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Stability of some of rice genotypes based on WAASB and MTSI indices

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Abstract

Ten rice genotypes were evaluated in a randomized complete block design with four replications in three regions of Iran during three cropping seasons. Likelihood ratio test (LRT) was shown the significant effects of genotype and genotype by environment interaction (GEI). Scree plot indicated the first three components explained 81.24% of GEI variation. Mosaic plot partitioned total sum of squares (TSS) and indicated genotype and GEI effects illustrated 52.72% and 47.28% of TSS, respectively. Heatmap plot also exhibited variations in the grain yield of genotypes across environments. The best linear unbiased predictors (BLUPs) of grain yield showed that G2, G5, G4, G10 and G6 had a higher prediction than the overall grain yield. The nominal yield plot indicated G4, G5, G6 and G10 had a small contribution in GEI and were more stable genotypes. In the fourth quarter of grain yield *vs* the weighted average of absolute scores (WAASB) biplot, G2, G5 and G10 were highly productive and stable. Based on a weight of 50:50 for grain yield and stability, G5, G6, G2, and G3 had the highest WAASBY values and were determined as stable genotypes. In WAASB/GY ratio plot, it is observed that G5, G6, G2, and G3 had the highest WAASBY values and were deyermined as stable genotypes. Factor analysis based on WAASBY values of all of the traits identified three factors with a cumulative variance of 79.35. Based on the multi-trait stability index (MTSI), G6 and G3 were selected. In conclusion, G5 was superior to all genotypes and can be used to determine the best cropping manangement in agronomic research experiments and for the introduction of new cultivars.

Key words: AMMI, BLUP, Factor analysis, Heatmap, Mosaic plot.

INTRODUCTION

Rice is one of the most important crop and staple food for a large proportion of people in many countries in Asia, especially in Iran. Environmental stresses such as drought, cold, heat, and deficiency or excess of nutrients affect crop yield production. Therefore, it is very important to evaluate different genotypes in different environments, to identify appropriate and stable genotypes for a wide range of environments or a specific environment (Sharifi, 2020). A better understanding of genotype by environment interaction (GEI) and stability in crops is used as a decision tool, particularly at the final stage of the variety introduction process, for screening breeding lines and recommendation of the released varieties (Yan and Kang, 2003).

The best linear unbiased predictor (BLUPs), as a classical approach, has been used in a few cases for evaluations of the genotype effects and their interaction with environments for quantifying genotypic stability in rice. Donoso-Ñanculao *et al.* (2015) analyzed ten rice genotypes in three locations during three growing seasons by BLUP and distinguished the high-yielding and stable genotypes. Balestre *et al.* (2010) also used BLUP for the stability of rice genotypes and observed the use of phenotypic means had a lower predictive potential than the use of BLUP. Olivoto *et al.* (2019a) proposed a new quantitative genotypic stability index, designated as the weighted average of absolute scores based on singular value decomposition (SVD) of BLUP-interaction effects (WAASB). It is the weighted average of absolute scores from SVD of the matrix of BLUPs for the GEI effects obtained by the linear mixed-effect model (LMM). They also introduced a superiority index, called WAASBY, which allows weighting between mean performance and stability (MPE). These indices combined the graphical tools of AMMI and the predictive accuracy of BLUP for stability analysis. Santos and Marza (2020) used these indices for selecting more productive and stable forage oat genotypes. Olivoto *et al.* (2019b) also suggested a multi-trait stability index (MTSI) for simultaneous selection regard to MPE for the analysis of multi-environment trials (METs) using both fixed and mixed effect models for several traits. The most important benefit of this approach is taking the advantage of nice graphical interpretations of AMMI and most predictively accurate of BLUP.

The other graphical tools for studying GEI in multi-environment trials (METs) are mosaic and doc plots, proposed by Laffont *et al.* (2007) and established a link between the partitioning of the total sum of squares (TSS) of GEI obtained by SVD and the partitioning of this TSS provided by the ANOVA. The mosaic plot, which simultaneously partitions TSS, facilitates the interpretation of the GGE biplot (Laffont *et al.*, 2013). In a dot plot, in which each panel and row represents a different genotype and environment, respectively, the yield is indicated by the position of the dot and can be used for evaluation response variable of a given genotype across environments and vice versa (Laffont *et al.*, 2007). Recently, the heat map plot was used for this purpose. Kumar Das *et al.* (2018) used this heatmap plot for the detection of the stable rice genotypes under different agro-ecological locations.

This study aims to evaluate the stability of rice genotypes using combining features of AMMI and BLUP techniques and other graphical tools.

MATERIALS AND METHODS

Experimental design and plant materials

This experiment was carried out for the evaluation of nine promising rice genotypes along with Shiroudi cultivar (as a check variety) in a randomized complete block design (RCBD), with four replications. Code and origin of the rice genotypes are shown in Table 1. The experimental fields were located in three different stations in Iran (Tonekabon, -20 m above sea level (ASL), 36°51’ N, 50°46’ E; Amol, 76 m ASL, 36°28' N, 52°23' E and Gorgan, 155 m ASL, 36°85' N, 54°44' E) during three cropping seasons of 2009-2012.

The 30-day old seedlings at the 4-5 leaf-stage were planted at all locations in 25×25 cm plant intervals in plots with the size of 20 m^2. The recommended dose of N, K and P were 250, 100 and 100 kg $ha^{-1}$of urea, potassium sulfate and ammonium phosphate. Half of the required N and all of K and P were used at the time of planting. The remaining urea was applied 30 and 60 days after planting. The weed control was done manually three times. No insecticides and herbicides were employed in the trials. The middle two rows of

Table 1. Code, parents and origin of rice genotypes.

