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CIÊNCIAS AGRÁRIAS

Selection of rice genotypes based on agronomic traits and commercial grain quality

Seleção de genótipos de arroz com base em caracteres agronômicos e de qualidade comercial de grãos

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ABSTRACT

The study aimed to select rice genotypes based on agronomic traits and commercial grain quality. The study was carried out in the 2014/15 and 2015/16 harvests in eight growing environments, located in the state of Rio Grande do Sul, Brazil. Fourteen rice genotypes were sown in each environment. The experiment was conducted in a randomized block design with four replications. The following agronomic traits were evaluated: number of days to flowering and grain yield as well as commercial grain quality traits: percentage of whole grains and percentage of chalky area in the grains. AMMI, GGE and MGIDI methodologies were used to select the best performing genotypes. Using the AMMI, GGE and MGDI methods, genotypes G9 and G1 performed close to the ideal ideotype for the number of days to grain flowering, yield and quality.

Keywords: *Oryza sativa*; adaptability; stability; selection index.

RESUMO

O objetivo do estudo foi selecionar genótipos de arroz com base em caracteres agronômicos e de qualidade comercial de grãos. O estudo foi realizado nas safras de 2014/15 e 2015/16 em oito ambientes de cultivo localizados no estado do Rio Grande do Sul, Brasil. Em cada ambiente, foram semeados 14 genótipos de arroz. O experimento foi conduzido em delineamento experimental de blocos ao acaso, com quatro repetições. Foram avaliados os caracteres agronômicos: número de dias para o florescimento e produtividade de grãos; e caracteres da qualidade comercial de grãos: percentagem de grãos inteiros e percentagem de área gessada dos grãos. Foram utilizadas as metodologias AMMI, GGE e MGIDI para a seleção de genótipos de maior desempenho. Pelos métodos AMMI, GGE e MGDI, os genótipos G9 e G1 apresentam desempenho próximo ao ideótipo ideal para número de dias para o florescimento, produtividade e qualidade de grãos.

Palavras-chave*: Oryza sativa; adaptabilidade; estabilidade; índice de seleção.*

1. INTRODUCTION

Rice (*Oryza sativa*) is one of the main staple foods consumed worldwide (Muthayya *et al*., 2014). With the growing demand for food and the need to increase agricultural grain yield, it is essential to seek to improve the traits of rice genotypes. The selection of genotypes with favorable phenological traits, such as higher grain yield and grain quality, has been the subject of research and development in agriculture (Streck *et al*., 2019; Adjah *et al*., 2020).

The selection of rice genotypes based on phenology, yield and grain quality requires a comprehensive approach, which involves analyzing different traits and evaluating a large number of genotypes (Streck *et al*., 2018). For this, methodologies that estimate adaptability and stability parameters, as well as multi-trait selection indices, are used. These methodologies have been widely applied in the selection of genotypes of rice (Facchinello *et al*., 2022), wheat (Loro *et al*., 2023) and soybean (Pradebon *et al*., 2023).

Studies were conducted with the aim of studying the interaction between genotypes and environments, as well as selecting rice genotypes based on yield and grain quality traits (Streck *et al*., 2018; Inabangan-Asilo *et al*., 2019; Streck *et al*., 2019; Facchinello *et al*., 2022). The results obtained by Streck et al. (2018), Streck et al. (2019) and

Inabangan-Asilo *et al*. (2019) revealed the possibility of selecting rice genotypes with high productive capacity, combined with grain quality.

However, Xu *et al*. (2015) and Kakar *et al*. (2019) showed that there is a negative relationship between grain yield and grain quality. These results indicate that the relationship between yield and commercial quality of grains traits is not yet fully consolidated. In addition, the studies highlighted that the agronomic and grain quality traits of rice are influenced by the genotype × environment interaction.

Therefore, the development and selection of genotypes with greater agronomic potential, combined with better grain quality, are essential to meet market demands and promote more sustainable production. In this context, the objective of this study was to select rice genotypes based on agronomic and commercial grain quality traits.

2. MATERIAL AND METHODS

The study was carried out in the 2014/15 and 2015/16 harvest in eight growing environments, located in the state of Rio Grande do Sul, Brazil: Capão do Leão - 2014/15 harvest (31º 45' 48" S 52º 29' 02" W, at 21 m), Capivari do Sul - 2014/15 harvest (30º 08' 42" S 50º 30' 53" W, at 12 m), Santa Vitória do Palmar - 2014/15 harvest (33º 31' 08" S 53º 22' 05" W , at 23 m), Alegrete - 2015/16 harvest (29º 46' 59" S 55º 47' 31" W, at 102 m), Capão do Leão - 2015/16 harvest (31º 45' 48" S 52º 29' 02" W, at 21 m), Mostardas - 2015/16 harvest (31º 06' 25" S 50º 55' 16" W, at 17 m), Uruguaiana - 2015/16 harvest (29º 45' 17" S 57º 05' 18" W, at 66 m) and Santa Vitória do Palmar - 2015/16 harvest (33º 31' 08" S 53º 22' 05" W , at 23 m). In each environment, 14 rice genotypes were sown, coded as follows: G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13 and G14. The experiment was in a randomized block experimental design, with four replications.

The experimental units consisted of nine rows of 5.0 m in length, spaced 0.17 m between rows. The useful harvesting area consisted of 4 internal rows of 4 m in length, to avoid any incident effect on the border. The sowing density used was 100 kg ha^{-1}, using a mechanical plot seeder. Soil preparation for sowing took place according to the conventional system. Base fertilization took place together with sowing, with an application corresponding to 300 kg ha^{-1} of NPK (5-20-20 formula). Topdressing nitrogen fertilization was 90 kg ha^{-1} in the form of urea, with 50% of the dose applied in stage V4 and the remainder in stage R0 (beginning of panicle emission). The irrigation system adopted was permanent flooding up to the R9 stage. Pest, weed and disease controls also took place in accordance with the technical recommendations for irrigated rice cultivation.

The rice genotypes in each environment were phenologically characterized, for which the number of days to flowering (NDF, days) was marked, considering the number of days from emergence to 50% of exposed panicles. Grains were harvested manually, and grain yield was estimated (GY, kg ha^{-1}), with grain moisture corrected to 13%. the percentage of whole grains (WG, %) was estimated. Then, the percentage of chalky grains (CG, %) was estimated.

