

MGIDI-BASED MULTI-TRAIT SELECTION AND GRAIN QUALITY ASSESSMENT IN SEGREGATING RICE (*ORYZA SATIVA* L.) POPULATION

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ABSTRACT

Consumption of nutrient-deficient rice contributes to global malnutrition and hunger, highlighting the need for nutritionally enriched rice cultivars. With this perspective, the Tunga x KHP 13 cross lines were evaluated during the wet season 23 at ZAHRS, Mudigere, to investigate MGIDI-assisted selection to identify lines of better performance. High values of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were for the number of filled grains per panicle (20.39% and 20.03%, respectively). Most characters showed minimal differences between PCV and GCV. Filled grains per panicle, productive tillers per plant, spikelets per panicle, tillers per plant, and panicle length showed a significantly positive association with grain yield. A positive direct effect on grain yield was observed for days to maturity, productive tillers per plant, panicle length and filled grains per panicle. The top 10 superior lines identified by MGIDI-based selection index were analyzed for quality parameters. Entry 40 (38.50, 33.65ppm), 33 (35.20, 32.35ppm), and 49 (30.29, 29.36 ppm) outperformed all other lines in zinc content in brown rice and milled rice, respectively. For iron content, these 3 lines, Entry 40 (13.40, 10.79 ppm), 33 (14.80, 12.92 ppm), and 49 (12.20, 11.43 ppm), have outperformed parents as well as other high-yielding lines. The correlation analysis of grain quality parameters with grain yield shows that all the traits, mainly Zn BR (0.30), Zn MR (0.28), Fe BR (0.38), Fe MR (0.19), total starch (0.28), amylose (0.36), and amylopectin (0.029) have a weak positive correlation.

KEYWORDS: correlation; GCV; iron; MGIDI; PCV; zinc

1. INTRODUCTION

Rice, a major staple cereal crop after wheat, belongs to the Poaceae family, having chromosome number $2n = 24$ (Prakash et al., 2024). 20% of the world's dietary energy is provided by rice alone, primarily in more than 17 Asian countries, as well as in countries in South and North America and Africa (Hori et al., 2022). In India, rice is cultivated on 42.70 Mha, accounting for 30 per cent of the net cultivated area of 142.20 Mha. Out of this, 93% is being cultivated during Kharif season (Anonymous, 2024).

Rice plays a significant and crucial role in advancing the UN Sustainable Development Goals (SDGs) in the world, especially SDG 1 (No Poverty), SDG 2 (Zero Hunger) and SDG 3 (Good Health and Well-being), as it serves as a vital source of calories (SDGs 2015). It is primarily consumed as polished white rice, which contains approximately 80% starch and 6-8% protein, whereas lipids, dietary fibre, minerals, and secondary metabolites are present in trace amounts (Kasote et al., 2022). Rice biofortification seemed to be an efficient and effective method to combat hidden hunger (Swamy et al., 2016), with initial efforts progressing in recent decades (Bouis & Saltzman, 2017). Currently, global efforts have released 37 Fe, Zn, protein and provitamin-A biofortified varieties with high polished grain Fe (>10 ppm), Zn (>28 ppm), and protein (>10%) content (Senguttuvel et al., 2023).

The demand for rice continues to rise to feed a growing population, with an estimated demand of about 137.30 million tonnes by 2050. To meet this target, production per unit area must increase from 2.20 t/ha to 3.3 t/ha. However, due

to demand from urbanization, competition from other crops and industrialization, there may be a decline in rice area by 6-7 Mha by 2050 (Mondal et al., 2022). Under such a scenario, the realistic productivity target would be around 3.90 t/ha. Hence, there is a need to increase productivity to feed the growing population by identifying high-yielding rice genotypes in the segregating population generated from a breeding program involving the most desirable parents (Kumar et al., 2024).

Estimation of genetic variability parameters like phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV), heritability and genetic advance as a percentage of mean (GAM) from germplasm and new variability created by crossing the best available varieties provides information on selecting superior individuals as parents for hybridization and getting good superior segregants (Harshraj et al., 2024). Estimation of heritability for each character in all the crosses will guide the selection for different traits. It is crucial to estimate the heritability component for all the traits. (Khalequzzaman et al., 2023). The genetic advance is the product of the heritability and selection differential component. High heritability, coupled with high genetic advance as a percentage of the mean, indicates the presence of additive gene action. Whereas high heritability, coupled with low genetic advance as a percentage of the mean, indicates the presence of epistatic and dominance effects. Hence, it is important to estimate genetic advance to carry out effective selection (Singh et al., 2022).

Knowledge of character association study forms the basis for selecting desirable genotypes. Correlation is an important measure for analyzing the association between traits and helps identify the most crucial traits for selection, mainly in segregating generations to increase yield (Barde et al., 2024). Path coefficient is a statistical measure that partitions the values of correlation coefficients into direct and indirect effects towards the dependent trait, with this, the contribution of each trait towards yield (dependent trait) can be measured (Thuy et al., 2023). Both correlation and path analysis are used in plant breeding to determine the nature of relationships between yield and yield-related components, to increase yield (Jyoti et al., 2026).

Fundamental objective in plant breeding is aiming for selection gain, guiding the development and progress of breeding programs to improve crop performance. Modern breeding programs seek to combine desirable traits into a single genotype, aiming to create an ideotype-a plant model with optimized traits for superior performance (Donald, 1968). The Multi-Trait Genotype-Ideotype Distance Index (MGIDI) offers a novel approach that addresses these limitations by incorporating data from multiple traits into the selection process (Olivoto & Nardino, 2021). Unlike conventional selection indices, MGIDI leverages multivariate techniques to account for trait correlations and efficiently selects genotypes based on their proximity to an ideal genotype.

Increasing of genetic variability is crucial in breeding efforts to increase Zn and Fe content. India had plenty of local rice varieties and landraces adapted to various ecological regions, such as, swampy, flood, acidic, rainfed, and dry lands, and the presence and absence of micronutrients due to pedological conditions (Pallavi et al., 2024). Tunga is a well-known rice cultivar in the hill zone of Karnataka, consumed for its superior grain quality and high yield (55 q/ha). However, over time, it has become increasingly susceptible to leaf blast and yield decline. With this background, the current study is being carried out to correct defects and improve the existing variety.