Genotype code	Parents	Origin
G1	Number 54 from IR 67015-22-6-2-(A37632)×(Amol3×Number 3)	Iran
G2	Number 58 from IR 67015-22-6-2-(A37632)×(Amol3×Number 3)	Iran
G3	Number 59 from IR 67015-22-6-2-(A37632)×(Amol3×Number 3)	Iran
G4	Number 134 from IR 67015-22-6-2-(A37632)×(Amol3×Number 3)	Iran
G5	Number 16 from IR 64669-153-2-3-(A8948)×(4 Surinam×Deylamani)	Iran
G6	Number 177 from IR 67015-22-6-2-(A37632)×(Amol3×Number 3)	Iran
G7	Number 81 from IR 67015-22-6-2-(A37632)×(Amol3×Number 3)	Iran
G8	Number 13 from 67015-22-6-2-(A37632)×Shiroudi	Iran
G9	Number 50 from IR 67015-22-6-2-(A37632)×(Amol3×Number 3)	Iran
G10	Shiroudi (check variety)	Iran

each plot were harvested at full maturity from 5 m^2 plots. The grain yield was adjusted for 14% moisture.

Statistical analysis

Estimating the WAASB and WAASBY indices

All statistical analyses were performed using metan (multi-environment trial analysis) (Olivoto and Lúcio, 2020) and gge (genotype plus genotype-by-environment) (Wright and Laffont, 2018) R packages.

WAASBi (weighted average of absolute scores based on SVD of BLUP-interaction effects of the ith genotype or environment) (Olivoto *et al.*, 2019a) is calculated by equation 1:

$$(1) \qquad WAASB_i = \frac{\sum_{k=1}^{p} \left| IPCA_{ik} \times EP_k \right|}{\sum_{k=1}^{p} EP_k}$$

Where, interaction principal component axis (IPCA$_{ik}$) is the score of the ith genotype (or environment) in the kth IPCA; and EP$_k$ is the amount of the variance explained by the kth IPCA.

WAASBY index for simultaneous selection based on grain yield (Y) and stability (WAASB) is obtained by equation 2 (Olivoto *et al.*, 2019a):

$$(2) \qquad WAASBY_i = \frac{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}{\theta_Y + \theta_S}$$

Where, WAASBYi is the superiority index for the ith genotype, that weights between performance and stability, θY and θS, are the weights for the response variable and the stability (WAASB) (Olivoto *et al.*, 2019b) assumed to be 50 and 50 in our study, indicating equally weight of grain yield and stability. In addition, 21 scenarios varying θY and θS (100/0, 95/5, 90/10,..., 0/100) were planned. Gi and Wi are the values of grain yield and WAASB for ith genotype. rGi and rWi are the rescaled values (0–100) for the response variable and WAASB, respectively. Because the best values for grain yield and WAASB are the maximum and minimum values, the transformations were carried out according to the following equations (Olivoto *et al.*, 2019b):

$$(3) \qquad rG_i = \frac{100-0}{G_{\max} - G_{\min}} \times (G_i - G_{\max}) + 100$$

and

$$(4) \qquad rW_i = \frac{0-100}{W_{\max} - W_{\min}} \times (W_i - W_{\max}) + 0$$

Multi-trait index based on factor analysis

The multi-trait stability index (MTSI) (Olivoto *et al.*, 2019b) was computed by equation 5:

$$(5) \qquad MTSI_i = \left[\sum_{j=1}^{f} (F_{ij} - F_j)^2 \right]^{0.5}$$

Where, the MTSI is the multi-trait stability index for the ith genotype, F$_{ij}$ is the jth score of the ith genotype, and F$_j$ is the jth score of ideotype. The genotype with the lowest MTSI is then closer to the ideotype and therefore presents a high MPE for all analyzed variables (Olivoto *et al.*, 2019b).

The steps to compute the MTSI are:

1- Define an ideotype a prior, i.e., which one is better to increase and which one is better to decrease (in terms of selection gains). The factor analysis of WAASBY is the first step to compute the MTSI index. Then, a Euclidean distance is used to compute the distance between the genotypes' scores to the ideotype's score.

2 - Provide weights for mean performance and stability. Here should explicitly consider a greater weight for GY.

3 - Compute the WAASBY index (which is compute with the waasb() function) of metan package, and use this model in the mtsi () function.

4 - Based on the ideotype defined, the function will try to find the better ones, close to the ideotype.

RESULTS AND DISCUSSION

Analysis of variance, estimation of variance components and predicted grain yield

Likelihood ratio test (LRT) showed the significant effects of environment and genotype by environment interaction (GEI) (Table 2). Analysis of variance indicated a significant effect of genotype on grain yield. The significant effect of GEI indicated the different performance of genotypes across environments. This variation in grain yield supports the requirement of more analysis for increasing the efficiency of the selection of genotypes. In another word, the presence of a significant GEI demonstrated the necessity of determining the performance and adaptation of genotypes based on evaluations in multiple locations and growing seasons. AMMI and BLUP analyses are important tools for obtaining an understanding of the factors involved in the forming of the GEI. Therefore, BLUP analysis is appropriate for such data (Olivoto *et al.*, 2019a). The other researchers have also indicated the significant effects of environment, genotype and GEI in rice multi-environment trials (Chandel *et al.*, 2010; Suwarto, 2011; Akter *et al.*, 2014; Bose *et al.*, 2014a; Rerkasem *et al.*, 2015; Sharifi *et al.*, 2017; Rahayu, 2020; Sadimantara *et al.*, 2020).