The analysis of individual variance was performed for each environment to verify the homogeneity of the residual variances of the variables. Then, the joint analysis of variance was performed at 5% significance by the F test. The estimation of variance components and genetic parameters was performed based on restricted maximum likelihood (REML), using the statistical model: $y = Xr + Za + Wp + e$, where y is a data vector; r are the effects of repetitions (fixed); a is the individual additive (random) genetic effects; p is the effect attributed to the genotype x environment interaction; e are the (random) residual effects; and X, Z and W represent the incidence matrices for these effects (Resende, 2007). This model allowed estimating the phenotypic variance (σ^2P), heritability in the broad sense (h^2_a), mean heritability of the genotype (h^2_{mg}), coefficient of determination of the effects of genotype x environment interaction ($GEIr^2$), genotypic correlation between performance genotypes x environments (rGE), genotypic coefficient of variation (CVg), residual coefficient of variation (CVr) and coefficient of variation of the ratio between genotypic coefficient of variation and residual coefficient of variation (CVratio).

The best unbiased linear predictions (BLUPs) were calculated for the variables, taking into account the available genetic information. The AMMI method was used, with the number of families (AMM_1, $AMMI_2$, ..., $AMMI_n$) defined through analysis of variance for each principal component. Simultaneously, the GGE methodology was used to select superior genotypes for the analyzed variables.

To carry out the selection of rice genotypes considering all the variables, the MGIDI selection index was used. For this, a plant ideotype was developed with the objective of increasing the duration of the number of days for flowering, grain yield and percentage of whole grains and reducing the percentage of chalky grains. This ideotype was used as a reference for applying the MGDI selection index. For this, maximum and minimum values of 100 and 0 were used, respectively, after reprogramming to obtain positive and negative gains, as proposed by Olivoto and Nardino (2021).

All statistical analyzes were performed using the R software, version 3.5.6 (R CORE TEAM, 2023). For this, the agricolae packages, version 1.3-5 (Mendiburu, 2021), were used to verify the assumptions of the analyses; metan, version 1.16.0 (Olivoto; Lucio, 2020), to apply analysis of deviance, BLUP and multiple feature selection indices; and ggplot2, version 3.3.6 (Wickham, 2016) to develop graphical representations.

3. RESULTS AND DISCUSSION

The genotypes × environments interaction showed a significant effect for all analyzed variables (Table 1). This indicates that rice genotypes responded differently under different environmental conditions. Therefore, the adequate positioning of the genotypes may depend on the specific traits of each environment. Thus, it is possible to identify which genotypes are more adapted and responsive under different conditions, allowing the selection of genotypes with superior agronomic performance (Loro *et al*., 2023).

Broad sense heritability ranged from 0.02 to 0.23 for number of days to flowering and percentage of chalky grains, respectively (Table 2). The selective accuracy was greater than 0.82 for number of days to flowering, percentage of whole grains and percentage of chalky grains. This indicates the reliability of genotype selection based on phenotypic information. Similar results for percentage of whole grains were also revealed by Streck *et al*. (2018) and Xu *et al*. (2015).

Grain yield, as it is governed by a large number of genes, showed the lowest broad-sense heritability (0.02) and selective accuracy (0.46). This indicates the greatest contribution of the environment to the expression of this characteristic (Pradebon *et al*., 2023). The contribution of environmental variation to rice grain yield was also reported by Adhikari *et al*. (2018) and Asante *et al*. (2019).

Table 1 – Joint analysis of variance for the variables number of days to flowering (NDF, days), grain yield (GY, kg ha^{-1}), percentage of whole grains (WG, unit) and percentage of chalky grains (CG, %) in 14 rice genotypes grown in eight environments.

Source	**DF**	**Pr(>F)**			
		NDF	**GY**	**WG**	**CG**
Env	7	0.000001	0.000001	0.000001	0.000001
Rep (Env)	24	0.028066	0.000003	0.000440	0.002599
Gen	13	0.000001	0.000114	0.000001	0.000001
Gen:Env	91	0.000001	0.000001	0.000001	0.000001
PC1	19	0.000001	0.000001	0.000001	0.000001
PC2	17	0.000001	0.000001	0.000001	0.000001
Residual	312				
Total	538				

Env: environments; Rep: repetition; Gen: genotypes;
PC1 and PC2: main components of the AMMI analysis; DF: degrees of freedom.

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Table 2 – Estimates of the variance components and genetic parameters of the variables number of days to flowering (NDF, days), grain yield (GY, kg ha^{-1}), percentage of whole grains (WG, unit) and percentage of chalky grains (CG, %) in 14 rice genotypes cultivated in eight environments.