2. MATERIALS AND METHODS

2.1. Experimental Location and Climate

A thorough performance evaluation of the F₄-F₅ advanced generation was conducted at the Zonal Agricultural and Horticultural Research Station (ZAHRS), Mudigere, during the wet season 2023. The research site was located in the Western Ghats of a typical hill zone (Region V and Zone-9) of Karnataka. It lies at 130° 7' North latitude and 740° 37' East longitude and an altitude of 982 m above mean sea level.

2.2. Developing F₄-F₅ segregating generation

The crossing programme was initiated during wet season 2019 to address the problems associated with the existing popular variety in the hill zone of Karnataka. The F₁ generation was produced in 2020, and the F₂ and F₃ generations were advanced through pedigree using the single-seed descent method. The F₃ seeds from the panicles of the primary tillers of the F₂ plants were harvested, cleaned, dried, and stored to advance the generation (F₃). From the F₃ seed lot, a subset of 60 lines was selected for evaluation in the F₄-F₅ generation. The breeding scheme is as shown on Figure 1.

2.3. Design of the Experiment

The augmented randomized complete block design was employed for the study, incorporating the parents and checks within all blocks. Within each block, the parent and checks were replicated. One-month-old seedlings were transplanted with a spacing of 20 cm × 20 cm. The recommended fertilizer dosage (Roy et al., 2021) and necessary agronomic practices were applied accordingly. The details of the experiment are provided in Supplementary Table S1, and the features of parents and checks are presented in Supplementary Table S2.

2.4. Evaluated Traits and Techniques

To evaluate the characteristics and performance of the genotypes, each observation namely, for days to 50 percent flowering (DFF), days to maturity (DM), plant height (PH), number of tillers per plant (NT), number of productive

tillers per plant (NPT), panicle length (cm) (PL), number of spikelets per panicle (SP), number of filled grains per panicle (NFG), panicle fertility (%) (PF), test weight (g) (TW), length and breadth ratio (LB) and grain yield per single plant (g) (GY) was noted on five randomly selected plants per line using standard agronomic procedures (Table 1).

2.5. Grain quality parameters

The top-performing lines were subjected to estimation of rice quality parameters, mainly zinc, iron, amylose content, and starch content. The zinc and iron content were estimated using the atomic absorption spectrophotometer (AAS) method by feeding the prepared mineral solution to the AAS, having appropriate hollow cathode lamps, after getting values for standard solutions, and the concentrations of zinc and iron were expressed in ppm (Lekha et al., 2023; Anil et al., 2026). Amylose content was estimated using the iodometric method. For amylose determination, 20 mg of rice flour was cooked at 100 °C for 15 min after treatment with 0.5 mL of ethanol and 4.5 mL of sodium hydroxide (NaOH). The reaction was then carried out by adding 100 µL of glacial acetic acid and 200 µL of potassium iodide, followed by incubation at room temperature for 20 min. The readings were taken at 620 nm using a multimode reader (Lauro et al., 1999). Total starch is estimated as per the Megazyme method (Tuano et al., 2022).

2.6. Statistical Evaluations.

The homogeneity of error variances for each trait was tested using Bartlett's test to verify the suitability of the data for combined analysis. All traits showed homogeneous variances. An analysis of variance (ANOVA) was then conducted for 12 morphological traits using RStudio software version 4.2.2 (R Core Team 2022). Descriptive statistics were used to summarize the performance of the segregating lines.

2.6.1. Estimates of the parameters of genetic variability

Variability among genotypes was assessed by calculating environmental (σ_e^2), genotypic (σ_g^2) and phenotypic (σ_p^2) variances as described below:

$$\text{Genotypic variance } (\sigma_g^2) = \frac{\text{MSS (genotype)} - \text{MSS (error)}}{\text{Number of blocks}}$$

$$\text{Phenotypic variance } (\sigma_p^2) = \sigma_g^2 + \sigma_e^2$$

Where, MSS (genotype) represents the genotype mean square, and MSS (error) represents the error mean square.

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were computed according to the method recommended by Burton and Devane (1953) as shown below:

$$\text{Phenotypic coefficient of variation, PCV} = \frac{\sigma_p}{\bar{x}} \times 100$$

$$\text{Genotypic coefficient of variation, GCV} = \frac{\sigma_g}{\bar{x}} \times 100$$

Where, σ_p represents the phenotypic SD of a particular trait, σ_g denotes the genotypic SD of a particular trait SD of a particular trait and $\bar{x}$ is the mean performance of particular trait.

Broad-sense heritability (h^2 bs) was calculated for each trait as per the following formula of Burton and DeVane (1953) and Johnson, Robinson, and Comstock (1955).

$$\text{Heritability, H} = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

The expected genetic advance (GA) resulting from the selection of 5% superior individuals was calculated as suggested by Burton and DeVane (1953) and Johnson, Robinson, and Comstock (1955).

$$\text{Genetic Advance (Expected)} = H \times \sqrt{\sigma_p^2} \times K$$

$$\text{Genetic advance as per cent of mean, GAM} = \frac{GA}{\bar{x}} \times 100$$

Where, K is 2.06 (standardized selection differential).

The PCV and GCV values were categorized based on standard thresholds, where values less than 15% were considered low, those ranging from 15 to 30% were considered moderate, and values exceeding 30% were classified as high. Broad-sense heritability (h^2 bs) estimates were similarly grouped: values below 40% were categorized as low, those between 40 and 60% as moderate, and values above 60% as high. Genetic advance as a percentage of mean (GAM) was classified into three categories: low (20%), moderate (10 – 20%), and high (>20%)

2.6.2. Correlation and path coefficient analyses

Correlation coefficients among the studied traits were estimated following the method of Al-Jibouri, Miller, and Robinson (1958). The correlation matrix was generated using RStudio software version 4.2.2. Path coefficient analysis was performed according to Dewey and Lu (1959) to partition the correlations into direct and indirect effects on marketable fruit yield per plant. This analysis was carried out using Windostat software version 8.0.

$$r_p(xy) = \frac{\text{Cov}_p(xy)}{\sqrt{\sigma_p^2(x) \times \sigma_p^2(y)}}$$

2.6.3. The MGIDI index

The MGIDI index theory is based on four key steps: (i) standardizing all traits to a range of 0 to 100, (ii) applying factor analysis to capture the correlation structure and reduce the data's dimensionality, (iii) designing an ideal

genotype using known or desired trait values, and (iv) calculating the distance between each genotype and the designed ideotype (7).

$$\text{MGIDI} = [\sum_{j=1}^f (\gamma_{ij} - \gamma_j)^2]^{0.5}$$

In this context, MGIDI_i represents the multi-trait genotype–ideotype distance index for the *i*th row/genotype/treatment, while γ_{ij} denotes the score of the *i*th row/genotype/treatment for the *j*th factor (1, 2, ..., *g*; *j* = 1, 2, ..., *f*), where *g* and *f* are the total number of rows/genotypes/treatments and factors, respectively. γ_j represents the score of the ideotype for the *j*th factor. The row/genotype/treatment with the smallest MGIDI value is closest to the ideotype and thus exhibits the most desirable values across all *p* traits. The proportion of the MGIDI index for the *i*th row/genotype/treatment explained by the *j*th factor (ω_{ij}) is calculated to highlight each genotype/treatment's strengths and weaknesses, expressed as Eq. 6

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=1}^f \sqrt{D_{ij}^2}}$$

Here, D_{ij} represents the distance between the *i*th genotype/treatment and the ideotype for the *j*th factor. A lower contribution from a factor suggests that the traits associated with that factor are closer to the ideotype.