Table 2. Likelihood ratio test, variance components and genetic parameters for grain yield of 10 rice genotypes evaluated in nine environments.

Statistics	Likelihood ratio test†	
	E	G×E
χ^2	17.27	20.08
p-value	0.00003243	7.416e-6
	Variance components	
	Estimates (%)	
σ^2_e	161364 (26.51)	
$\sigma^2_{Env/block\ variance}$	45306(7.44)	
σ^2_i	94009 (15.44)	
$\sigma^2_{Residual}$	307972 (50.60)	
σ^2_P	608647	
	Analysis of variance	
MSG	2750733	
p-value	6.549e-9	

G: Genotype, E: Environment.
σ^2_e: Environmental variance, $\sigma^2_{Env/block\ variance}$: Environmental/ block variance, σ^2_i: Variance of G×E interaction, $\sigma^2_{Residual}$: Residual variance, σ^2_P: Phenotypic variance.

Evaluation of the ratio of the estimated variance components to the phenotypic variance by restricted maximum likelihood indicated that 50.60% of the phenotypic variance was explained by residual variance, while environment, environment/block and GEI variances accounted for 26.51%, 7.44% and 15.44% of phenotypic variance, respectively (Table 2). Since environment (and as a result environment/ block and GEI) is considered as random effects, the phenotypic variance is partitioned into environmental, environmental/block, GEI and residual (error) variance components. Genotypic variance will be taken into account when we have a complete random model, i.e., only the intercept is a fixed effect and all the others are random.

Scree plot, which was used to determine the number of principal components and the contribution of each of them in GEI, indicated that the first three components explained 81.24% of GEI variation (Figure 1-A). Since the first and second principal components account for 48.8% and 22.5% of the GEI variation, respectively, the interpretation of stability based only on these two principal components may lead to the wrong conclusion. Therefore, to prevent such erroneous conclusions, we used the weighted average of absolute scores based on SVD of BLUP-interaction effects (WAASB) as a stability index. Olivoto *et al.* (2019a) declared that when the explaining GEI by the first two IPCA was low to moderate, it needs to be cautious in interpretation and with the increase in GEI pattern, the variation is retained in a larger number of axes, tending to be captured in the last IPCA axes.

Mosaic plot was used for partitioning of the total sum of squares (TSS) (Figure 1-B). The dark-colored areas of this plot revealed that 52.72% of the total variation is illustrated by the differences between genotype means. The light-colored areas correspond to the variation due to genotype-by-environment effects (47.28%) of the total variation. The panels of the mosaic plot are corresponding to principal component axes and indicate the first two IPCAs, account for 61.02 and 13.02% of the TSS, respectively. These first two principal components, account for 74.04% of the TSS, 98.72% of the SSG, and 46.52% of the SSGE. The rows of mosaic plot in each column divide axis into portions caused by SSG and SSGE. This view of the mosaic plot indicated that the first IPCA had a very large contribution from SSG (84.96%) and was considered as a genotype axis, so that, the distance between the points of a given genotype to this axis is highly correlated with the distances between the genotype means. The sum of squares of second IPCA had a much higher contribution to GE (98.42%) effects than G (1.58%) effects and is labeled as a GEI axis.

Variation of grain yield indicated the existence of diversity in the studied genotypes, so that, G9 (5126.28 kg ha^{-1}) and G2 (6528.14 kg ha^{-1}) had the lowest and the highest grain yield, respectively (Figure 1-C). The average grain yield of all of the genotypes across environments was 6166.92 kg ha^{-1}. A heatmap was used for considering GEI in which each column represented a different genotype across environments and each row corresponded to a different environment for a given genotype. Heatmap also exhibited variations in the grain yield of genotypes across environments (Figure 1-C). In this heatmap plot, it is obvious that G10 and G2 have the highest grain yield in many environments, while G9 has the lowest grain yield in all of the environments except for E1. This heatmap plot also provides a clear visualization of the stability

