Selection of tropical wheat lines based on classical and modern parameters of adaptability and stability

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Abstract

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The differential response of lines to the variation of environments makes it necessary to use robust biometric tools for efficient evaluation and selection of wheat lines in tropical regions of Brazil. The objective of this work was to select tropical wheat lines with high grain yield, adaptability, and stability for the Central region of Brazil using classic and modern methodologies. For this purpose, three experiments were conducted in the agricultural years of 2018 and 2019 in the state of Minas Gerais, Brazil. The treatments were 26 tropical wheat lines developed by the UFV's Wheat Breeding Program, in addition to two commercial cultivars (checks). Four methodologies were used of adaptability and stability: AMMI, GGE Biplot, Lin and Binns and HMRPGV. The VI 14194, VI 14127, VI 14026 and BRS 264 lines have high grain yield and broad adaptability and stability according to all four methods. AMMI and GGE biplot pointed line VI 141045 with high productivity, adaptability and specific stability for the Alto Paranaíba region.

Keywords: Triticum aestivum L; genotype by environment interaction; AMMI; GGE Biplot; Lin and Binns; HMRPGV
Abbreviations: AEC*:* average environment coordination; AMMI*:* additive main-effects and multiplicative interaction; GEI*:* genotype-environment interaction; GGE*:* genotype plus genotype-environment interaction; GY*:* grain yield; HMGV*:* harmonic mean of the genotypic values; HMRPGV*:* harmonic mean of the relative performance of genotypic values; MET*:* multi-environment trials; REML/BLUP*:* Restricted maximum likelihood/Best linear unbiased prediction; RPGV*:* relative performance of the genotypic values

Introduction

Worldwide, it is estimated that 222.7 million hectares of wheat will be harvested in the 2020/21 harvest, an increase of 2.63% compared to the 2019/20 harvest. The estimated world production of wheat is of 773.6 million tons. In Brazil, the total production expected for the 2021 harvest is 6.1 million tons for the 2021 harvest, a negligible amount when compared to the largest world producer (China), with an expected production of 136.4 million tons for the 2021 harvest (CONAB, 2021). These data reinforce the importance of genetic improvement for the development of cultivars that are more productive and adaptable to tropical conditions so helping Brazil to become self-sufficient in the production of this cereal.

The differential behavior of the lines according to the variation of the environments is known as genotype-environment

interaction (GEI). The presence of significant GEI influences the selection and recommendation of cultivars, requiring the use of criteria and methodologies to quantify such a GEI, increasing the accuracy of selection of superior lines (Cruz et al., 2012). The performance evaluation of lines in multi-environment trials (MET) is a useful tool in the identification and quantification of GEI. The results of MET analysis allow the understanding of the relative contribution of lines and GEI components in the performance of cultivars (Yan, 2000).

Several methodologies can be used to estimate parameters of adaptability and stability in wheat. Among several, we can cite multivariate parametric models (Zobel et al., 1988; Gauch et al., 1996; Yan, 2000), non-parametric models (Lin & Binns, 1988) and mixed models (Resende, 2007).

Methodologies such as Additive main-effects and multiplicative interaction (AMMI, Zobel et al., 1988; Gauch et al., 1996) and Genotype plus Genotype-Environment interaction (GGE Biplot) (Yan, 2000) allow the evaluation of the performance of lines based on biplot interpretation, being very useful and widely used by breeders due to the visual aspect of data interpretation. The method proposed by Lin & Binns (1988) and modified by Carneiro (1998) allows the partitioning of environments into favorable and unfavorable environments, having a great application due to the ease of interpretation and selection of the best lines. The Harmonic mean of the relative performance of genotypic values (HMRPGV) proposed by Resende (2007) is advantageous because it allows to make an integrated evaluation of stability, adaptability and productivity. AMMI, GGE biplot, HMRPGV and Lin & Binns (1988) modified by Carneiro (1998) methods has particularities and is not always unanimous in the selection of promising lines. It is up to the breeder to determine the most appropriate methodologies according to his objectives.

The use of different methodologies for the investigation of the environment genotype interaction in wheat has been reported in the literature (Singh et al., 2019). However, the scarcity of studies related to the selection and recommendation of lines using the parameters of adaptability and stability of tropical wheat lines in Central Brazil justifies the accomplishment of this work, since it presents classic and modern methodologies. In light of this, the objective of this work was to select tropical wheat lines with high grain yield, adaptability, and stability for the Central region of Brazil using classic and modern methodologies.