3. RESULTS

3.1. Analysis of Variance

The variance analysis indicated substantial differences ($p \leq 0.01$) among the segregating lines and the lines exhibited significant variation compared to their respective parent for all the quantitative traits, DFF, DM, PH, NT, NPT, PL, SP, NFG, PF, TW, LB ratio and GY(g). To further visualize trait variation across all genotypes, informative boxplots (Figure 2) were shown to illustrate the range, mean, and variability of each trait. The ANOVA results are presented in Table 2.

3.2. Genetic variability parameters

The genetic variability parameters are shown in Figure 3. The genetic parameter estimates revealed that for the trait NFG, the PCV and GCV were high (21.33% and 20.30%, respectively). PCV and GCV values were low for DFF, DM, PH, and PF. Moreover, the heritability values were high for all traits. High heritability coupled with high GAM were recorded for NFG (92.36%, 40.25%), SP, TW, NT, NPT, L/B ratio. Moderate heritability and high GAM were observed for GY (58.13%, 21.19%). Platykurtic and positively skewed distributions were recorded by DFF, NT, NPT, PL, SP, NFG, TW, and GY. A negatively skewed, platykurtic distribution is shown by PF and DM. A positively skewed, leptokurtic distribution was observed for TW and PH. The frequency distribution curve of all traits is shown in Supplementary Figures S1 and S2.

3.3. Trait association analysis

The association of grain yield was highly significant and positive with NPT (0.85) followed by NT (0.79), NFG (0.78), SP (0.73), PL (0.64), PF (0.48), TW (0.34) and L/B ratio (0.30). PH (-0.23), DM (-0.12) and DFF (-0.098) were negatively correlated with grain yield. The results of the correlation are shown in Figure 4.

A highly positive direct effect on yield was exhibited for DM (0.7308) followed by NPT (0.432), PL (0.2429), SP (0.1854), NFG (0.0985), L/B ratio (0.0437), PF (0.0109) and test weight (0.007). DFF (-0.712), PH (-0.0737) and NT (-0.0307) exhibited negative direct effect. The path analysis results are shown in Figure 5.

3.4. MGIDI-based selection index

3.4.1. Eigenvalues and Varimax Factor Loadings

The eigenvalue analysis and varimax factor loadings identified three principal components with eigenvalues greater than 1, collectively accounting for 69.9% of the total trait variance (Table 3). Post-varimax rotation enhanced interpretability, with an average communality (*h*) of 0.699 across traits. Communalities ranged from 0.26 for PL to 0.96 for NPT, indicating that the factors captured a substantial portion of each trait's Variance. The 12 traits analyzed were grouped into three factors (FA): FA1 (PH, PL, SP, NFG, TW, LB, PF, GY), FA2 (DFF, DM), and FA3 (NT, NPT). FA1, encompassing PH, PL, SP, NFG, TW, LB, PF, and GY, accounted for the greatest variation in the dataset, underscoring its importance for identifying genotypes suitable for further breeding.

3.4.2. Predicted Selection Gain

The selection gains (SG) the MGIDI indexes indicated that both indexes effectively achieved desired gains across all evaluated traits (Table 4). The MGIDI index demonstrated an overall selection gain of 85.23% for traits targeted for improvement and -0.105% for traits requiring reduction. Among the traits, NFG showed the highest selection gain with 16.4%, followed by SP with 13.1% for MGIDI. Selection gain for other traits is mentioned in the Table 4. These results underscore the efficacy of indexes in enhancing breeding objectives and achieving balanced genetic improvements across multiple traits.

3.4.3. Selected Genotypes by MGIDI Index

The genotypes selected by the MGIDI Index include Entry 50, 24, 35, 9, 19, 17, 10, 32, 56, 48 (Figure 6). Entry 48, 56, were found exactly at the cutoff point in the MGIDI index and entry 32, 10, 17 were found near to the cutoff point in the MGIDI index suggesting they possess potentially valuable traits that warrant further investigation. MGIDI demonstrates effectiveness in identifying superior genotypes, contributing to balanced trait selection and enhancing breeding efficiency.

3.4.4. Strength and Weakness view

The radar plot depicts the proportional contribution of each factor axis to the MGIDI index for individual genotypes. Each spoke of the radar represents a genotype. The concentric circles represent increasing contribution to MGIDI from the center (lower contribution) toward the periphery (higher contribution). The colored polygons correspond to: FA1 (red), FA2 (green), and FA3 (blue). The dashed black line indicates the average contribution across all genotypes and serves as a reference baseline (Figure 7).

The radar visualization allows identification of strengths and weaknesses: Genotypes with higher FA1 contribution exhibit greater deviation in yield and yield-contributing traits. Higher FA2 contribution indicates divergence in phenological traits (flowering and maturity). Greater FA3 contribution reflects an imbalance in tillering traits.

3.5. Grain quality parameters

Based on the mean performance of the segregating population, the top 10 best-performing lines were identified through MGIDI analysis and analyzed for quality parameters, particularly zinc and iron, in both brown rice and milled rice. In addition to the total starch content, amylose and amylopectin content are also analyzed as they affect the rice cooking quality, especially the amylose content. The high-yielding lines were outperforming the parents in almost all quality aspects. Entry 48 (38.50, 33.65 ppm), 56 (35.20, 32.35 ppm), and 32 (30.29, 29.36 ppm) have outperformed all other lines in terms of zinc content in brown rice and milled rice, respectively. To iron content these 3 lines, Entry 48 (13.40, 10.79ppm), 56 (14.80, 12.92ppm), and 32 (12.20, 11.43ppm) has outperformed parents as well as other high-yielding lines. The details of zinc, iron and quality parameters of high-yielding lines are represented in Table 5.