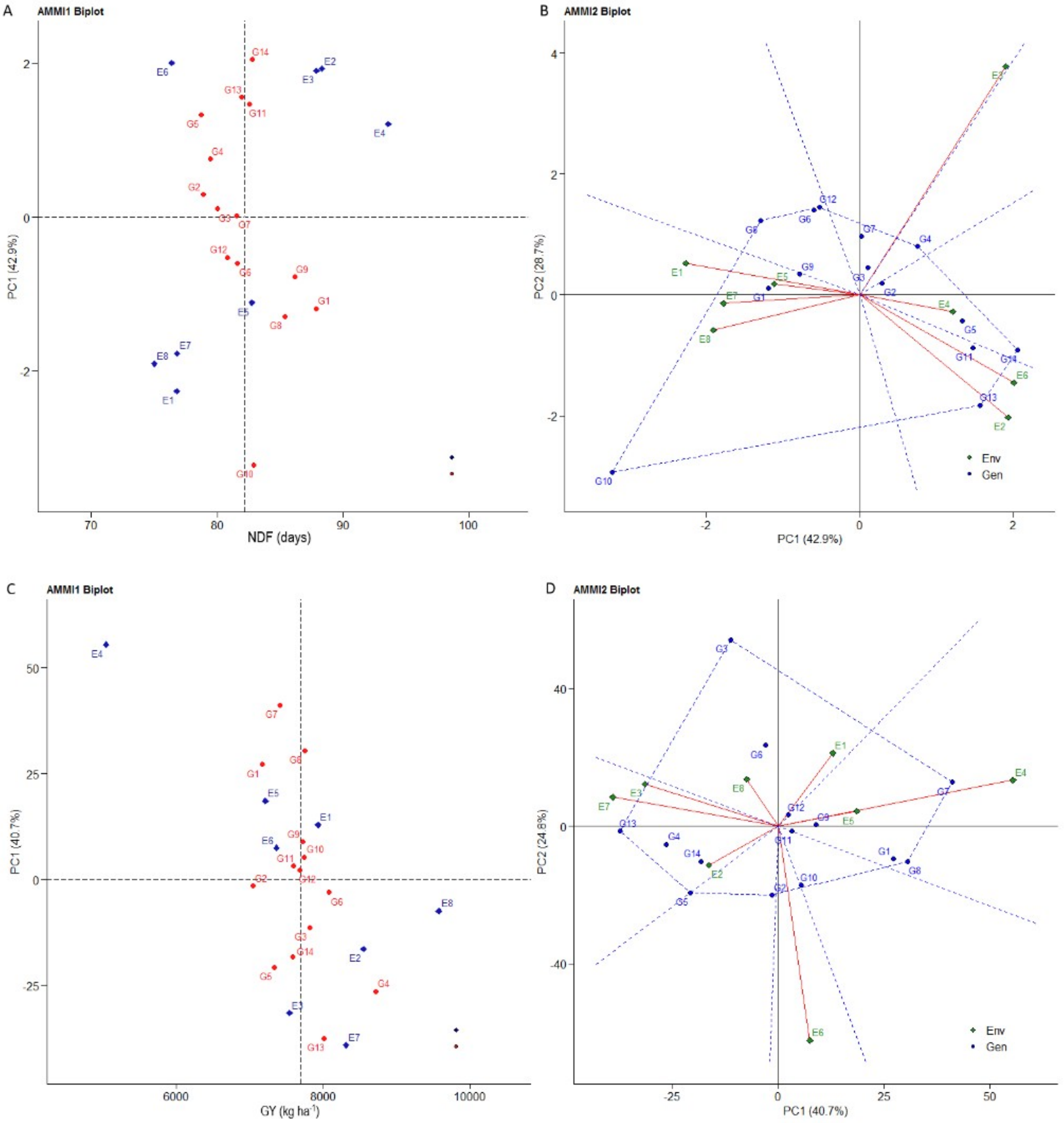
Parameters	**NDF**	**GY**	**WG**	**CG**
σ^2P	40.56	2530014.43	22.57	4.14
h^2_a	0.11	0.02	0.14	0.23
$GEIr^2$	0.26	0.27	0.45	0.37
h^2_{mg}	0.69	0.21	0.67	0.79
Ac	0.83	0.46	0.82	0.89
rGE	0.29	0.27	0.53	0.48
CV_g	2.59	2.60	2.92	7.19
CV_r	6.08	17.96	5.01	9.64
CV_{ratio}	0.43	0.14	0.58	0.75

σ^2P: phenotypic variance; h^2_a: broad sense heritability; h^2_{mg}: average heritability of the genotype; $GEIr^2$: coefficient of determination of the effects of genotype x environment interaction; rGE: genotypic correlation between performance genotypes x environments; CVg: genotypic coefficient of variation: CVr: residual coefficient of variation; CVratio: coefficient of variation of the ratio between genotypic coefficient of variation and residual coefficient of variation. Font: Authors.

The percentage of chalky grains showed the highest coefficient of genotypic variation (7.19%). This indicates that phenotypic variation was largely determined by genotype, so selection for this trait based on phenotype can be effective. Similar results were observed by Adjah *et al*. (2020).

By the AMMI analysis, the G1 and G9 genotypes showed the highest average number of days to flowering (Figure 1A).

Figure 1 – Biplot AMMI$_1$ (A and C) and AMMI$_2$ (B and D) for the variables number of days to flowering (NDF) and grain yield (GY) for 14 rice genotypes evaluated in eight environments.



E1: Capão do Leão - 2014/15; E2: Capivari do Sul - 2014/15;
E3: Santa Vitória do Palmar – 2014/15; E4: Alegrete - 2015/16;
E5: Capão do Leão - 2015/16; E6: Mostardas – 2015/16;
E7: Uruguaiana - 2015/16; and E8: Santa Vitória do Palmar – 2015/16.

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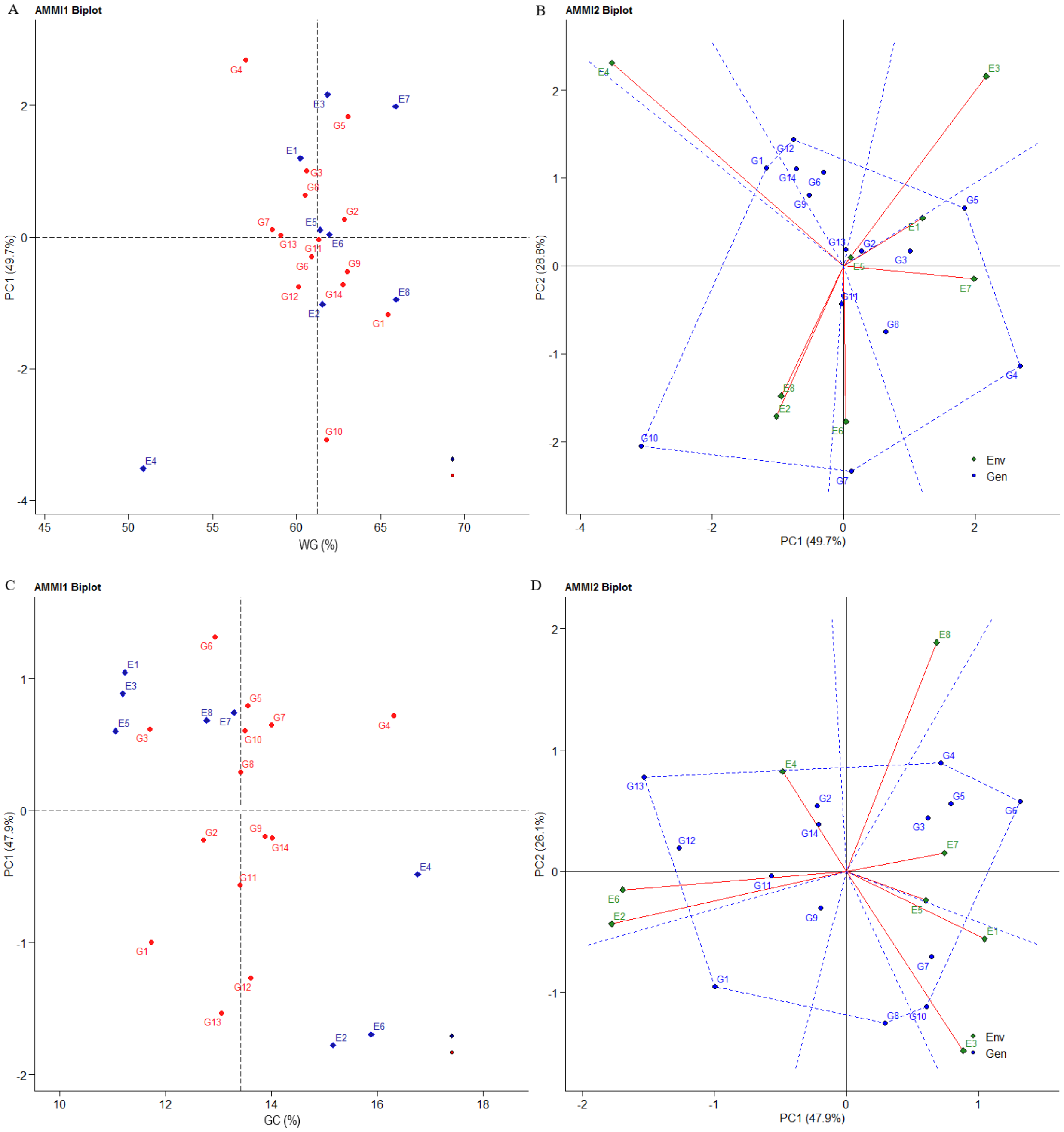
While the greatest stability was expressed by the G2 and G3 genotypes (Figure 1A and B). These genotypes expressed a lower number of days to flowering than the general average of the genotypes. Therefore, it is possible to identify early and late genotypes with stability in the environments. Genotypes G9, G11 and G12 showed the greatest stability in relation to grain yield. Among them, the G9 genotype showed a grain yield above the general average of the evaluated genotypes (≥ 7,700 kg ha^{-1}). In addition, it is worth highlighting the better adaptability of the G9 genotype in the E5 and E4 environments. This indicates that the G9 genotype has a promising potential to be considered in genetic improvement programs aimed at increasing grain yield. The average grain yield was similar to that reported by Rosa *et al.* (2015), with grain yield of rice genotypes between 7.938 and 9.759 kg ha^{-1}.

