlations with major yield and morphological traits (Fig 2; Table S4A and S4B). This inverse relationship highlights an inherent trade-off between growth duration and productivity. While early maturing genotypes are advantageous in agro-ecologies with limited growing seasons, they may incur yield penalties due to shorter vegetative growth and grain filling periods. Conversely, later maturing genotypes often leverage extended photosynthetic and reproductive phases to achieve higher yield potential. This finding is corroborated by [60], who examined the relationships between yield and agronomic traits across 7,686 rice varieties representing four ecotypes (indica inbred, indica hybrid, japonica inbred, and japonica hybrid), concluding that a longer growth period accounted for higher grain yield across all ecotypes. These findings are crucial for tailoring breeding objectives to specific production environments, balancing maturity duration with yield optimisation. Beyond

yield associations, several morphological traits exhibited strong positive correlations, including panicle length with plant height, grain length, and culm length. These strong interrelationships suggest the involvement of shared genetic or physiological pathways regulating plant architecture, possibly related to internode elongation and panicle initiation. Similarly, panicle number showed strong positive correlations with grain width, tiller number, and hundred grain weight, implying that reproductive efficiency and sink capacity may play critical roles in determining yield output. However, these interpretations remain speculative and warrant further investigation to confirm underlying mechanisms.

Multivariate analysis identified key traits and distinct genotype groupings

The PCA revealed a clear distribution of phenotypic variation among the evaluated genotypes based on their trait profiles. The first two principal components captured most of the phenotypic diversity, explaining 91.77% of the total variance. PC1 represented the primary dimension of variation, driven mainly by yield-related and phenological traits (Table 2; Fig S1a). Strong positive loadings for grain yield, hundred-grain weight, grain width, panicle number, and tiller number characterise this axis as a yield–productivity dimension. These associations reflect genotypes with higher reproductive output, larger grains, and more tillers. In contrast, heading and maturity days contributed negatively to PC1, supporting the previously noted inverse relationship between early maturity and yield potential. This exemplifies a well-known agronomic trade-off where early-maturing cultivars tend to yield less than those with longer growth durations due to penalties from shortened vegetative phases [61]. Reduced growth duration limits assimilate accumulation, leading to lower yield potential, whereas later-maturing cultivars benefit from extended photosynthetic activity that supports higher productivity. This aligns with [62], who found a negative correlation between days to 50% maturity and grain yield in sorghum and suggested that increasing this trait could enhance both grain yield and carbon sequestration potential. High cos^2 values (Table S5) for these variables further emphasise their strong representation on this axis, confirming their central role in shaping the primary gradient of agronomic differentiation. PC2 captured variation in plant morphology and structural development, evidenced by high positive loadings for plant height, panicle

length, grain length, and culm length (Table 2; Fig S1b). The grain length-to-width ratio also contributed positively, supporting the interpretation of this component as a structural growth axis that separates genotypes with elongated plant and grain forms from those with more compact architectures. Yield-related traits such as grain yield, hundred-grain weight, and grain width exhibited negative loadings on PC2, suggesting an inverse relationship between vegetative elongation and yield efficiency. This pattern aligns with resource allocation trade-offs, where excessive vegetative growth can divert assimilates away from reproductive structures. Moderate cos^2 values for grain length, plant height, and panicle length (Table S5; Fig 3b) highlight the secondary but meaningful importance of these traits in defining phenotypic variability beyond yield and maturity in this dataset. [33] and [63] previously underscored the significance of traits contributing to PC1 and PC2 in explaining dataset variability. Thus, these traits could be prioritised in rice breeding programmes.

The PCA biplot revealed structured clustering of traits into three major association groups. The first group, consisting of traits such as plant height, grain length, and panicle length, represented vertical growth and architectural attributes. The second encompassed yield and yield-related parameters, including grain yield, hundred-grain weight, and panicle number, while the third group, composed of heading and maturity days, showed a strong negative correlation with the yield group, reinforcing the fundamental yield–phenology trade-off. Genotypic distributions within the biplot mirrored these trait associations. Accessions from KUMASI-CRI aligned closely with yield-related traits, indicating a breeding emphasis on productivity and grain mass. KAFACI accessions are associated with phenological traits, suggesting adaptation to longer growth cycles, while AFRICARICE and NYANKPALA-SARI accessions were more diffusely distributed, implying greater variability or intermediate adaptation across trait clusters. At the genotype level (Fig S1c), accessions such as AgKE99-56, SA38-SARI, AGRA-CRI-LOL-1-11, and AGRA-CRI-LOL-2-7 can be classified as tall and elongated types. Late-maturing accessions include WAB 2085-TGR2-WAT4-1-1, SA52-SARI, SA14-SARI, and WAIQ1-SARI, while high-yielding lines comprise KBR 2, SA38-SARI, AgKE99-56, JKE56-30, and SR34053(#5-52)-1-4-2-10-1-2.