Both the parents had Tunga (81.30%, 18.28%), KHP 13 (79.96%, 23.30%) starch and amylose content respectively. The correlation analysis of grain quality parameters with grain yield shows that all the traits, mainly, Zn BR (0.30), Zn MR (0.28), Fe BR (0.38), Fe MR (0.19), total starch (0.28), amylose (0.36), and amylopectin (0.029) have a weak positive correlation, is mentioned in Figure 8. It shows the significant impact of different grain quality parameters on rice grain quality. Amylose has a significant positive correlation with all the traits except amylopectin, where it is highly negatively correlated (-0.55). The Zn BR content had a weak negative correlation with total starch (-0.088).

4. DISCUSSION

Several superior high-yielding rice varieties have been developed and released in the hill zone of Karnataka. There were earlier attempts to improve the yield in rice that involved conventional pedigree breeding by crossing with different varieties. However, such approaches often adversely affect grain quality traits. The present study reports the application of crossing programme to improve the superior variety traits by intercrossing with KHP 13 to develop semi dwarf, high-yielding varieties and to overcome the problem of existing varieties, while preserving their unique grain quality attributes.

The ANOVA indicates that the lines differ significantly for the traits studied. The present experiment documented the presence of wider variation for genetic variability parameters in and among the lines of the population of rice for DFF, DM, PH, NT, NPT, PL, SP, NFG, PF, TW, LB and GY (g). These findings were found similar to those obtained by Venkatesan et al. (2019) and Akshay et al. (2022).

Most of the traits studied show ample variation, suggesting that these traits can be improved by selection. In most of the traits studied, the difference between the PCV and GCV values was minimal, indicating that these traits were less influenced by the environment. High PCV and GCV values indicate higher magnitude of variability present in the material studied. Hence, it indicates high variability in the population for selection. These results obtained were analogues to the results obtained by Rajendar et al. (2014), Nezam et al. (2018), Seneega et al. (2019), Sathishkumar et al. (2020) and Yadav et al. (2022). Low PCV and GCV values indicate that the traits under study were less influenced by the environment. All the studied characters showed close phenotypic and genotypic coefficients of variation, indicating additive gene action in their expression (Raia et al., 2016). These results were found in accordance with those obtained by Gangashetty et al. (2013) for L/B ratio, Mallimar et al. (2015) for L/B ratio and NFG, Savitha and Usha (2015) for NPT, GY, Nishanth et al. (2017) for L/B ratio, Ram et al. (2017) for NFG, Longkho et al. (2020) for NFG, TW, Sudeepthi et al. (2020) for GY, TW and Ardiarini and Aridedjo (2022) for NT. The investigation revealed that in both crosses estimates of GCV for all the traits studied were slightly less than PCV estimates indicating the influence of the environment on the lines' performance (Akshay et al., 2022).

These insights into the skewness and kurtosis of the traits provide valuable information about their distribution patterns across the genotypes in the study. Maximizing the genetic gain concerning the traits with positively skewed distribution requires intense selection from the existing variability. These distribution components studies, such as skewness (third-degree statistic) and kurtosis (fourth-degree statistic) provide information regarding the nature of gene

action (Fisher et al., 1932) and the number of genes affecting the traits, respectively (Robson et al., 1956). The parameters d and h in the genetic expectations of skewness ($-3/2 d^2 h$) reflect additive gene effects and dominant gene effects, respectively. Both skewness and kurtosis have greater predictive potential than first- and second-degree statistics for revealing interaction genetic effects (Choo et al., 1982). Most of the traits show a normal distribution.

It is necessary to estimate the heritability for each character. This will give a precise estimate of the heritable portion of the variability. The genetic advance is commonly predicted as the product of the heritability ratio and the selection differential (Sood et al., 2026). The results found were similar to those obtained by Sudhir et al. (2017) for NPT, NFG, Singh et al. (2021) for NPT, L/B ratio, and TW. Sadimantara et al. (2014), Nishanth et al. (2017) for PH, PL, DM and Sudeepthi et al. (2020) for PF and PL.

Improvement in grain yield is the top most important trait in rice breeding. It can be reached by direct selection of easily observable characters. However, this requires a good understanding of how different traits are associated with grain yield and among themselves (Devi et al., 2022). The positive association indicates that selection for these traits will directly improve grain yield (Sudeepthi et al., 2020). Analysis of path coefficient measures the direct and indirect contributions of independent variables to the dependent variable. It is used to partition values of correlation coefficients into direct and indirect effects on dependent variable (Savitha et al., 2015). Focusing on traits that positively affect yield will help boost production.

The evaluation of genotypes based on multiple correlated traits is a major challenge in plant breeding programs. To overcome this limitation, multivariate approaches such as factor analysis combined with the Multi-trait Genotype–Ideotype Distance Index (MGIDI) have been proposed to facilitate simultaneous selection for multiple traits (Olivoto & Nardino, 2021). In the present analysis, a radar (spider) plot was used to visualize the contribution of different factor axes (FAs) to the MGIDI index in rice genotypes. This dimensionality reduction approach minimizes multicollinearity and allows interpretation at the factor level rather than at the individual trait level (Hair et al., 2010). Because MGIDI measures the Euclidean distance between a genotype and an ideotype in a multi-trait space, a larger contribution of a factor indicates that the genotype is farther from the ideotype for the traits grouped under that factor (Olivoto & Nardino, 2021). Genotypes showing relatively smaller and balanced contributions across all factor axes are considered closer to the ideotype and are therefore more desirable for selection. Conversely, genotypes with disproportionately large contributions from a specific factor indicate targeted areas for trait improvement (Pallavi et al., 2024). MGIDI helps in identifying trait groups responsible for inferior performance, prioritizing traits for improvement in specific genotypes (Roka et al., 2024). Select genotypes with balanced multi-trait performance. Enhance selection efficiency under complex breeding objectives. Thus, the radar plot serves as a powerful diagnostic tool within the MGIDI framework for multi-trait selection in rice breeding programs.