The G2 genotype exhibited the highest percentage stability of whole grains, as well as expressed a mean higher than the general mean of the genotypes. This genotype showed adaptability to environments E1, E3, E5 and E7 (Figure 2A and B). Streck *et al*. (2018) also showed rice genotypes adapted to some environments. For the percentage of chalky grains, it is expected to select genotypes to reduce this characteristic. Therefore, the G3 genotype showed an average percentage of chalky grains lower than the general average of the genotypes, as well as showing relative stability for the characteristic.

The percentage of chalky grains is related to the quality of the rice grain (Edwards *et al*., 2017) and occurs due to an arrangement between the starch and protein granules resulting from adverse climatic and cultivation conditions, as well as genetic factors (Gong *et al*., 2017). Therefore, the greater the percentage of chalky grains, the lower the market value of the grains. This indicates that the G3 genotype may be a suitable choice for genetic improvement programs aimed at reducing the percentage of chalky grains in rice grains (Figure 2C and D).

The G4 genotype exhibited the highest average grain yield in the eight evaluated environments (Figure 3). However, this genotype showed the highest percentage values of chalky grains. Therefore, although it is the most productive genotype, its grains have low commercial quality, due to the higher percentage of chalky grains. The G1 genotype, on the other hand, presented the highest number of days to flowering, percentage of whole grains and low percentage of chalky grains. Thus, it was noticed that this genotype exhibits essential traits for grain quality, however it expresses low grain yield.

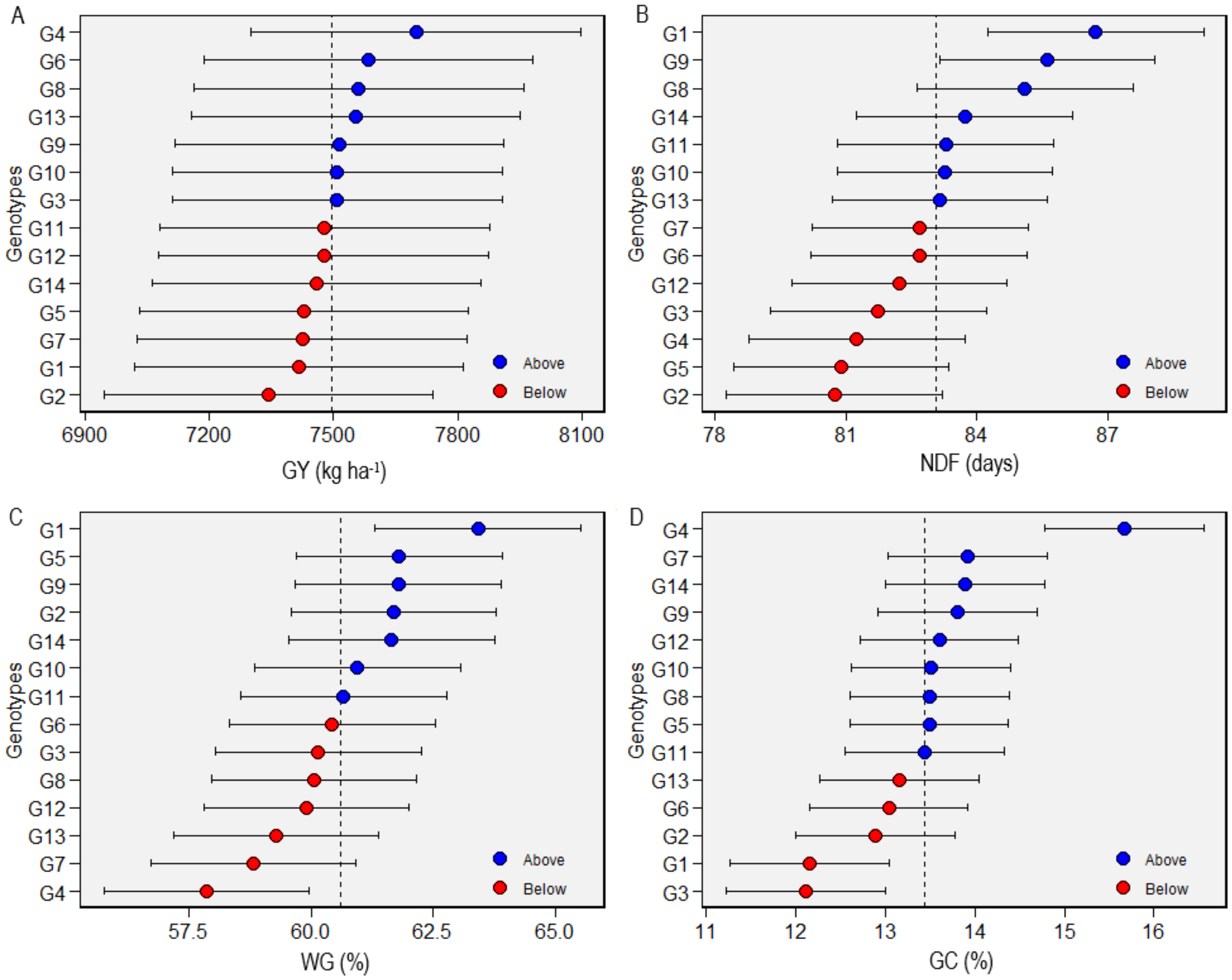
Figure 2 – Biplot AMMI$_1$ (A and C) and AMMI^2 (B and D) for the variables percentage of whole grains (WG) and percentage of chalky grains (CG) for 14 rice genotypes evaluated in eight environments.