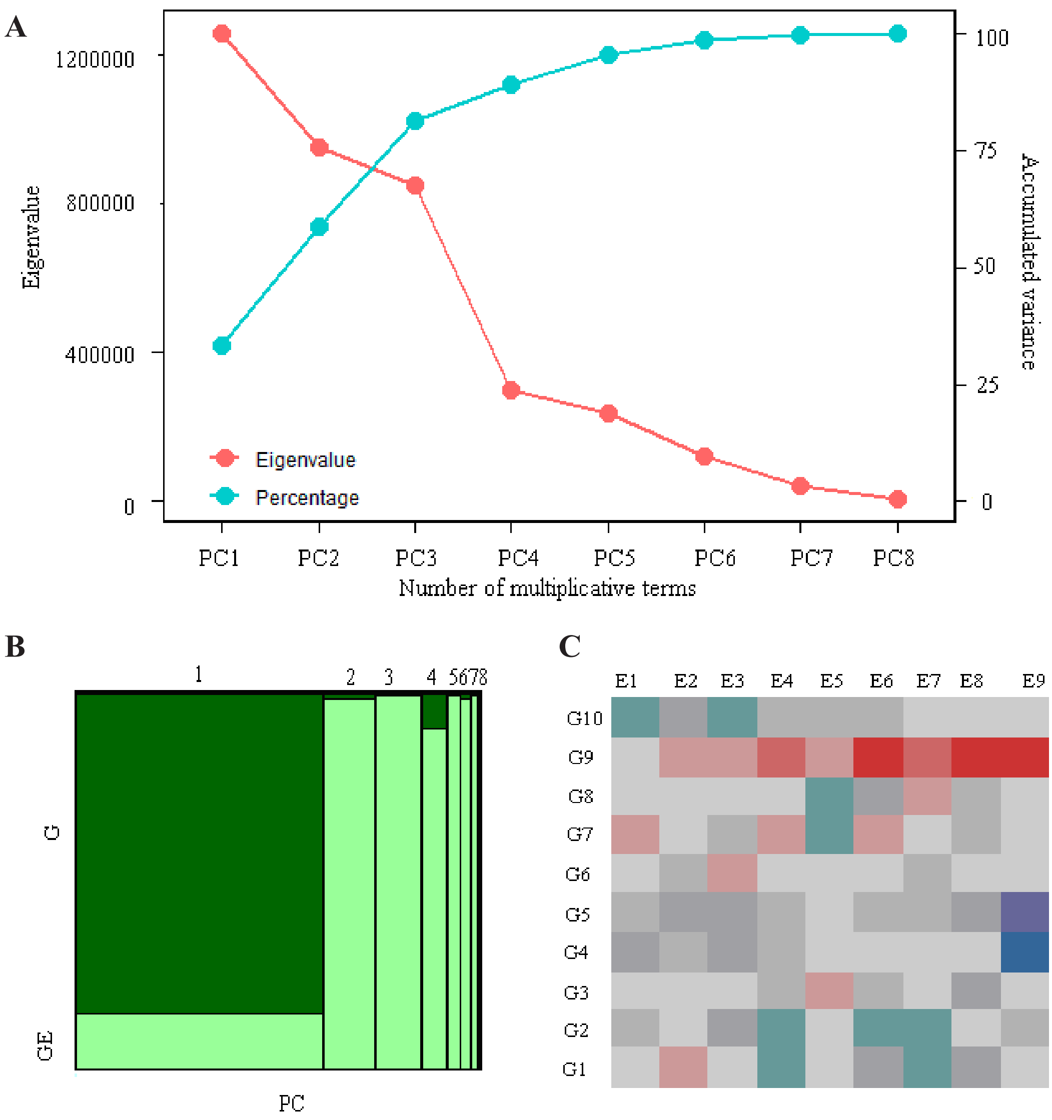

Figure 1. Pre-analysis of genotype×environment interaction (GEI) for grain yield of 10 rice genotypes in nine environments. **A:** Eigenvalues of the BLUP_GEI matrix, **B:** Mosaic plot of GEI principal components, **C:** Heatmap plot of GEI.

of G10, G5 and G2. In the heatmap plot, the yield of all genotypes in each environment, give information about the variance within each environment, while the yield of each genotype in separate columns of environments is more useful for investigating variance across environments (Laffont *et al.*, 2007). Although, a similar interpretation can be derived from the biplot, the heatmap plot provides a clearer visualization according to the phenotypic expression of response variable. This graphical method was also used for the detection of the stable rice genotypes across environments by Kumar Das *et al.* (2018).

Comparing the best linear unbiased predictors (BLUPs) of grain yield showed that G2, G5, G4, G10 and G6 had a higher prediction than the overall grain yield and therefore, were superior genotypes. G9 had the lowest predicted grain yield and had a significant difference from the other genotypes (Figure 2).

Nominal yield plot (Figure 3-A) was used to draw a line with the equation y=a+bx for each genotype, in which, x is the environmental IPCA1 score; a, is the total average of the response variable of a given genotype across environments and b, is the IPCA1 score of the given genotype. G4, G5, G6 and G10, due to the lowest IPCA1 scores (coefficients b or line slope), had a small contribution in GEI and therefore, had more stability, while grain yields of G1, G2, G3, G7, G8 and G9 differed from one environment to another and were unstable. The comparison of this plot with predicted grain yield with BLUP (Figure 2) showed that G4 and G5, in addition to stability in all environments, also had a high-predicted grain yield.

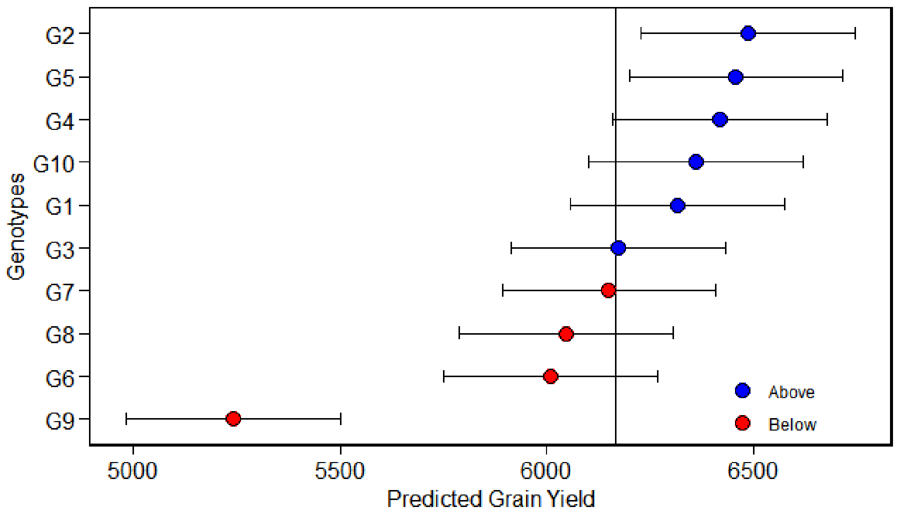

Figure 2. Best linear unbiased prediction (BLUPs) of grain yield for nine rice genotypes. The genotypes above and below the BLUPs are indicated by blue and red circles, respectively. horizontal error bars present 95% confidence intervals of BLUPs in a two-tailed t-test.