Consumer preference is the main objective in current crop improvement. To satisfy consumers and provide nutritional benefits, focusing on quality parameters is a must (Anil et al., 2026). As rice is consumed all over the world, improving its nutritional aspects plays a major role in eradicating malnutrition and improving public health. Among micronutrients, zinc and iron are essential for the body (Bollinedi et al., 2022). Based on the amylose content, the grain texture after cooking will be different. Hence, the high-yielding lines are analyzed for zinc and iron in both brown rice and milled rice forms. Other than these, the quality of the rice is mainly affected by the total starch, amylose and amylopectin content (Tuaño et al., 2022). The medium- to high-amylose content lines (lines 48, 56, 32) have good cooking quality, such as firm and non-sticky rice. These lines will also reduce the rate of digestion and play a role in reducing the glucose response. The lines identified with superior grain quality and yield also have good grain type, like slender and medium slender lines, which are preferred by consumers. The grain type of the lines is shown in the Figure 9.

5. CONCLUSION

Most of the traits have ample scope for variation for selection. High values of PCV and GCV were observed for NFG. Selecting by analyzing the segregating population for variation and forwarding it to the next generation are the key steps in crop improvement. Grain yield had a strong association with NFG, SP, NPT, NT, PL and TW and they have showed high values of heritability coupled with high values of GAM, which indicates that they are governed by additive gene action. Rather than making a direct selection for grain yield per plant, making an indirect selection in segregating variable population of rice based on both grain yield per plant and yield contributing characters like NPT, NFG, and PF will be rewarding through MGIDI based selection. Entry 40, 33, and 49 have outperformed parents as well as other high-yielding lines in terms of zinc and iron. These identified lines are carefully evaluated in future generations.

Acknowledgements

The authors sincerely thank the College of Agriculture, Shivamogga, KSNUAHS, Shivamogga for providing the facilities to complete the research work.

Authors' contributions

H.M Anil carried out the study conception, design, and research part of the paper. Material preparation and data collection were performed by C.N Nimish Bhushan and H. M Anil. Jyoti IT participated in the sequence alignment. L.R Preethi, M. L Sachin and G. Moulya participated in the table's arrangements. Anil Lalsingh Chavan helped with the rearrangement of the subheadings and finishing. The first draft of the manuscript was written by H. M Anil. All authors commented on previous versions of the manuscript. All authors read and approved the final manuscript.

Funding

No funding was received for this research work.

Declarations

Conflict of interest Authors declare no conflict of interest. All authors have read the manuscript and consented to publish.

Ethical approval Not applicable.

Supplementary data

Supplementary figures

Fig. S1: Frequency distribution of F_4 population of cross Tunga x KHP 13 for days to 50 per cent flowering, days to maturity, plant height, No. of tillers per plant, No. of productive tillers per plant, panicle length.

Fig. S2: Frequency distribution of F_4 population of cross Tunga x KHP 13 for number of spikelets per panicle, number of filled grains per panicle, test weight, L/B ratio, panicle fertility and grain yield.

Supplementary tables

Table S1: Details of the Experimental Design

Table S2: Characteristics of check variety involved in the experiment

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Table 1. Description of traits with their respective units

Trait	Trait code	Unit measured
Days to 50% Flowering	DFF	Count
Days to Maturity	DM	count
Plant Height	PH	cm
Number of tillers per plant	NT	count
Number of productive tillers per plant	NPT	count
Panicle length	PL	cm
Number of spikelets per panicle	SP	count
Number of filled grains per panicle	NFG	count
Panicle fertility	PF	%
Test weight	TW	grams
Length and breadth ratio	LB	count
Grain yield per single plant	GY	grams/plant

Table 2. Analysis of variance for yield and yield contributing characters in F₄ population of cross Tunga x KHP 13

Traits	Factor	SG (%)	Goal
PH	FA1	-0.105	Decrease
PL	FA1	6.49	Increase
SP	FA1	13.1	Increase
NFG	FA1	16.4	Increase
TW	FA1	8.09	Increase

LB	FA1	6.58	Increase
PF	FA1	3.26	Increase
GY	FA1	10.4	Increase
DFF	FA2	2.07	Increase
DM	FA2	2.67	Increase
NT	FA3	8.79	Increase
NPT	FA3	7.38	Increase

Table 3. Eigenvalues, explained Variance, factorial loading after varimax rotation, and communalities

Traits	FA1	FA2	FA3	communalities
DFF	0.11	0.92	0.15	0.89
DM	0.04	0.94	-0.03	0.88
PH	-0.52	-0.28	-0.03	0.35
NT	-0.24	-0.04	-0.94	0.94
NPT	-0.21	-0.07	-0.95	0.96
PL	-0.45	-0.21	-0.08	0.26
SP	-0.81	-0.06	-0.4	0.83
NFG	-0.83	-0.08	-0.44	0.88
TW	-0.7	0.14	-0.16	0.53
LB	-0.78	-0.02	-0.01	0.61
PF	-0.47	-0.07	-0.37	0.37
GY	-0.86	-0.03	-0.42	0.91
Eigen values	5.33	1.8	1.26	
Variances	44.4	15	10.5	
Acculamated	44.4	59.4	69.9	

Table 4. Selection Gain Percentage of MGIDI

Entry	Zn BR	Zn MR	Fe BR	Fe MR	TS	AC	AMP	GY
Tunga	26.39	22.81	12.3	10.01	81.3	18.28	63.02	36.81
KPR 1	29.4	27.06	14.4	13.33	83.2	23.5	59.7	34.6
KHP 13	27.4	24.6	12.3	8.43	79.96	23.3	56.66	34.48
48	38.5	33.65	13.4	10.79	78.4	26.6	51.8	37.67
24	33.4	29.99	12.3	10.62	72.4	21.3	51.1	33.5
9	28.4	25.21	11.3	9.18	84.3	19.75	64.55	31.6
35	29.4	25.85	13.4	10.07	78.4	19.3	59.1	29.6
56	35.2	32.35	14.8	12.92	76.25	28.2	48.05	33.58
19	26.8	21.17	11.75	8.86	71.3	19.3	52	26.5
32	30.29	29.36	12.2	11.43	79.2	20.3	58.9	29.2
48	31.3	29.3	14.29	13.31	85.29	22.4	62.89	29.15
10	35.3	30.43	12.3	11.21	80.3	25.68	54.62	30.5
17	29.4	26.5	10.3	8.4	73.4	21.36	52.04	27.2

Table. 5. The details of zinc, iron, total starch, amylose and amylopectin content of high-yielding lines