E1: Capão do Leão - 2014/15; E2: Capivari do Sul - 2014/15;
E3: Santa Vitória do Palmar – 2014/15; E4: Alegrete - 2015/16; E5: Capão do Leão - 2015/16;
E6: Mostardas – 2015/16; E7: Uruguaiana - 2015/16; and E8: Santa Vitória do Palmar – 2015/16.

Font: Authors.

Figure 3 – Prediction of variables number of days to flowering (NDF), grain yield (GY), percentage of whole grains (WG) and percentage of chalky grains (CG) for 14 rice genotypes. Blue and red circles represent genotypes that had BLUP above and below BLUP means, respectively. The horizontal error bars represent the 95% confidence interval of the prediction.



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Liu *et al.* (2022) revealed similar results, in which they observed difficulty in promoting the simultaneous increase in grain yield and characters referring to the industrial quality of grains. Different results were reported by Xu *et al*. (2015), in which they did not show a negative correlation between grain yield and grain quality traits. However, these authors indicated that grain yield may be increased up to 8,500 kg ha^{-1} without impacting grain quality. Therefore, grain yield above this limit can promote the reduction of traits that confer the commercial quality of rice grains, such as the grain yield evidenced in this present study.

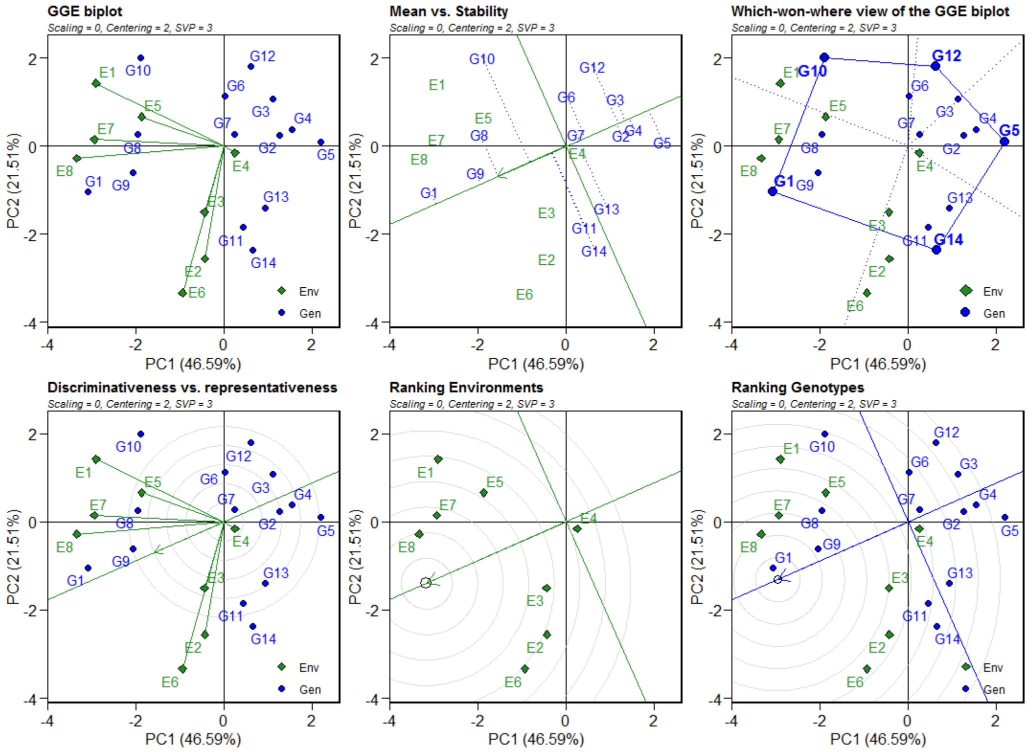
Based on these results, there is a negative relationship between grain yield and grain quality. These conclusions may be relevant for genetic improvement programs, as they highlight the need to seek a balance between grain yield and grain quality when selecting promising genotypes for future studies and development of rice genotypes. Similar results were in a study carried out by Kakar *et al*. (2019), in which they showed a negative correlation between the percentage of whole grains and grain yield, while a positive correlation was observed between the percentage of broken grains and grain yield.

Genotypes with longer duration of days to flowering have greater tolerance to high temperatures. Therefore, the objective of the selection is to increase the number of days for the flowering of the rice genotypes. Thus, it was possible to observe that the G1 genotype had the highest number of days for flowering and the greatest stability (Figure 4). Therefore, it was classified as the ideal genotype. This indicates that this genotype had the highest number of days to flowering with high stability between growing environments. The highest number of days for flowering of the G1 genotype was observed in environments E6, E7 and E8. Environments E3 and E8 were considered ideal for evaluating the number of days for the genotypes to flower.