The identification of two dominant axes, yield–phenology (PC1) and plant architecture (PC2), provides a strategic framework for designing idotypes and guiding selection targets. Genotypes with high PC1 scores and moderate PC2 scores represent optimal genotypes that combine strong yield potential with stable maturity and moderate plant stature, minimising lodging risks. High PC1 and low PC2 genotypes are shorter, high-yield lines suited for mechanised production and intensive management systems. Low PC1 and high PC2 genotypes express tall, early-maturing forms suitable for low-input environments or competitive weed suppression. By positioning genotypes within the PC1–PC2 space, breeders can effectively exploit combinations of phenology, productivity, and architecture to develop varieties that balance yield potential with structural resilience and ecological adaptability.

Cluster analysis serves to identify distinct and diverse genotypes for hybridisation programmes, thereby fostering the development of breeding material with a broader genetic base [64]. Here, the cluster dendrogram revealed a three-cluster groups (Figs 4a-4b; Table S7), further highlighting the substantial diversity within the rice collection. Genotypes in cluster 1 exhibited superior plant architectural traits, while those in cluster 2 were characterised by longer growth durations. Cluster 3 genotypes showed superiority in yield-related traits. A three-way hybridisation programme incorporating accessions from each cluster could be an effective strategy to develop high-yielding rice varieties with balanced phenology and optimised plant architecture. Conversely, within-cluster hybridisation may yield reduced genetic gain due to the close relatedness of genotypes in each cluster [64].

Multi-trait genotype–ideotype distance index indicated desirable gains for most studied traits

Genotype selection based on a single trait is often unreliable, as improvement in one characteristic may negatively affect others. To address this, the MGIDI was applied to identify genotypes exhibiting an optimal combination of agronomic traits. From 295 rice genotypes evaluated, 44 were selected as closest to the ideal profile. Notable among these were SA2-SARI, Togo Marsha, SA51-SARI, KBR 12, NERICA-L 41, JKE56-30, CRI-AMANKWATIA, AGRA-CRI-LOL-1-21, AGRA-CRI-LOL-2-29, ARICA

2, and AGRA-CRI-LOL-2-27 (Fig 5; Table S8). These elite genotypes demonstrated strong, balanced performance and hold significant potential for breeding programs aimed at improving grain yield alongside key agronomic traits [15]. MGIDI's effectiveness in identifying superior genotypes has also been demonstrated in rice [65-67] and other cereals such as wheat [68], and barley [24].

MGIDI facilitated robust multi-trait selection, resulting in significant genetic gains across yield-related and phenological traits. Grain yield, hundred-grain weight, tiller number, and panicle number (Table 3) showed substantial positive genetic gains, reflecting marked improvements in productivity components and demonstrating MGIDI's capability to overcome challenges posed by genetic correlations and trade-offs. Concurrently, traits related to phenology and plant architecture (heading date, maturity date, culm length, and sterile lemma length) exhibited significant negative gains, consistent with our breeding objectives to reduce these traits. Shortened heading and maturity dates improve adaptation to shorter growing seasons and reduce environmental stress exposure, while decreased culm length enhances lodging resistance, critical for agronomic stability. For example, plant types with short culms and long, upright leaves have been reported to substantially increase grain yield [69]. The simultaneous improvement of yield and favourable modifications to growth duration and plant stature highlights the comprehensive efficiency of MGIDI-based selection.