This comparison also indicated that although G5 and G2 had similar predictive averages, their line pattern was quite different because the IPCA1 score of G5 and G2 were 1.16 and 15.32, respectively, which indicates the instability of G2 and stability of G5. Although G2 had the highest predicted average (Figure 2), its line equation had a downward slope compared to other stable genotypes. Also, G6, which was stable in Figure 2-C, had a very low predicted grain yield (Figure 2), so it could not be considered as a superior genotype. Because of drawing of this plot nominal yield is based on the first principal component, which explains only 48.8% of GEI variation, concluding with such a plot alone, can be misleading, so additional analyses are needed based on other principal components. For this reason, the third type of biplot was used based on all of the significant principal components (Figure 3-B). However, one application of nominal yield plot is to specify genotypes for each environment and our results indicated that G7 and G8 were the most suitable genotypes for environment 5 and most unsuitable for E4 and E6. On the other hand, G1 and G2 were suitable for E4 and E6 and unsuitable for E2 and E5. This interpretation is important because in most cases, no genotype is superior everywhere and always, and the introduction of genotypes adaptable to any environment is needed (Olivoto *et al.*, 2019a).

The third type of biplot (grain yield *vs* WAASB) is divided into four quarters (Figure 3-B), in which simultaneous interpretation is performed for average grain yield and stability with WAASB index. Genotypes or environments located in the first quarter, due to their high contribution to GEI, are unstable genotypes or discriminate environments and their performance is lower than the average overall performance (Olivoto *et al.*, 2019a). In this quarter, G8, G7, and G9 were unstable due to high WAASB values. Special compatibility for these genotypes can be examined for some environments. Thus, G7 can be considered adaptable with E5, which the heatmap plot also showed a similar result. In this quarter, E8 had a high discrimination ability due to its highest WAASB index. In the second quarter, G1 and G4 (with higher grain yields) were unstable genotypes due to the high values of WAASB index. In the third quarter, G3 and G6 had lower-than-average overall performance, but they can be considered stable due to low WAASB values. In the fourth quarter, G2, G5 and G10 were highly productive and stable due to the large grain yield and low WAASB values. In nominal yield plot (Figure 3-A), G2 was less stable compared to the other two genotypes (G5, and G10), while based on the WAASB index (Figure 3-B) it was stable. Because all significant principal components used in the calculation of the WAASB index, it shows a better stability interpretion, and the selected genotypes with this index have more reliable stability. The nominal yield plot (Figure 3-A) was used to identify compatible genotypes for specific environments, but the third type of biplot (GY×WAASB) (Figure 3-B), which simultaneously interprets stability and grain yield, can be used for broad adaptation and the identification of stable genotypes for all environments. The WAASB×GY biplot (Figure 3-B) can be used for a simultaneous interpretation of productivity and stability.