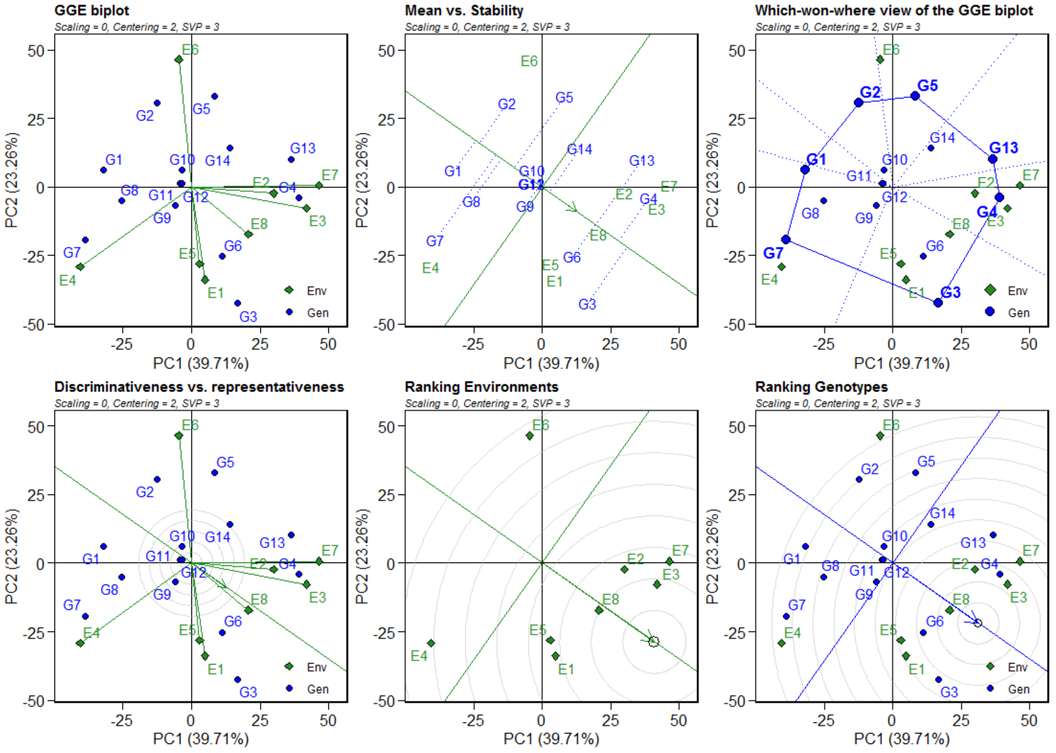
Through the GGE biplot analysis, it was observed that the G4 and G6 genotypes were the most productive with phenotypic stability (Figure 4). Therefore, among the evaluated genotypes, the G4 and G6 genotypes presented a stable performance close to the ideal genotype, established by the GGE analysis. The G4 genotype had the best productive response when evaluated in environments E2, E3 and E7. While the G6 genotype expressed better performance in environments E1, E5 and E8. Environments E3 and E8 were considered ideal for expressing the highest grain yield of the genotypes.

The G1 genotype had the highest percentage of whole grains, associated with high stability in the expression of this trait (Figure 5). Therefore, it was characterized as being the closest genotype to the ideal for the percentage of whole grains. The highest percentage of whole grains was expressed by this genotype in environments E4 and E5, and these environments were considered close to the ideal to evaluate this characteristic.

Figure 4 – GGE biplot for the variables number of days to flowering (NDF) and grain yield (GY) for 14 rice genotypes evaluated in eight environments.



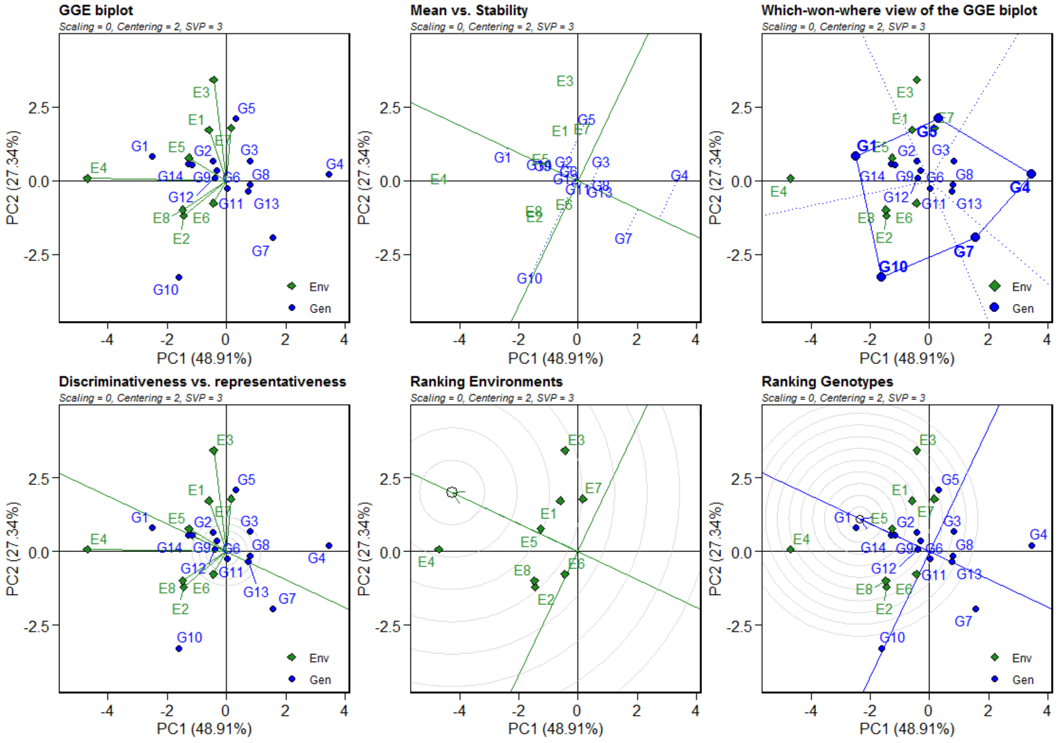
NDF (days)



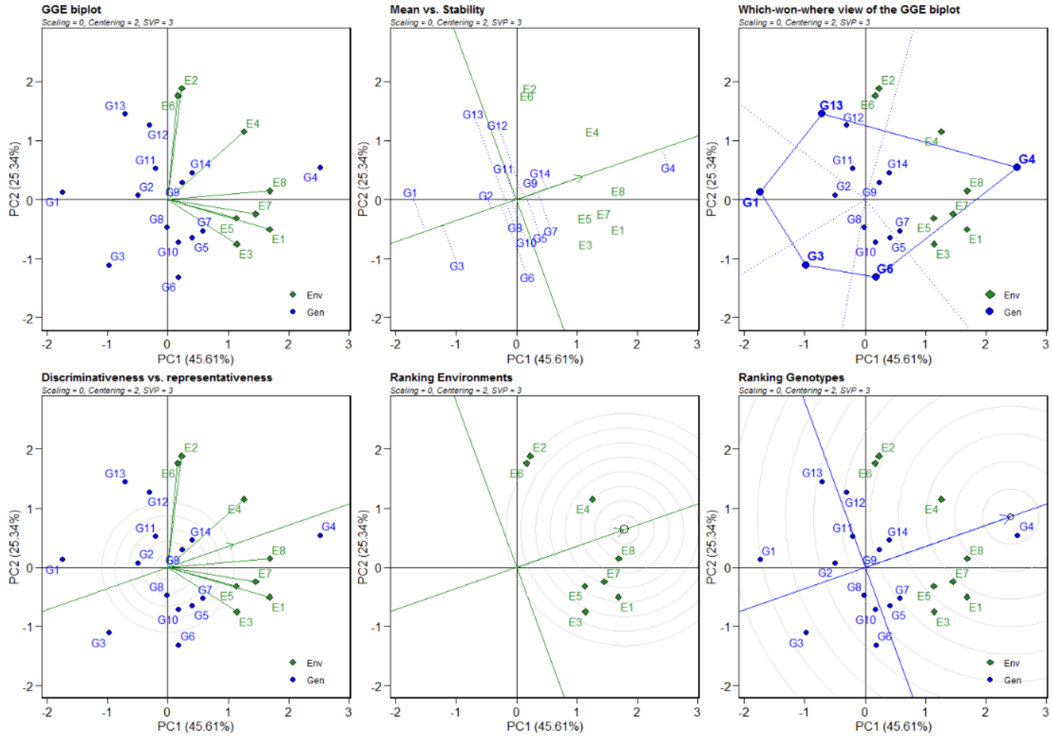
GY (kg ha^{-1})