However, undesirable genetic gain was observed in plant height, where selection led to a slight increase contrary to the target reduction (Table 3). This may stem from genetic correlations between plant height and positively selected traits such as grain yield, hundred-grain weight, tiller number, and panicle number (Fig 2b), or from limitations in the index's capacity to fully resolve complex trait interrelationships. Additionally, grain width showed an unintended increase despite a target reduction, while grain thickness and grain length-to-width ratio exhibited little gains opposite to their goals. These deviations illustrate the challenge of balancing genetic gains across multiple, sometimes conflicting, trait objectives. To mitigate such outcomes, breeders should apply careful parental selection and strategic crossing schemes aimed at breaking unfavourable genetic linkages, thereby improving trait balance in subsequent generations. Overall, these findings confirm MGIDI's utility as a powerful tool for

ideotype-driven breeding [30,70] while identifying areas for refinement to optimise selection outcomes.

The strength and weakness analyses further revealed distinct trait groupings corresponding to genotype clusters captured by factor analysis. Genotypes including Sahel 134, SR34053(#5-52)-1-4-2-10-1-2, Togo Marshall, CRI-1-11-15-21, SR35276-2-4-3-1-1, and Tog7291 (Fig 6) were notable for strong contributions from grain yield, hundred-grain weight, panicle number, and grain width (FA1, Table 3), reflecting a coherent genetic architecture underpinning key productivity traits. Conversely, genotypes such as AGRA-CRI-LOL-1-21, SA51-SARI, ART152-3-1-1-B-B, SA61-SARI, KBR 12, and ART248-1-97-1-B-B excelled in grain morphology and plant structure traits, including grain length, grain length-to-width ratio, culm length, and plant height (FA2, Table 3). This differentiation highlights complementary trait profiles emphasising grain quality and plant architecture, impacting both market preferences and agronomic adaptability, including lodging resistance. The clear delineation of genotypes along these factors provides strategic insight for breeding programs, suggesting that crossing genotypes dominant in different factors can generate progeny combining high yield potential with desirable grain and structural attributes, facilitating the development of rice varieties that balance productivity and quality.

Although this study demonstrates the potential of MGIDI for identifying promising rice genotypes, certain limitations must be addressed to enhance the applicability of the results. Effective crop improvement depends on selecting genotypes that perform consistently across multiple traits and diverse environmental conditions. However, this study was conducted in a single environment without replication across multiple locations, which limits the assessment of genotype stability and genotype-by-environment interactions. Additionally, genotypes were evaluated only under optimal growing conditions and were not exposed to abiotic stresses such as drought or heat, restricting insight into their performance under adverse conditions. Future research should incorporate multi-location trials and stress screening to facilitate the development of rice varieties with stable performance and resilience across a broad range of environments.

Conclusions

This study provides insight into the extent of variability among 295 Ghanaian rice genotypes for key agronomic and yield traits. Substantial diversity and high heritability (>60%) were observed across all measured traits, offering valuable opportunities to identify genotypes with desirable trait combinations for further evaluation and selection. The correlation analysis revealed significant positive associations between several traits, such as grain yield, grain width, hundred grain weight, panicle number, tiller number, and grain thickness, indicating that these attributes contribute directly and substantially to yield formation and could be simultaneously improved with minimal trade-offs. In contrast, the negative relationships observed between phenological traits (including heading and maturity days) and most other traits highlight an inherent trade-off between growth duration and productivity. PCA showed that all measured traits contributed to at least one of the two significant principal components, underscoring their importance in explaining the overall variability within the dataset. Hierarchical cluster analysis grouped the 295 rice genotypes into three clusters, further confirming the diversity within the collection. The MGIDI identified 44 promising rice accessions, including SA2 SARI, Togo Marshal, SA51 SARI, KBR 12, NERICA L 41, JKE56 30, CRI Amankwatia, and AGRA CRI LOL 1 21, which can serve as progenitors in rice improvement programs aimed at enhancing agronomic performance and yield potential. For breeding implications, the study demonstrates the importance of exploiting complementary trait groups. Crosses between early-maturing, stress-escape donors and high-yielding late-maturing lines can generate transgressive segregants with superior yield stability under variable conditions. Likewise, integrating genotypes with high grain quality attributes into breeding pipelines ensures the release of varieties that satisfy both production and market demands. The clustering of genotypes independent of geographic origin emphasises that diverse sources can be successfully recombined, broadening the genetic base of national breeding programs. Future research should incorporate multi-location trials and stress screening to facilitate the development of rice varieties with stable performance and resilience across diverse environments.