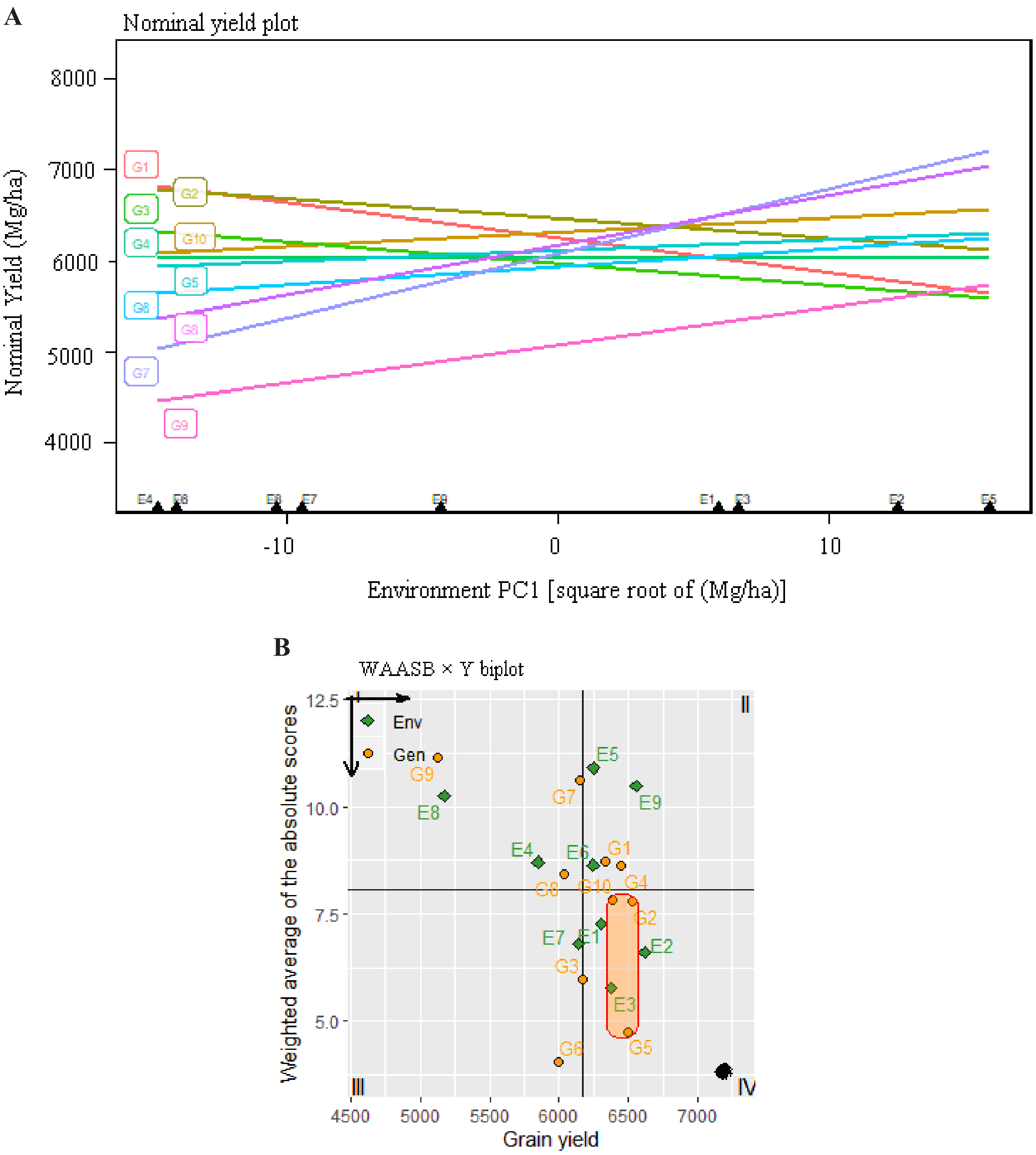

Figure 3. Diagrams for analysis of the grain yield in 10 rice genotypes evaluated over nine environments (combinations of three cultivation years in three locations). **A:** Nominal grain yield plot, **B:** Biplot of the grain yield vs WAASB. a hypothetical highly productive and broadly adapted genotype is depicted by a black circle in the right corner and horizontal and vertical black arrows in the left corner indicate the direction of the increase in grain yield and stability, respectively.

AMMI-based stability indices, such as ASV, have been used successfully in rice to quantify stability (Akter *et al.*, 2014; Bose *et al.*, 2014 a, b; Sharifi *et al.*, 2017; Kumar Das *et al.*, 2018; Rahayu, 2020; Sadimantara *et al.*, 2020). In the present study, since the scores of some genotypes are low in the first two IPCAs (such as G2 and G6), the selection or deletion of these genotypes by indices based on the first two principal components or the corresponding biplots may be incorrect and lead to misinterpretation. Therefore, when the explanation of the first two components is low, the WAASB index is recommended based on the BLUP matrix and the results are more reliable (Olivoto *et al.*, 2019b). Comparing nominal yield plot with the third type of biplot, based on all of the significant principal components, shows the superiority of the WAAS index.

Genotype ranking based on the weights for stability and performance (grain yield)

Figure 4 identifies genotypes by simultaneous selection criteria based on average grain yield (GY) and WAASB stability index. Based on a weight of 50:50 (i.e., having equal importance for grain yield performance and stability), G5, G6, G2, and G3 had the highest WAASBY values (Figure 4) and were stable genotypes. Previously, it was shown that G2 and G5 were superior genotypes in terms of grain yield and stability due to their placement in the fourth quarter (Figure 3-B).

Figure 5 shows the change in the ranking of genotypes according to the weight of grain yield (GY) and stability (WAASB). In the first column on the left side, the ranking of genotypes based on solely the WAASB index indicated that G5 and G6 were the most stable genotypes; while G7 and G9 were the most unstable genotypes. In the last column on the right side, the rankings of genotypes were based solely on grain yield, making G2 and G5 the most superior genotypes. The black rectangle is ranking the genotypes based on the equal weight of stability and grain yield, which is similar to the ranking of genotypes in Figure 4; and therefore, G5 and G6 were the best genotypes when grain yield and stability are equally important. The clusters shown on the left side are used to identify genotypes with similar performance regarding stability and grain yield. Cluster 1 includes G7, G9 and G8, which, according to previous plots, were poorly productive and unstable genotypes. G1 and G4 in the second cluster were high-yielding but unstable genotypes. In the third cluster, there is a stable but low-yielding genotype (G6), which was also a genotype with the yield lower than average grain yieldbut stable (Figure 3-B). In the last cluster, there were G2, G5, G10, and G3, which were highly productive and stable.

A key choice to be made for the WAASB measure is the weights assigned to stability and mean performance. This is a very old problem. A clear explanation of weight for mean performance is attributed to GY; because it is preferable to select highly productive genotypes that do not perform well regarding the broad stability and then consider the adaptability of these genotypes to specific environments to make better recommendations. The blue rectangle in Figure 5 ranks genotypes based on the highest weight for grain yield (65), which therefore, indicated , G5 followed by G6, G2, G10 and G3 as the best genotypes, while, G9 and G7 were the most undesirable genotypes.