E1: Capão do Leão - 2014/15; E2: Capivari do Sul - 2014/15; E3: Santa Vitória do Palmar – 2014/15; E4: Alegrete - 2015/16; E5: Capão do Leão - 2015/16; E6: Mostardas – 2015/16; E7: Uruguaiana - 2015/16; and E8: Santa Vitória do Palmar - 2015/16. Font: Authors.

Figure 5 – Biplot GGE for the variables percentage of whole grains (WG) and percentage of chalky grains (CG) for 14 rice genotypes evaluated in eight environments.



WG (%)



GC (%)

E1: Capão do Leão - 2014/15; E2: Capivari do Sul - 2014/15; E3: Santa Vitória do Palmar – 2014/15; E4: Alegrete - 2015/16; E5: Capão do Leão - 2015/16; E6: Mostardas - 2015/16; E7: Uruguaiana - 2015/16; and E8: Santa Vitória do Palmar - 2015/16. Font: Authors.

The percentage of chalky grains is a parameter that indicates the quality of rice grains (Edwards *et al*., 2017). It is expected that this percentage is the minimum possible, so that the grains have greater acceptance by the consumer and, therefore, greater commercial value. Therefore, the selection of genotypes needs to check the reduction of this characteristic. Therefore, it was observed that G1 could be selected, since it presented the lowest average expression of the percentage of chalky grains with relative stability. It was possible to identify that the G1 genotype exhibited the lowest percentage of chalky grains in all environments. In addition, environments E2 and E3 presented favorable environmental conditions to reduce the percentage of chalky grains.

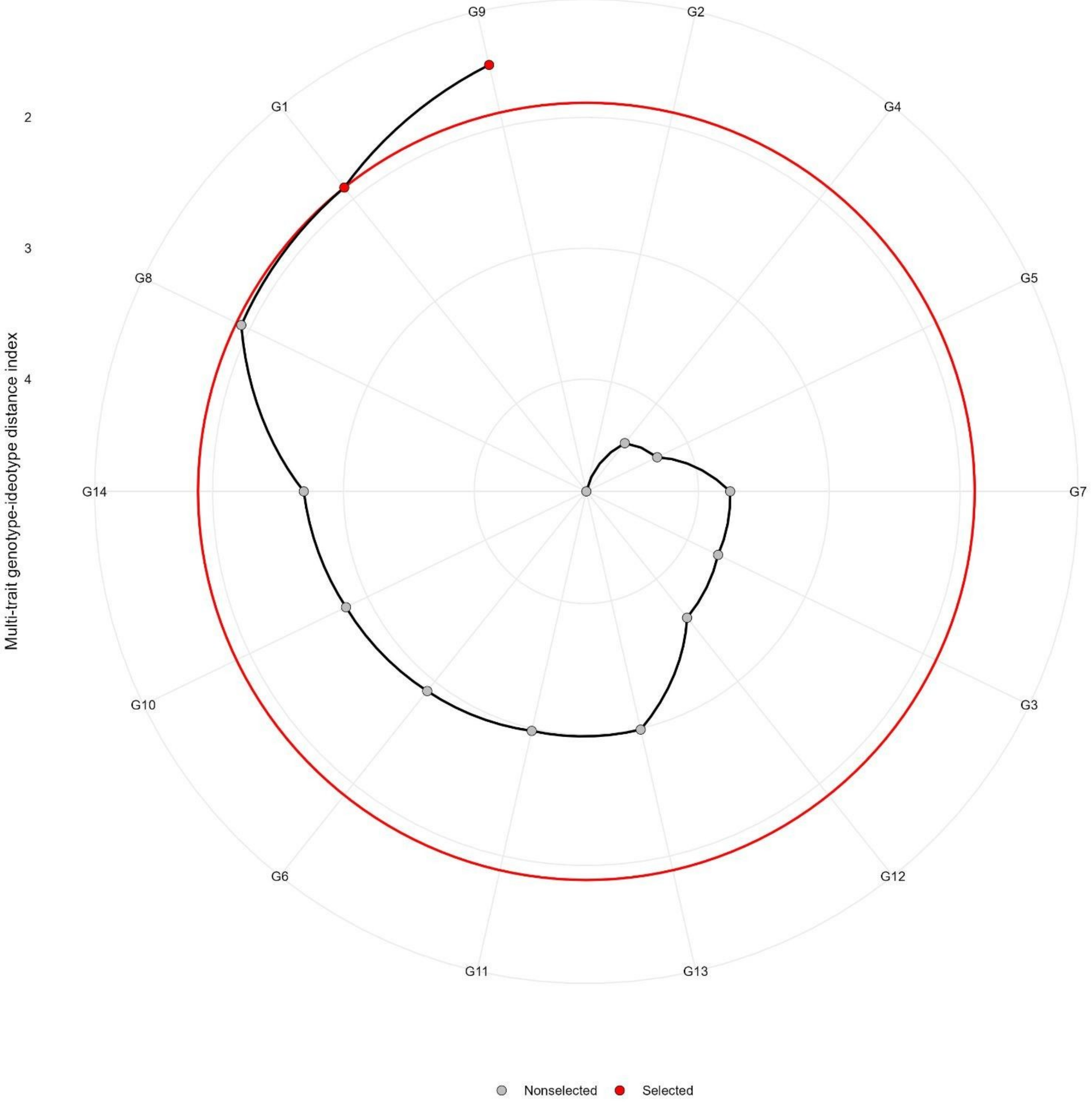
Therefore, it can be inferred that, based on the GGE analysis, the G1 genotype proved to be the closest to the ideal genotype, presenting a greater number of days for flowering, a greater percentage of whole grains and a smaller percentage of chalky grains, in addition to exhibit high stability in these traits. However, it was characterized by lower grain yield. Therefore, the G4 and G6 genotypes were considered the closest to the ideal genotype for grain yield.