Material and Methods

Field experiments and plant material
Three experiments were conducted in the 2018 and 2019 harvest seasons in the cities of Rio Paranaíba and Viçosa in the state of Minas Gerais, Brazil. The trial located in Rio Paranaíba was carried out at the experimental farm of the Cooperativa Agropecuária do Alto Paranaíba (Coopadap) (19º21′31″S; 46º07′22″ W, at 1150 m altitude) in 2018 and 2019. The trial located in Viçosa, was carried out in the experimental area Professor Diogo Alves de Melo (20º45′14″S; 42º52′55″ W, at 648 m altitude) belonging to the Department of Agronomy of the Federal University of Viçosa (UFV), in 2019, totaling three environments. The experiments were carried out during the months of May to August and June to October, for Rio Paranaíba and Viçosa, respectively.

Twenty-six tropical wheat lines in the value for cultivation and use (VCU) stage developed by the UFV Wheat Breeding Program were used, in addition to two commercial cultivars recommended for sowing in the Center-South region of Brazil: BRS 264 (Embrapa) and CD 151 (Coodetec). The experimental design used was a randomized complete block design with three replications. Each plot was composed of six, 5-m-long cultivar rows, spaced at a 0.2 m, with a sowing density of 350 seeds m^{-2}. Only the three central cropping rows were considered as a useful area for evaluation.

Management
The experiments were carried out under sprinkler irrigation to supply the water needs of the crop during its development. Fertilizations were carried out according to the chemical analysis of the soil to meet the nutritional requirements of the crop. For sowing, 300 kg ha^{-1} of the formulated 08-28-16 (nitrogen, phosphorus, and potassium) were applied. In coverage, 90 kg ha^{-1} of nitrogen was applied in the form of urea (45%) split into two stages of development (tillering and booting stages). The other cultural treatments were carried out according to the technical recommendations for the cultivation of wheat (Embrapa, 2018).

Evaluated trait
After harvesting, the plants in each plot were threshed to obtain the grain mass, which were weighed and standardized to 13% moisture. Finally, the values were transformed to kg ha^{-1} to determine the grain yield estimate (GY).

Statstical analyses
•   Analysis of variance
Initially, individual analysis of variance and the homogeneity test of the residual variances were performed using the Hartley F-maximum test, using the criterion that the relationship between the largest and the smallest residual mean square do not exceed the 7:1 ratio. Then, a joint analysis of variance was performed, assuming all the model effects, ex-

cept the residual, to be fixed. After a significant interaction, GEI was decomposed into a simple and complex part (Cruz and Castoldi, 1991) and with the dissimilarity between environments. These analyzes were made using the GENES software (Cruz, 2016).

• Modern method – Mixed models

For the analysis of adaptability and stability via mixed models the method of the harmonic mean of the relative performance of the genotypic values (HMRPGV) proposed by Resende (2007) was used. Genotypic values were predicted by the REML/BLUP methodology in the Selegen software (Resende, 2016): $y = X_r + Z_g + W_i + e$, where y is the vector of the data; r is the vector of the replication effects (fixed effect); g is the vector of the genotypic effects (random effect) ($g \sim N(0, \sigma_g^2)$), where σ_g^2 is the matrix of genotypic variances; i is the vector of the GEI (random effect); and e is a vector of (random) errors ($e \sim N(0, \sigma_g^2)$), where σ_g^2 is the matrix of residual variance. X, Z e W corresponds to the incidence matrices for r, g and i, respectively.

The harmonic mean of the genotypic values (HMGV), relative performance of the genotypic values (RPGV) and harmonic mean of the relative performance of the genotypic values (HMRPGV) were obtained by the following expressions: $HMGV = n/\sum_{j=1}^{n}(1/Vg_{ij})$, where n is the number of environments where the genotype j; Vg_{ij} is the genotypic value of the genotype i in the environment j; $RPGV = 1/n \times (\sum_{j=1}^{n} Vg_{ij})/M_j$, where M_j is the average performance of lines in the environment j; $HMRPGV = n/\sum_{j=1}^{n} \times 1/ Vg_{ij}/\mu_j$. Finally, the RPGV and HMRPGV of each genotype were multiplied by the general average of the lines. These values were also estimated in the Selegen software (Resende, 2016).