In the fourth cluster of Figure 5, G2, G5, G10, and G3 were highly productive and stable genotypes, while based on the nominal yield plot (Figure 3-A),

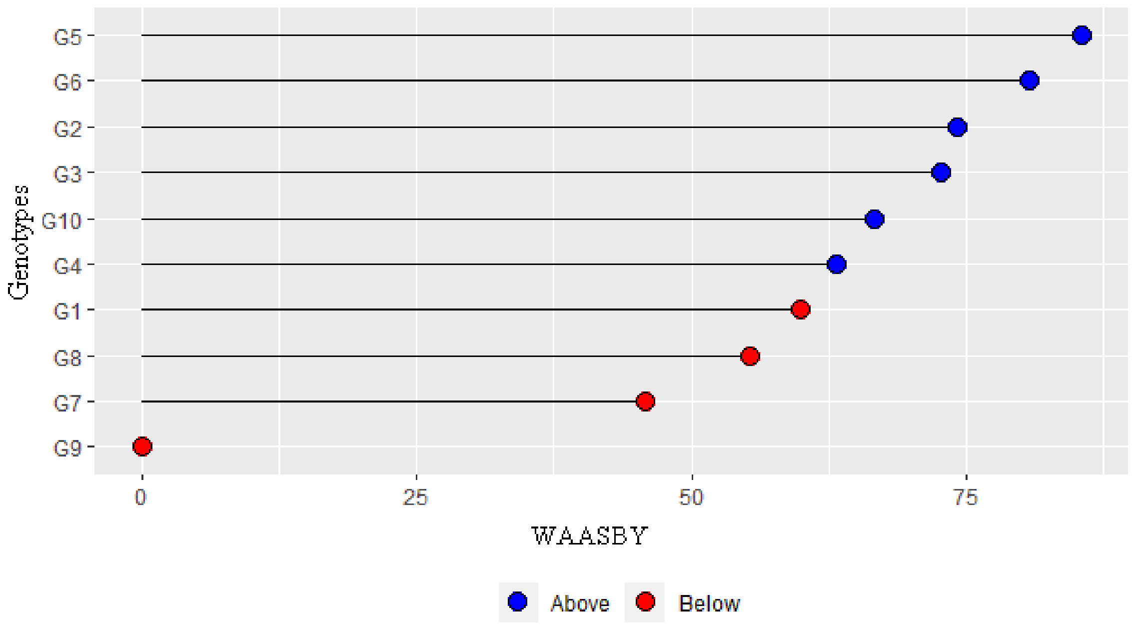

Figure 4. Estimated values of WAASB and mean performance (Y) (WAASBY) for 10 rice genotypes considering the weights of 50 (grain yield) and 50 for (stability).

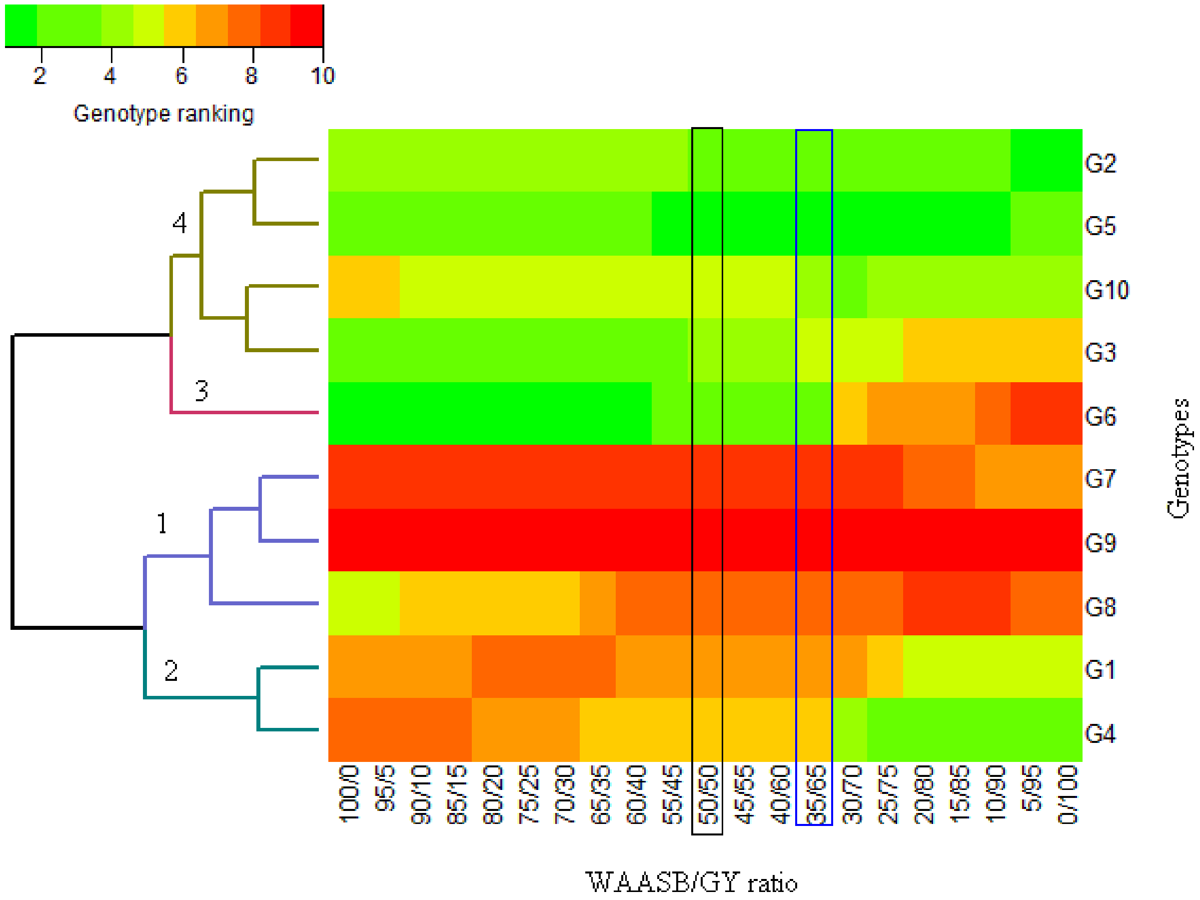

Figure 5. Ranks of 10 rice genotypes considering different weights for stability and yielding. The farthest-left ranks were obtained considering the stability only. The farthest right-ranks were obtained considering the grain yield only. Between the extremes, the ranks were obtained different weights for stability and yield. The four clusters represent four classes of genotypes: (1) Poorly productive and unstable genotypes, (2) productive but unstable genotypes, (3) stable but poorly productive genotypes, and (4), highly productive and stable genotypes.