Acknowledgements

We are grateful to the rice team at Council for Scientific and Industrial Research-Crops Research Institute for their varied contributions toward this research.

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Declarations

Funding

No funding was received to assist with the preparation of this manuscript

Conflicts of interest/Competing interests

The authors declare no conflicts of interest

Ethics

The rice (Oryza sativa L.) accessions used in this study were obtained from cultivated sources and were not collected from the wild. The collection and use of the plant material complied with all relevant institutional, local, and national guidelines regulating plant cultivation and agricultural research in Ghana. No endangered or protected plant species were involved in this study, and therefore no specific permits or licenses were required.

Consent to publish

Not applicable. This manuscript does not contain any individual person's data in any form.

Consent to participate

Not applicable

Data available on request

The datasets generated and/or analyzed during the current study are available from the corresponding author upon reasonable request.

REFERENCES

1. Mohidem, N. A., Hashim, N., Shamsudin, R., & Che Man, H. (2022). Rice for Food Security: Revisiting Its Production, Diversity, Rice Milling Process and Nutrient Content. *Agriculture*, *12*(6), 741. https://doi.org/10.3390/agriculture12060741

2. United States Department of Agriculture, F. A. S. (2019). No Title. *Ghana: Ghana Grain and Feed - Update*.

3. Ministry of food and Agriculture. (2022). No Title. *Facts and Figures: Agriculture in Ghana*.

4. Ouédraogo, S.A., Bockel, L., Abedi, A., Arouna, A. and Gopal, P. (2021). *Rice value chain in Ghana – Prospective analysis and strategies for sustainable and pro-poor growth*. FAO. https://doi.org/10.4060/cb1659en

5. Ministry of Food and Agriculture. (2025). Feed Ghana Programme (FGP) A Four-Year Agricultural Transformation Programme (2025 - 2028).

6. Ministry of Food and Agriculture. (2024). Facts and Figures: Agriculture in Ghana.

7. United States Department of Agriculture, Foreign Agricultural Service. Ghana: Ghana Grain and Feed – Update. 2024.

8. Frimpong BN, Asante BO, Asante MD, Ayeh SJ, Sakyiamah B, Nchanji E, et al. (2023). Identification of Gendered Trait Preferences among Rice Producers Using the G+ Breeding Tools: Implications for Rice Improvement in Ghana. Sustainability. 2023;15(11):8462.

9. Jahufer, M. Z. Z., & Casler, M. D. (2015). Application of the Smith-Hazel Selection Index for Improving Biomass Yield and Quality of Switchgrass. *Crop Science*, *55*(3), 1212–1222. https://doi.org/10.2135/cropsci2014.08.0575

10. Olivoto, T., & Nardino, M. (2021). MGIDI: toward an effective multivariate

selection in biological experiments. *Bioinformatics*, *37*(10), 1383–1389. https://doi.org/10.1093/bioinformatics/btaa981

11. Donald, C. M . (1968). The breeding of crop ideotypes. *Euphytica*, *17*, 385–403. https://doi.org/doi.org/10.1007/BF00056241

12. Ceron Rojas JJ, C. J. (2018). *Linear selection indices in modern plant breeding*. Springer.

13. Hazel, L. N. (1943). The Genetic Basis for Constructing Selection Indexes. *Genetics*, *28*(6), 476–490. https://doi.org/doi.org/10.1093/genetics/28.6.476, *Studies*, *10*(2), 30. https://doi.org/10.5539/jps.v10n2p30
14. Smith, H. F. (1936). A Discriminant Function For Plant Selection. *Annals of Eugenics*, *7*, 240–250.

15. Vinoth, P. K., Manonmani, S., Raveendran, M., Sritharan, N., Sudha, M., Puja, M., Bonipas, A., & Babu, C. (2025). Comparison of traditional selection indices and the Multi-Trait Genotype Ideotype Distance Index (MGIDI) for improving rice (Oryza sativa L.) cultivars. *Plant Science Today*. https://doi.org/10.14719/pst.5475

16. Graham, M. H. (2003). Confronting Multicollinearity In Ecological Multiple Regression. *Ecology*, *84*(11), 2809–2815. https://doi.org/10.1890/02-3114

17. Bizari EH, Pereira EM, Di AO, Unêda-Trevisoli SH. Selection indices for agronomic traits in segregating populations of soybean. Rev Ciênc Agron. 2017;48(1):110–117.