• Classical methods

The Lin and Binns (1988) methodology were used to determine the performance of the 28 lines evaluated against the three tested environments. In this method, the general performance of the lines is given by the average square of the distance between the average of the cultivar and the maximum average response for all sites, so that lines with lower values correspond to the lines with better performance. The stability parameter estimate is given by the following expression: $P_{ig} = \sum_{j=1}^{n} (Y_{ij} - M_j)^2/2n$ where: P_{ig} is the estimate of the stability parameter for genotype i; Y_{ij} is the grain yield of the i-th genotype in the j-th environment; M_j is the maximum grain yield in the environment j; n is the number of environments. Then, the model described above was decomposed to group the genotypes into favorable and unfavorable environments according to the methodology proposed by Carneiro (1998): $P_{if} = \sum_{j=1}^{f} (Y_{ij} - M_j)^2/2f$ and $P_{id} = \sum_{j=1}^{f} (Y_{ij} - M_j)^2/2d$, where: P_{if} is the estimate of the stability parameter for the favorable environments; P_{id} is the esti-

mate of the stability parameter for the unfavorable environments; f is the number of favorable environments; and d is the number of unfavorable environments.

The AMMI analysis (Zobel et al., 1988; Gauch et al., 1996), adjusts the genotypic and environmental additive effects through analysis of variance (ANOVA) and then adjusts the multiplicative effects of the interaction using the principal component analysis (PCA), according to the model (Zobbel et al., 1988) $Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{n} \lambda_k \gamma_{ik} \alpha_{jk} + p_{ij} + \epsilon_{ij}$, where: Y_{ij} is the grain yield of the genotype i in the environment j; μ is the grand mean; g_i is the fixed effect of the genotype i; e_j is the fixed effect of the environment j; λ_k is the k-th singular value of the interaction matrix; γ_{ik} is the k-th singular vector of the i-th genotype; α_{jk} is the k-th singular vector of the j-th environment; p_{ij} is the residual of the model; e ϵ_{ij} is the polled random error. This analysis was performed in the R software version 4.0.2 (R Core Team, 2018) using the function performs_ammi () of the R package metan (Olivoto & Lúcio, 2020) version 1.7.0.

The analysis via GGE Biplot allows the graphical visualization of the data matrix. It considers the main effect of the genotype together with the genotype-by-environment interaction. Such a methodology is described by the following model (Yan et al., 2000): $Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{1i} \eta_{1j} + \lambda_2 \xi_{2i} \eta_{2j} + \epsilon_{ij}$, where: Y_{ij} is the grain yield of the genotype i in the environment j; μ is the grand mean; β_j is the effect of the environment j; λ_1 e λ_2 are the eigenvalues associated with PC1 and PC2 respectively; ξ_{1i} e ξ_{2i} are the scores for PC1 and PC2 axes, respectively, for the genotype i; η_{1j} e η_{2j} are the scores for PC1 and PC2 axes, respectively, for the environment j; and ϵ_{ij} is the polled random error.

Results and Discussion

Individual analysis of variance

There was a significant difference ($p < 0.05$) for grain yield of the lines in the three environments (Table 1). The general average in Rio Paranaíba 2018, Rio Paranaíba 2019, and Viçosa 2019, were 5633.68 kg ha^{-1}, 3364.58 kg ha^{-1} and 3987.71 kg ha^{-1}, respectively. The CV for these locations was 7.09%, 10.7%, and 10.98%. It is observed that the coefficients of variation were of low magnitude. The coefficients of genotypic determination (h2) were 82.62%, 68.78%, and 85.81% for Rio Paranaíba 2018, 2019, and Viçosa 2019, revealing a greater contribution of the genotypic constitution.

• *Joint analysis of variance, genetic parameters, and environmental dissimilarity*

The result of the joint analysis of variance revealed a significant ($p < 0.05$) difference for the GEI component, show-

ing the differential behavior of the lines in the environments. For genotype and environment effects, there was also a significant (p <0.05) difference (Table 1).

The analysis of variance allows the partitioning of phenotypic variance into three components: genotypic component, GEI component, and residual variance. The component estimates in Table 1 revealed that there was a greater contribution of the GEI interaction component to grain yield, characterizing 50.20% of the phenotypic variance, while the residual variance and the genotypic component, corresponds to 33.10% and 16.70%, respectively, of the total variance. It was observed that 67% of the GEI variance is represented by

genotypic effects, indicating that the genotypic constitution of the lines contributed significantly to the average performance. Even so, it is known that quantitative characters such as grain yield are strongly influenced by the effect of the environment (Piepho et al., 2012).