G2 and G3 were unstable. This indicates the unique role of the WAASB/GY ratio plot in identifying and selecting stable genotypes based on simultaneous selection based on stability and grain yield. Olivoto *et al.* (2019a) stated that WAASB is a mixed-effect model version of the AMMI-based stability indices and have some advantages such as outperform the mixed-effect model to fixed-effect models in terms of predictive accuracy, robustness due to less sensitivity to outliers and joint interpretation of stability and productivity in a bidimensional plot considering all the IPCAs of the model. WAASB has the potential to provide reliable estimates of stability and allowing a joint explanation of performance and stability in a bidimensional plot considering two or more IPCAs. When only the first IPCA is considered, the ranking of some genotypes could be mistakenly calculated. In addition, WAASBY, as a simultaneous selection index, may be useful when different weights should be assigned for the performance of the response variable and stability (Olivoto *et al.*, 2019b). Olivoto *et al.* (2019a) also stated considering genotypes or environments have random effects, thus characterizing a mixed model, the GEI will always be random, which allows the estimation of scores for genotypes and environments and therefore, the same procedures (use of WAASB and WAASBY indices) may be used considering an LMM with random effect for environment or even a completely random-effect model.

Exploratory factor analysis

Factor analysis based on WAASBY values of the measured traits identified three factors with a cumulative variance of 79.35 (Table 3). After the rotation of the varimax, the average communality (b) was 0.79. The first factor includes grain yield, plant height and the number of unfilled grains; the second factor contains the number of tillers and the number of filled grains and the third factor included the thousand grain weight and panicle length (Table 3).

Table 3. Eigenvalues, explained variance, factorial loadings after varimax rotation, and communalities obtained in the factor analysis.

VAR	FA1	FA2	FA3	Communality	Uniquenesses
GY	-0.8874	-0.06602	-0.02387	0.7925	0.2075
PH	-0.7904	-0.05723	0.2098	0.672	0.328
TN	-0.3778	-0.8147	0.08449	0.8137	0.1863
UfGN	-0.9668	0.000883	-0.03651	0.9361	0.06387
FGN	-0.1802	0.8873	-0.08021	0.8263	0.1737
PL	0.3934	0.0459	-0.7686	0.7476	0.2524
TGW	0.1726	-0.108	0.8514	0.7663	0.2337
Eigenvalues	2.83	1.58	1.14		
Variance (%)	40.46	22.61	16.28		
Cumulative variance (%)	40.46	63.07	79.35		
Mean				0.7934979	

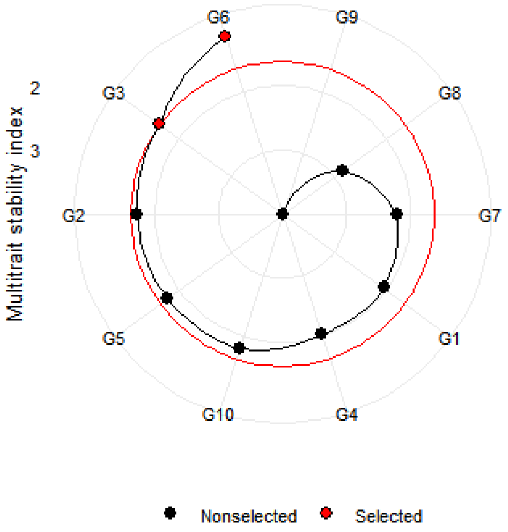

Figure 6. Genotype ranking and selected genotypes for MTSI considering a selection intensity of 15%. This plot is a MTSI (radar) plot, which shows the genotype ranking in ascending order for the MTSI index. The selected genotypes are shown in red and the spiral depicts the cutpoint according to the selection pressure.

Multi-trait stability index (MTSI) and genotype selection

Figure 6 shows the rankings of genotypes based on the multi-trait stability index (MTSI) and indicates G6 (MTSI=1.11) and G3 (MTSI=1.63) as the selected genotypes. The red circle (MTSI=1.63) indicates the cutting point (Olivoto *et al.*, 2019b).

The MTSI Index is a unique and easy selection process that allows simultaneous selection based on performance and stability for breeders and agronomists when having multi trait data (Olivoto *et al.*, 2019a). However, in this study, the results of this index are somewhat different from the results of the WAASBY index only for grain yield (Figure 4 and Figure 5), which may be due to the differential selection of the negative for some traits and positive for other traits.

CONCLUSION

The combination of AMMI and BLUP analyses according to the weight of grain yield (GY) and stability (WAASB) indicated that G2, G5, G10 and G3 had high performances and wide stabilities and can be used for future selection or recommendation programs. Based on the MTSI index, G3 and G6 were selected and due to the low performance of G6; G3 could be a desirable genotype. Based on all of the indices, it seems that G3 and G5 had a significant advantage over all genotypes, while G5 had higher performance and was stable in many methods. Therefore, G5 can be used to determine the best crop manangement to produce the highest grain yeld in research and extension experiments to introducenew cultivars.

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CONFLICTS OF INTEREST

The authors hereby declare that the study was carried out without any financial and/or commercial relationship that could result in a potential conflict of interest.

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