ANOVA – Mean Sum of Square													
Source of Variation	DF	Mean Sum of Square											
		DFF	DM	PH	NT	NPT	PL	SP	NFG	PF	TW	L/B	GY
Block	5	4.48	5.47	1.13	0.01	67.24	0.66	0.31	10.07	6.51	0.91	37.96	10.05
Genotypes + Checks	63	30.02 *	47.51 **	28.32 *	0.12 **	1189.66 **	4.04 **	4.18 **	30.97 **	53.48 **	8.02 **	1027.39 **	13.02 **
Genotypes	59	20.42 *	49.62 **	22.43 *	0.11 **	673.04 **	2.11 **	2.39 **	26.69 **	42.28 *	8.21 **	620.4 **	10.11 *
Checks	3	1.82	4.50	2.86	0.02	83.8	0.76	1.39 *	3.85	170.14 **	10.28 *	133.56	10.23
Checks vs. Genotypes	1	671.43 **	39.43 *	558.58 **	1.27 **	38965.87 **	127.85 **	120.39 **	489.05 **	609.35 **	3.51	31016.72 **	183.31 **
Error	15	12.05	8.47	9.39	0.01	51.44	0.35	0.33	4.12	14.94	1.94	53.75	4.05

* Significant at 5% level of significance ** Significant at 1% level of significance

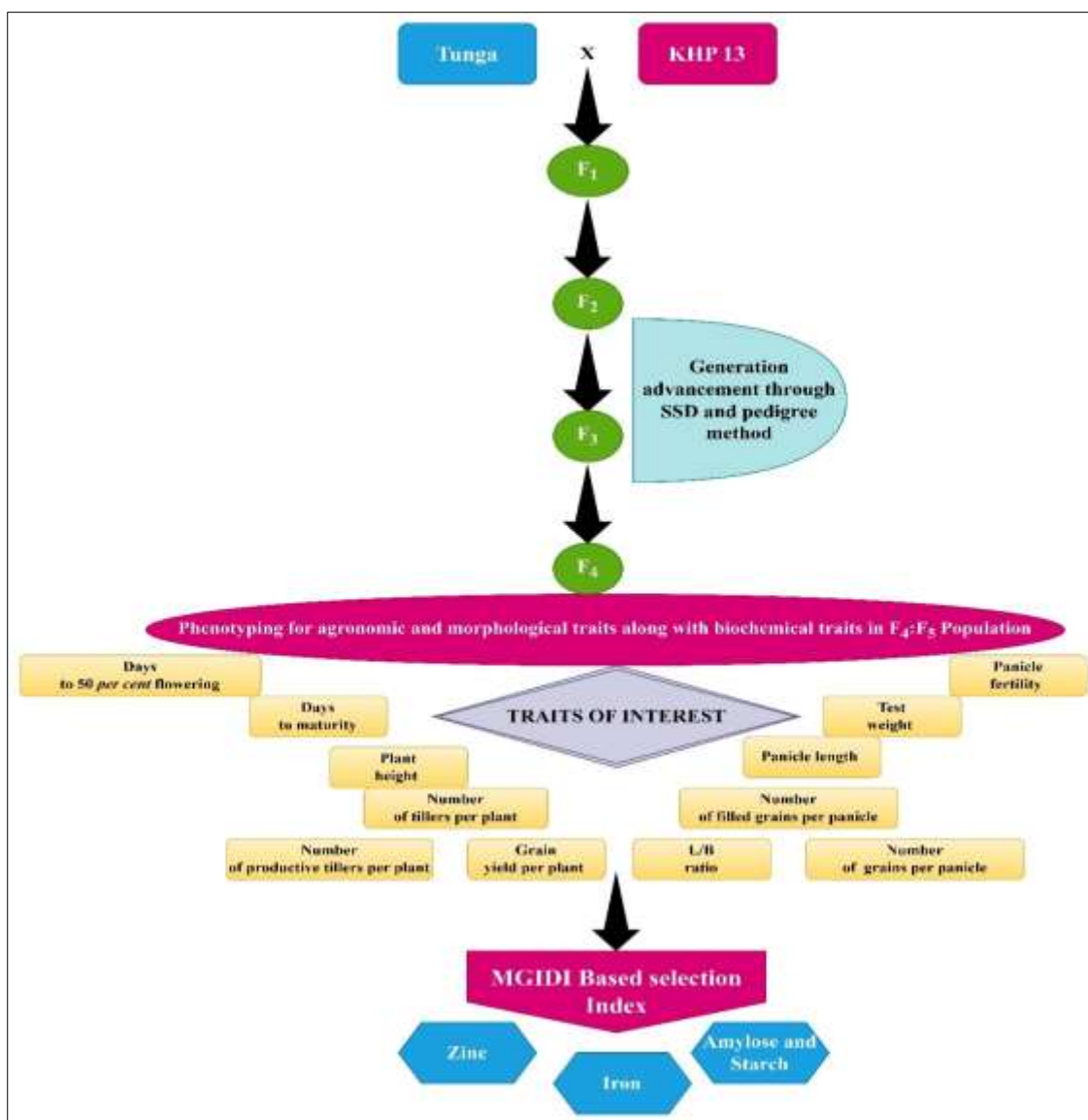


Figure. 1. Flowchart of the breeding procedure of cross Tunga × KHP 13.