18. Al Mamun, S. M. A., Ivy, N. A., Khan, M. A. I., Rehana, S., Sultana, M. S., Adhikary, S. K., & Islam, M. M. (2024). Genotype Selection from Azide-Induced Rice Mutants Using Multitrait Genotype–Ideotype Distance Index (MGIDI): Unveiling Promising Variants for Yield Improvement. *Advances in Agriculture*, *2024*(1). https://doi.org/10.1155/2024/5719580

19. Asante, M. D., & Adjah, K. L. (2025). Genetic Diversity and Selection of High Performing Cultivars for Grain Yield and Yield Components Improvement in Rice. In *Food Science and Agriculture: Research Highlights Vol. 2* (pp. 166–189). BP International. https://doi.org/10.9734/bpi/fsarh/v2/4320

20. Debsharma, S. K., Syed, M. A., Ali, M. H., Maniruzzaman, S., Roy, P. R., Brestic, M., Gaber, A., & Hossain, A. (2022). Harnessing on Genetic Variability and Diversity of Rice (Oryza sativa L.) Genotypes Based on Quantitative and Qualitative Traits for Desirable Crossing Materials. *Genes*, *14*(1), 10. https://doi.org/10.3390/genes14010010

21. Jalalifar, Reza; Sabouri, Atefeh; Mousanejad, Sedigheh; Dadras, A. R. (2023).

Estimation of Genetic Parameters and Identification of Leaf Blast-Resistant Rice RILs Using Cluster Analysis and MGIDI. *Agronomy*, *13*(11), 2730. https://doi.org/doi.org/10.3390/agronomy13112730

22. Mamun, AA., Islam, MM., Adhikary, SK and Sultana, M. (2022). Resolution of Genetic Variability and Selection of Novel Genotypes in EMS Induced Rice Mutants Based on Quantitative Traits through MGIDI. *International Journal Of Agriculture & Biology*, *28*(2), 100–112. https://doi.org/DOI: 10.17957/IJAB/15.1957

23. Pallavi, M.; Maruthi Prasad, B. P.; Shanthi, P.; Reddy, V. L. N.; Nirmal Kumar, A. R. (2024). Multi trait genotype-ideotype distance index (MGIDI) for early seedling vigour and yield related traits to identify elite lines in rice (Oryza sativa L.). *Electronic Journal of Plant Breeding*, *15*(1), 120. https://doi.org/10.37992/2024.1501.020

24. Pour-Aboughadareh, A., Sanjani, S., Nikkhah-Chamanabad, H., Mehrvar, M. R., Asadi, A., & Amini, A. (2021). Identification of salt-tolerant barley genotypes using multiple-traits index and yield performance at the early growth and maturity stages. *Bulletin of the National Research Centre*, *45*(1), 117. https://doi.org/10.1186/s42269-021-00576-0

25. Klein, L.A., Marchioro, V.S., Toebe, M., Olivoto, T., Meira, D., Meier, C., et al., (2023). Selection of superior black oat lines using the MGIDI index. *Crop Breeding and Applied Biotechnology*, *23*(3), 1. https://doi.org/10.1590/1984-70332023v23n3a25

26. Ahsan, A. F. M. S., Alam, Z., Ahmed, F., Akter, S., & Khan, M. A. H. (2024). Selection of waterlogging tolerant sesame genotypes (Sesamum indicum L.) from a dataset using the MGIDI index. *Data in Brief*, *53*, 110176. https://doi.org/10.1016/J.DIB.2024.110176

27. Singamsetti, A., Zaidi, P. H., Seetharam, K., Vinayan, M. T., Olivoto, T., Mahato, A., Madankar, K., Kumar, M., & Shikha, K. (2023). Genetic gains in tropical maize hybrids across moisture regimes with multi-trait-based index selection. *Frontiers in Plant Science*, *14*. https://doi.org/10.3389/fpls.2023.1147424

28. Atakora, K., Essilfie, M. E., Agyarko, K., Dapaah, H. K., & Santo, K. G. (2023). Evaluation of Yield and Yield Components of Some Cowpea (<i>Vigna unguiculata</i> (L.) Walp) Genotypes in Forest and Transitional Zones of Ghana. *Agricultural Sciences*, *14*(07), 878–897. https://doi.org/10.4236/as.2023.147059