To simultaneously identify productive genotypes with higher grain quality, the MGIDI analysis was used (Olivoto; Nardino, 2021). An ideotype was defined to increase the number of days to flowering, grain yield and percentage of whole grains, with a reduction in the percentage of grain chalk. In addition, the highest weights for selection were given to the traits number of days to flowering, percentage of whole grains and percentage of chalky grains. Therefore, it was observed that it was possible to identify two genotypes with performance close to the established ideotype (Figure 6). The selected genotypes were G9 and G1, in that order, with the best balance in the expression of the evaluated traits, standing out as the best options for simultaneously obtaining high grain yield and grain quality. Streck *et al*. (2018) also identified promising genotypes for agronomic and for commercial quality of grains traits.

Faced with the difficulties in selecting productive traits and grain quality, it was possible to simultaneously identify genotypes with a balance between these traits. Therefore, the AMMI, GGE and MGIDI analyses, used simultaneously, indicated that the selection of the G1 and G9 genotypes can be promising to promote greater grain yield and number of days to flowering, associated with better grain quality in agricultural crops.

In addition, producers and consumers of this cereal can use these genotypes in genetic improvement programs as genitors for the development of rice genotypes that meet the grain yield and grain quality criteria required.

Figure 6 – MGIDI index for selection of rice genotypes evaluated in eight environments in relation to the variables number of days to flowering (NDF), grain yield (GY), percentage of whole grains (WG) and percentage of chalky grains (CG).



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4. FINAL CONSIDERATIONS

Using the AMMI, GGE and MGDI methods, genotypes G9 and G1 present performance close to the ideal ideotype for number of days to flowering, grain yield and grain quality.

5. REFERENCES

ADHIKARI, B. N. *et al*. Genetic variability, heritability, genetic advance and correlation among yield and yield components of rice (*Oryza sativa* L.). **Journal of Agriculture and Natural Resources**, v, 1, n. 1, p. 149-160, 2018.

ADJAH, K. L. *et al*. Genetic variability, heritability and correlations for milling and grain appearance qualities in some accessions of rice (*Oryza sativa* L.). **Physiology And Molecular Biology of Plants**, v. 26, n. 6, p. 1309-1317, 2020.

ASANTE, M. D.; ADJAH, K. L.; ANNAN-AFFUL, E. Assessment of genetic diversity for grain yield and yield component traits in some genotypes of rice (*Oryza Sativa* L.). **Journal of Crop Science and Biotechnology**, v. 22, n. 2, p. 123-130, 2019.

EDWARDS, J. D.; JACKSON, A. K.; MCCLUNG, A. M. Genetic architecture of grain chalk in rice and interactions with a low phytic acid locus. **Field Crops Research**, v. 205, p. 116-123, 2017.

FACCHINELLO, P. H. K. *et al*. Adaptability and stability of irrigated rice elite lines for grain quality. **Brazilian Journal of Agriculture**, v. 97, n. 2, p. 137-153, 2022.

GONG, J. Y. *et al*. Dissecting genetic basis of grain shape and chalkiness traits in hybrid rice using multiple collaborative populations. **Molecular Plant,** v. 10, n. 10, p. 1353-1356, 2017.

INABANGAN-ASILO, M. A. *et al*. Stability and G× E analysis of zinc-biofortified rice genotypes evaluated in diverse environments. **Euphytica**, v. 215, n. 61, p. 1-17, 2019.

KAKAR, K. *et al*. Morphological observation and correlation of growth and yield characteristics with grain quality and antioxidant activities in exotic rice varieties of Afghanistan. **Agriculture**, v. 9, n. 8, p. 167, 2019.

LIU, Q. *et al*. Characteristics of population quality and rice quality of semi-waxy japonica rice varieties with different grain yields. **Agriculture**, v. 12, n. 2, p. 241, 2022.

LORO, M. V. *et al*. Wheat grain biofortification for essential amino acids. **Pesquisa Agropecuária Brasileira**, v. 58, e02860, 2023.

MENDIBURU, F. **agricolae**: Statistical Procedures for Agricultural Research. R package version 1.3-5. 2021. Disponível em: https://CRAN.R-project.org/package=agricolae. Acesso em: 31 oct. 2023.

MUTHAYYA, S. *et al*. An overview of global rice production, supply, trade, and consumption. **Annals of the New York Academy of Sciences**, v. 1324, p. 7-14, 2014.

OLIVOTO, T.; LÚCIO, A. D. metan: an R package for multienvironment trial analysis. **Methods in Ecology and Evolution**, v. 11, n. 6, p. 783-789, 2020.

OLIVOTO, T.; NARDINO, M. MGIDI: toward an effective multivariate selection in biological experiments. **Bioinformatics**, v. 37, n. 10, p. 1383-1389, 2021.

PRADEBON, L. C. *et al*. Soybean adaptability and stability analyzes to the organic system through AMMI, GGE Biplot and mixed models methodologies. **Ciência Rural**, 53, n. 9, e20220262, 2023.

R CORE TEAM. **R**: a language and environment for statistical computing. Vienna: R Foundation for Statistical Computing, 2023.

RESENDE, M. D. V. **Software SELEGEN – REML/BLUP**: sistema estatístico e seleção genética computadorizada via modelos lineares mistos. Colombo: Embrapa Florestas, 2007.

ROSA, H. T. *et al*. Simulação do crescimento e produtividade de arroz no Rio Grande do Sul pelo modelo SimulArroz. **Revista Brasileira de Engenharia Agrícola e Ambiental**, v. 19, n. 12, p. 1159-1165, 2015.

STRECK, E. A. *et al*. Adaptability and stability of flood-irrigated rice cultivars released to the subtropical region of Brazil. **Pesquisa Agropecuária Brasileira**, v. 53, n. 10, p. 1140-1149, 2018.

STRECK, E. A. *et al*. Genotypic performance, adaptability and stability in special types of irrigated rice using mixed models. **Revista Ciência Agronômica**, v. 50, n. 1, p. 66-75, 2019.

XU, Q.; CHEN, W.; XU, Z. Relationship between grain yield and quality in rice germplasms grown across different growing areas. **Breeding Science**, v. 65, n. 3, p. 226-232, 2015.

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