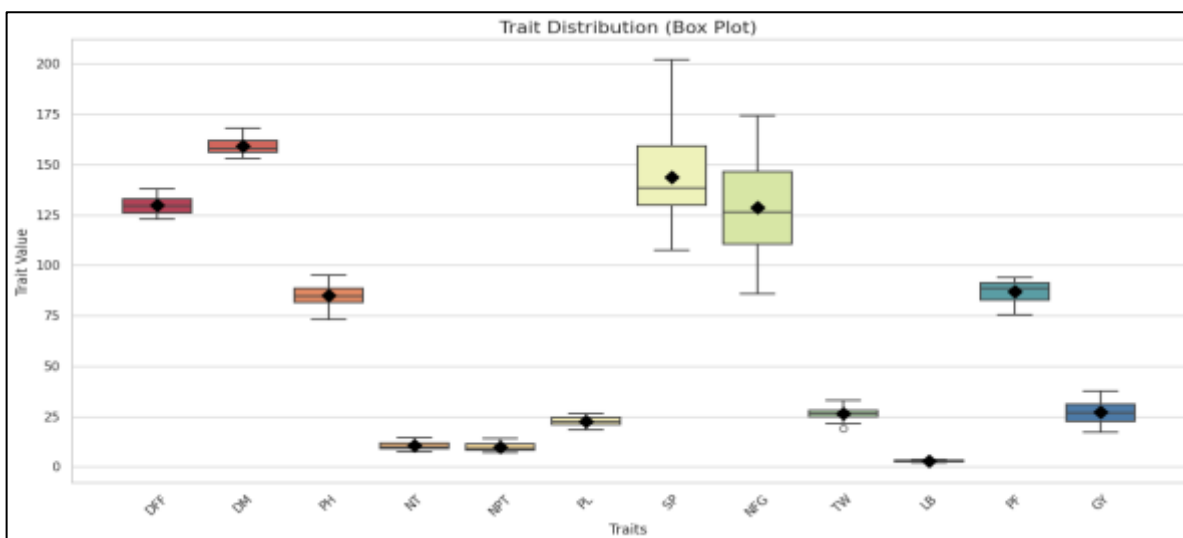


Figure. 2. Visualization of the trait variations across the population

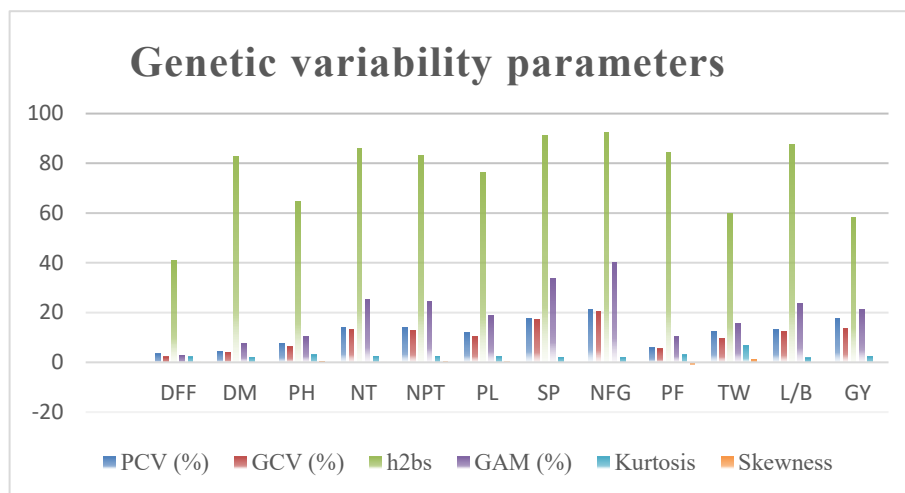


Figure. 3. Bar graph describing genetic variability parameters of segregating lines
DFF = Days to 50% flowering **DM** = Days to maturity **PH** = Plant height (cm)
NT = Number of tillers per plant **NPT** = Number of productive tillers per plant **PL** = Panicle length (cm)
SP = Number of spikelets per panicle **NFG** = Number of filled grains per panicle **PF** = Panicle fertility (%)
TW = Test weight (g) **L/B** = Length Breadth ratio (mm) **GY** = Grain yield per plant (g)