29. Owusu Danquah, E., Frimpong, F., Yeboah, S., Tetteh, E. N., Weebadde, C., Ennin, S. A., Agyeman, K., Amankwaa-Yeboah, P., Akley, E. K., Hayford, P., & Snapp, S. (2022). Pigeonpea (Cajanus cajan) and white yam (Dioscorea rotundata) cropping system: Improved resource use and productivity in Ghana. *Annals of Agricultural Sciences*, *67*(1), 60–71. https://doi.org/10.1016/j.aoas.2022.05.001

30. Oteng-Darko, P.Amponsah, S.K., Annan Afful, E. and Dzomeku, B. M. (2013). Installation of Drip Irrigation at CSIR-Crops Research Institute, Ghana. *International Journal of Engineering Research & Technology (IJERT)*, *2*(2).

31. Adu MO, Asare PA, Asare-Bediako E, Amenorpe G, Ackah FK, Afutu E, et al. (2018). Characterising shoot and root system trait variability and contribution to genotypic variability in juvenile cassava (Manihot esculenta Crantz) plants. Heliyon. 2018;4(6):e00665.

32. Adu, M. O., P. A. Asare, D. O. Yawson, et al. 2022. “Root System Traits Contribute to Variability and Plasticity in Response to Phosphorus Fertilization in 2 Field-Grown Sorghum [Sorghum bicolor (L.) Moench] Cultivars.” Plant Phenomics 2022: 0002. https://doi.org/10.34133/plant phenomics.0002.

33. de Mendiburu, F. (2023). *agricolae: Statistical Procedures for Agricultural Research* (1.3-7). CRAN or R-project.org. https://doi.org/10.32614/CRAN.package.agricolae.

34. Wickham H., Vaughan D., Girlich, M. (2024). *tidyr: Tidy Messy Data* (1.3.1). CRAN or R-project.org. https://cran.r-project.org/package=tidyr

35. Wickham H, François R, Henry L, Müller K, V. D. (2023). *dplyr: A Grammar of Data Manipulation* (1.1.4). CRAN or R-project.org. https://cran.r-project.org/package=dplyr

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

37. Shabanimofrad, M., Rafii, M. Y., Megat Wahab, P. E., Biabani, A. R., & Latif, M. A. (2013). Phenotypic, genotypic and genetic divergence found in 48 newly collected Malaysian accessions of Jatropha curcas L. *Industrial Crops and Products*, *42*, 543–551. https://doi.org/10.1016/j.indcrop.2012.06.023

38. Sivasubramaniam, S and Madhava Menon, P. (1973). Heterosis and inbreeding depression in rice. *Madras Agricultural Journal*, *60*(7), 1139–1140.

39. Khan, M. A. R., Mahmud, A., Islam, M. N., Ghosh, U. K., & Hossain, M. S.

(2023). Genetic variability and agronomic performances of rice genotypes in different growing seasons in Bangladesh. *Journal of Agriculture and Food Research*, *14*, 100750. https://doi.org/10.1016/J.JAFR.2023.100750

40. Lingaiah, N. (2020). Genetic Variability and Correlation Studies in Yield Traits of Elite Rice (Oryza sativa L.) Genotypes. *Indian Journal of Pure & Applied Biosciences*, *8*(6), 359–363. https://doi.org/10.18782/2582-2845.8428

41. Rathan, N. D. (2019). Variability and Path Coefficient Studies for Yield and Yield Related Traits in Rice (Oryza sativa L.). *International Journal of Agriculture Environment and Biotechnology*, *12*(4). https://doi.org/10.30954/0974-1712.12.2019.5

42. Russinga, A. M., Srividhya, A., Reddy, V. L. N., & Latha, P. (2020). Studies on Variability, Heritability and Genetic Advance for Yield and its Related Traits in Rice (Oryza sativa L) Genotypes. *International Journal of Current Microbiology and Applied Sciences*, *9*(9), 3180–3186. https://doi.org/10.20546/ijcmas.2020.909.393

43. Tessema, G. L., Mohammed, A. W., & Abebe, D. T. (2022). Genetic variability studies for tuber yield and yield attributes in Ethiopian released potato (Solanum tuberosum L.) varieties. *PeerJ*, *10*, e12860. https://doi.org/10.7717/peerj.12860

44. Pravallika, Y., Kumar, R. B., Kumar, J. ., & Kumar, ADVSLP, A. (2022). Studies on Genetic Variability, Heritability, Genetic Advance for Yield, and Yield Components in Rice Landraces. *Journal of Rice Research*, *15*(2). https://doi.org/10.58297/PDTR9988

45. Johnson HW, Robinson HF, Comstock RE. Estimates of Genetic and Environmental Variability in Soybeans. Agron J. 1955;47(7):314–318.