The CVg, responsible for quantifying the share of the genotypic variation in the total variation, was 6.56% (Table 1). It is also observed that the residual variation coefficient (CVe = 9.22%), as well as the relative coefficient (CVg / CVe = 0.71), were satisfactory for the set of tests, which allows inferring high accuracy and good precision in conducting the experiments (Resende and Duarte, 2007). In this work, a high

Table 1. Individual analysis of variance for the three environments, Analysis of variance for the AMMI model, genetic parameters for grain productivity (kg ha⁻¹) and estimates of the correlation between environments (upper diagonal) and percentage values of the complex part (lower diagonal) resulting from the decomposition of the interaction between genotypes and pairs of environments by the methodology of Cruz & Castoldi (1991) of 28 tropical wheat lines evaluated in three environments in the State of Minas Gerais in the years 2018 and 2019

Individual analysis					
Environments	MS	Fc (p <0.05)	Mean	CVe	h^2
Rio Parnaíba 2018	918635.29	5.75	5633.68	7.09	82.62
Rio Parnaíba 2019	414943.75	3.20	3364.58	10.70	68.78
Viçosa 2019	1353480.27	7.05	3987.71	10.98	85.81
Joint analysis and AMMI					
Source of variation[1]	DF	MS	Fc (p < 0.05)	GEI explained (%)	GEI accumulated (%)
Block/Env	6	357717.77			
Genotype (G)	27	886617.41*	5.56		
Environment (A)	2	115910623.90*	324.03		
GxA	54	886230.05*	5.56		
PC1	28	1266368.40*	7.94	74.10	74.10
PC2	26	476850.30*	2.99	25.90	100.00
Residual	162	159521.42			
Genetic parameters					
Mean		4332.64			
		80788.44			
		242236.21			
		159521.42			
H² (%)		82.01			
ICC		33.62			
CVe (%)		9.22			
CVg (%)		6.56			
CVg/CVe		0.71			
Dissimilarity between environments					
Ambientes	Rio Parnaíba 2018	Rio Parnaíba 2019		Viçosa 2019	
Rio Parnaíba 2018		0.22		-0.13	
Rio Parnaíba 2019	80.32			0.02	
Viçosa 2019	104.96	84.31			

[1] , Genotypic variance; , Genotype-environment interaction variance; , residual variance; H², Genotypic coeficient of determination; ICC, intraclass correlation coefficient; CVe, residual coefficient of variation; CVg, genotypic coefficient of variation

* Significant at 5% probability error

value was obtained for the coefficient of genotypic determination (H^2 = 82.01%), which indicates that a large part of the observed phenotypic variance is due to the genotypic variance of the lines.

The decomposition of the GEI revealed that there was a predominantly complex interaction (Table 1). This result can be explained due to the low values found in the correlation estimate between environments. Cruz et al. (2012) classified the GEI as simple and complex. The simple interaction is characterized by the differential response of the lines according to the variation of the environment; however, there is no change in the ranking of the lines in terms of productive performance. In the complex interaction, there is an inversion

in the ranking of superior lines. Thus, the genotype of superior performance in one environment may not have the same performance in another. This fact minimizes the magnitude of the association between phenotypic and genotypic values, influences the prediction of selection gains, and makes it difficult to recommend broadly adapted lines (Shukla et al., 2015). In this case, the breeder is responsible for assessing its magnitude and significance, as well as adopting procedures to minimize or take advantage of it (Cruz et al., 2012).