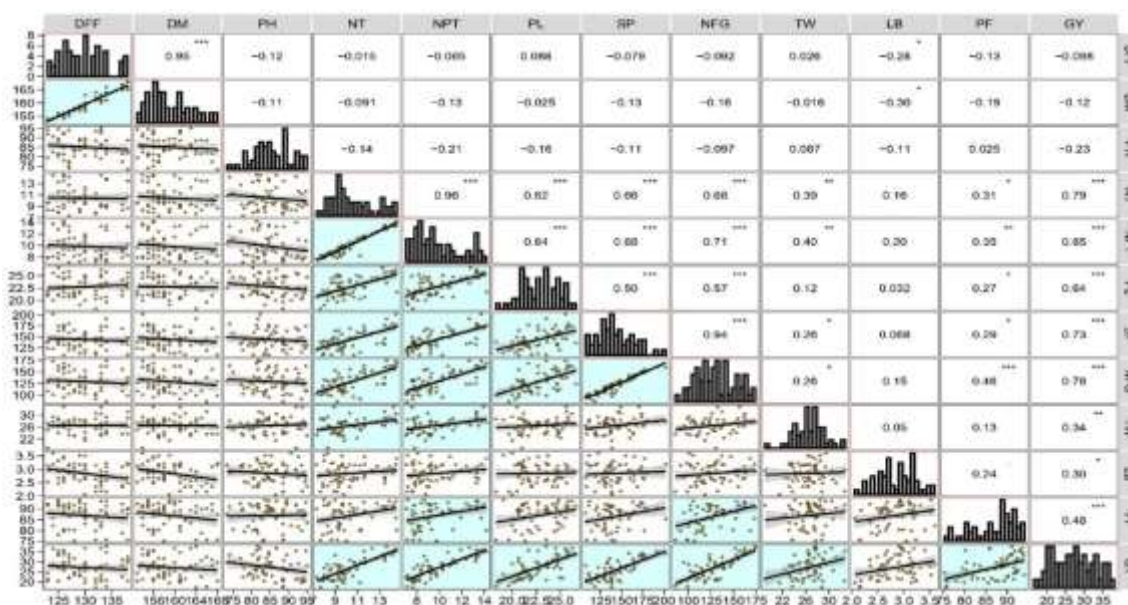


Figure. 4. Correlation among yield and yield contributing characters

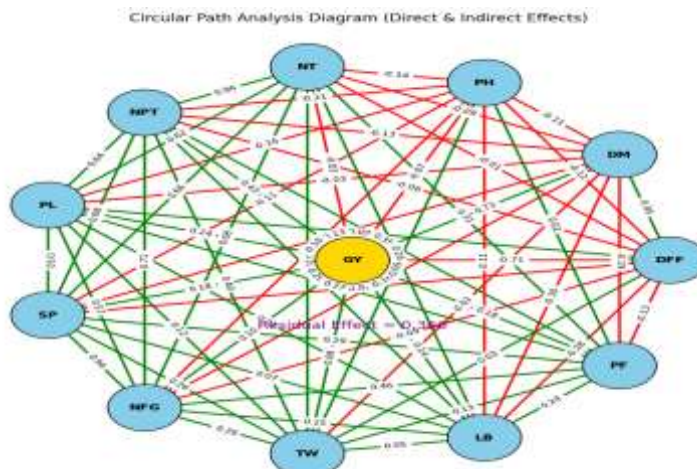


Figure. 5. Path analysis among yield and yield contributing characters

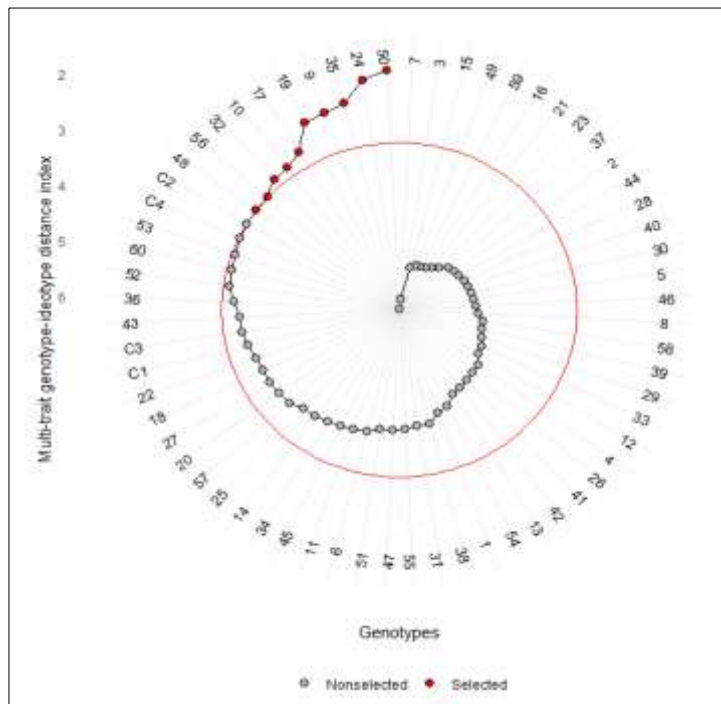


Figure. 6. Genotype ranking in ascending order for the MGIDI index. The selected genotypes are shown in red in the electronic version of the article. The circle represents the cut-point according to the selection pressure.

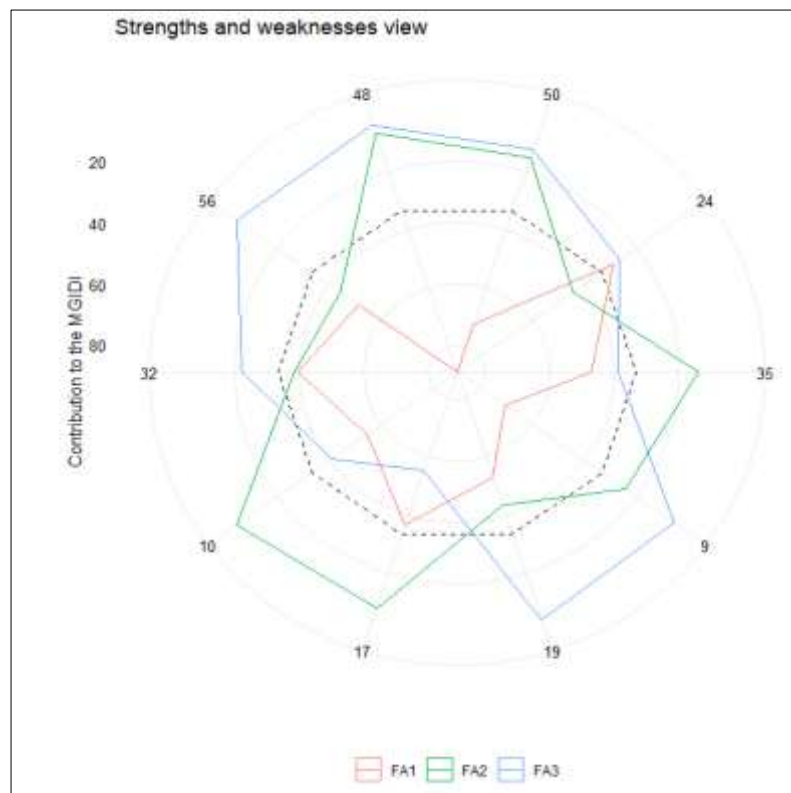


Figure. 7. The strengths and weaknesses of the selected genotypes are shown in the proportion of each factor on the computed multi-trait genotype–ideotype distance index (MGIDI). The most minor the proportion explained by a factor (closer to the external edge), the closer the traits within that factor are to the ideotype. The dashed line shows the theoretical value if all the factors had contributed equally

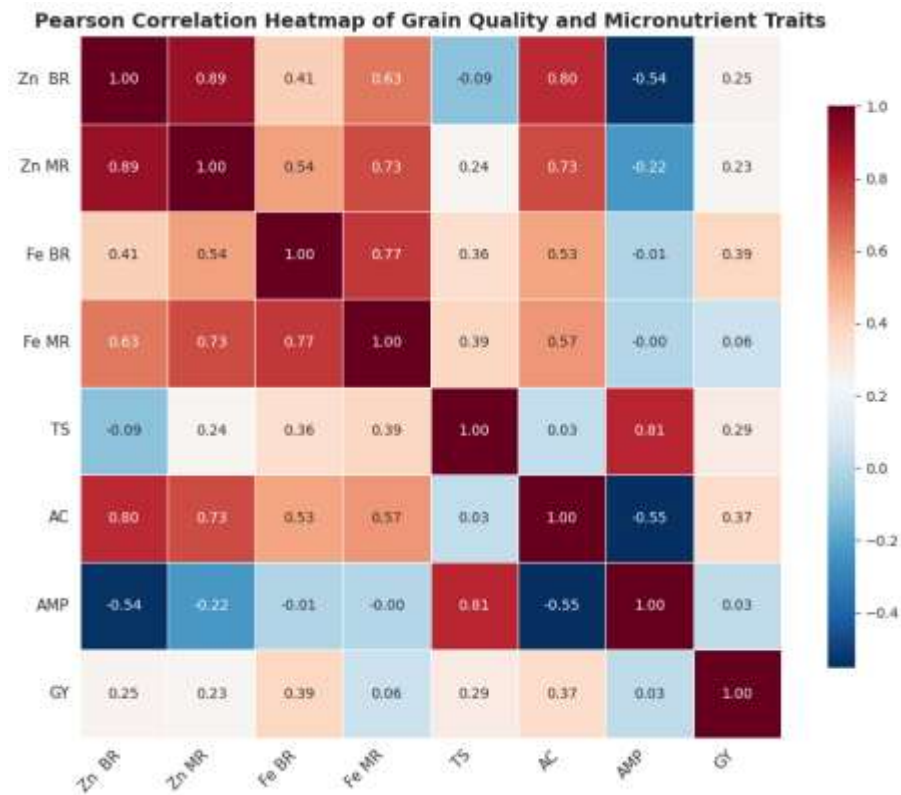


Figure. 8. Correlation of grain quality parameters with grain yield



Figure. 9. Promising high-yielding lines and their grain type