46. Lê, S., Josse, J., & Husson, F. (2008). FactoMineR : An R Package for Multivariate Analysis. *Journal of Statistical Software*, *25*(1). https://doi.org/10.18637/jss.v025.i01

47. Kassambara, Alboukade, Mundt, F. (2020). *factoextra: Extract and Visualize the Results of Multivariate Data Analyses* (1.0.7). CRAN or R-project.org. https://doi.org/10.32614/CRAN.package.factoextra

48. Kaiser, H. F. (1960). The Application of Electronic Computers to Factor Analysis. *Educational and Psychological Measurement*, *20*(1), 141–151. https://doi.org/10.1177/001316446002000116

49. Tabachnick, B. G., & Fidell, L. S. (1996). *Using Multivariate Statistics* ,

HarperCollins College Publishers. https://books.google.com.gh/books?id=V9NlQgAACAAJ

50. Manschadi, A. M., Hammer, G. L., Christopher, J. T., & DeVoil, P. (2008). Genotypic variation in seedling root architectural traits and implications for drought adaptation in wheat (Triticum aestivum L.). *Plant and Soil*, *303*(1–2), 115–129. https://doi.org/10.1007/s11104-007-9492-1

51. Charrad, M., Ghazzali, N., Boiteau, V., & Niknafs, A. (2014). NbClust : An R Package for Determining the Relevant Number of Clusters in a Data Set. *Journal of Statistical Software*, *61*(6). https://doi.org/10.18637/jss.v061.i06
52. Galili, T. (2015). dendextend: an R package for visualizing, adjusting and comparing trees of hierarchical clustering. *Bioinformatics*, *31*(22), 3718–3720. https://doi.org/10.1093/bioinformatics/btv428

53. Asante MD, Adjah KL, Mondal S, Pradhan P, Das B, Kumar D, et al. Agro-morphological and genetic diversity studies in Rice (Oryza sativa L.) germplasm using microsatellite markers. IOP Conf Ser Earth Environ Sci. 2025;13(1).

54. Demeke, B., Dejene, T., & Abebe, D. (2023). Genetic variability, heritability, and genetic advance of morphological, yield related and quality traits in upland rice (Oryza Sativa L.) genotypes at pawe, northwestern Ethiopia. *Cogent Food & Agriculture*, *9*(1). https://doi.org/10.1080/23311932.2022.2157099

55. Hallajian, M. T., Ebadi, A. A., & Kordrostami, M. (2024). Advancing rice breeding for drought tolerance: a comprehensive study of traditional and mutant lines through agronomic performance and drought tolerance indices. *BMC Plant Biology*, *24*(1), 1087. https://doi.org/10.1186/s12870-024-05771-5

56. Sheeba, A., Yogameenakshi, P., Aananthi, N., Sasikumaran, S., & Vimala, G. (2023). Studies on Genetic Diversity and Variability in Rice (Oryza sativa L.) Genotypes. *International Journal of Plant & Soil Science*, *35*(20), 1237–1243. https://doi.org/10.9734/ijpss/2023/v35i203922

57. Tezera, M. (2021). Variability, Heritability and Genetic advance of introduced upland rice genotypes at Fogera in North Western Ethiopia. *Journal of Plant Stud. 10(2):30*

58. Opoku, V. A., Adu, M. O., Asare, P. A., Asante, J., Hygienus, G., & Andersen, M. N. (2024). Rapid and low-cost screening for single and combined effects of drought and heat stress on the morpho-physiological traits of African eggplant (Solanum aethiopicum) germplasm. *PLOS ONE*, *19*(1), e0295512. https://doi.org/10.1371/journal.pone.0295512

59. Mondal, S., Pradhan, P., Das, B., Kumar, D., Paramanik, B., Yonzone, R.,

Barman, R., Saha, D., Karforma, J., Basak, A., Dey, P., & Seleiman, M. F. (2024). Genetic characterization and diversity analysis of indigenous aromatic rice. *Heliyon*, *10*(10), e31232. https://doi.org/10.1016/j.heliyon.2024.e31232

60. Sarif, H. M., Rafii, M. Y., Ramli, A., Oladosu, Y., Musa, H. M., Rahim, H. A., Zuki, Z. M., & Chukwu, S. C. (2020). Genetic diversity and variability among pigmented rice germplasm using molecular marker and morphological traits. *Biotechnology & Biotechnological Equipment*, *34*(1), 747–762. https://doi.org/10.1080/13102818.2020.1804451

61. Hygienus G, Opoku VA, Andersen MN, Asare PA, Adu MO. Genotypic Variation in Root System Architecture in Okra (Abelmoschus esculentus (L.) Moench) for Adaptive Breeding in Soil Resource-Limited Environments. J Agron Crop Sci. 2025;211(4).

62. Rathod, M. R., Vidyapeeth, M. K., Jadhav, I. A., Manish, I., Chavhan, V., Pawar, I. A., Jadhav, A. B., Chavhan, M. V, & Pawar, A. V. (2023). Correlation studies in rice (Oryza sativa L.) genotypes for yield and its yield contributing traits. ~ *1529 ~ The Pharma Innovation Journal*, *12*(7), 1529–1531. www.thepharmajournal.com

63. Li, R., Li, M., Ashraf, U., Liu, S., & Zhang, J. (2019). Exploring the Relationships Between Yield and Yield-Related Traits for Rice Varieties Released in China From 1978 to 2017. *Frontiers in Plant Science*, *10*. https://doi.org/10.3389/fpls.2019.00543

64. Dwivedi, S. L., Reynolds, M. P., & Ortiz, R. (2021). Mitigating tradeoffs in plant breeding. *IScience*, *24*(9), 102965. https://doi.org/10.1016/j.isci.2021.102965

65. Ngidi, A., Shimelis, H., Abady, S., Chaplot, V., & Figlan, S. (2024). Genetic variation and association of yield, yield components, and carbon storage in sorghum (Sorghum bicolor [L.] Moench) genotypes. *BMC Genomic Data*, *25*(1)

66. Kassambra, A. (2017). *Practical Guide To Principal Component Methods in R: PCA, M(CA), FAMD, MFA, HCPC, factoextra*. STHDA. https://books.google.com.gh/books?id=eFEyDwAAQBAJ

67. Maranna, S., Nataraj, V., Kumawat, G., Chandra, S., Rajesh, V., Ramteke, R., Patel, R. M., Ratnaparkhe, M. B., Husain, S. M., Gupta, S., & Khandekar, N. (2021). Breeding for higher yield, early maturity, wider adaptability and waterlogging tolerance in soybean (Glycine max L.): A case study. *Scientific Reports*, *11*(1), 22853. https://doi.org/10.1038/s41598-021-02064-x

68. Vinoth PK, Manonmani S, Raveendran M, Sritharan N, Sudha M, Puja M, et al. Comparison of traditional selection indices and the Multi-Trait Genotype

Ideotype Distance Index (MGIDI) for improving rice (Oryza sativa L.) cultivars. Plant Sci Today. 2025

69. Mohanty, T.A., Dharmalingam, K., Swaminathan, M., Ramalingam, S., Narayanan, M.B., & Natarajan, S. (2025). Multi-trait selection indices for identifying elite rice genotypes in rice breeding programs. *Plant Science Today*. https://doi.org/10.14719/pst.6215

70. Habib, M. A., Azam, M. G., Haque, M. A., Hassan, L., Khatun, M. S., Nayak, S., Abdullah, H. M., Ullah, R., Ali, E. A., Hossain, N., Ercisli, S., & Sarker, U. (2024). Climate-smart rice (Oryza sativa L.) genotypes identification using stability analysis, multi-trait selection index, and genotype-environment interaction at different irrigation regimes with adaptation to universal warming. *Scientific Reports*, *14*(1), 13836. https://doi.org/10.1038/s41598-024-64808-9109696

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