According to Santos et al. (2016), when there is a complex interaction, the simple analysis of the GEI does not provide sufficient information on the performance of lines across the environments, requiring further studies on adaptability and
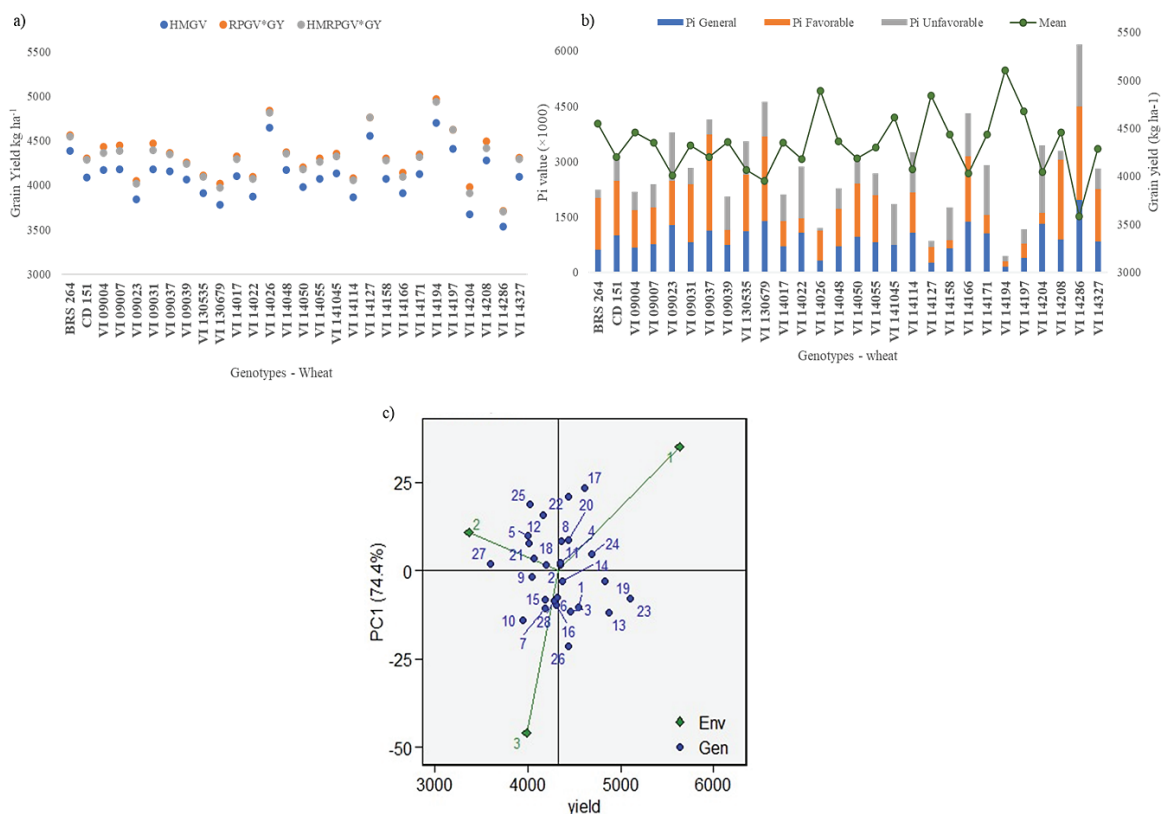

Fig. 1. A – Stability of genotypic values (HMGV), adaptability of genotypic values multiplied by the general average (RPGV * GY) and stability and adaptability of genotypic values multiplied by the general average (HMRPGV * GY) for grain yield (kg ha⁻¹); B – Adaptability and stability parameters obtained by the method of Lin & Binns (1988) modified by Carneiro (1998) through the decomposition of Pi into favorable and unfavorable environments; C– AMMI1 biplot for grain yield (kg ha⁻¹) of 28 tropical wheat lines evaluated in three environments in the State of Minas Gerais in 2018 and 2019

Lines: 1 = BRS 264; 2 = CD 151; 3 = VI 09004; 4 = VI 09007; 5 = VI 09023; 6 = VI 09031; 7 = VI 09037; 8 = VI 09039; 9 = VI 130535; 10 = VI 130679; 11 = VI 14017; 12 = VI 14022; 13 = VI 14026; 14 = VI 14048; 15 = VI 14050; 16 = VI 14055; 17 = VI 141045; 18 = VI 14114; 19 = VI 14127; 20 = VI 14158; 21 = VI 14166; 22 = VI 14171; 23 = VI 14194; 24 = VI 14197; 25 = VI 14204; 26 = VI 14208; 27 = VI 14286 e 28 = VI 14327. Environments: 1 = Rio Paranaíba 2018; 2 = Rio Paranaíba 2019 e 3 = Viçosa 2019

stability for the selection and recommendation of lines.

- *Harmonic mean of the relative performance of genotypic values*

The genotypic values of stability (HMGV), adaptability based on GY scale (RPGV * GY), and simultaneous selection by stability and mean performance based on GY scale (HMRPGV * GY) of the 28 lines evaluated in the three environments by the HMRPGV methodology are shown in Figure 1a.

The top six lines (VI 14194, VI 14026, VI 14127, VI 14197, BRS 264 and VI 14208) with the best genotypic values for stability (HMGV) and adaptability (PRGVG * GY) were also the best performers in the joint analysis of adaptability and stability of the genotypic values multiplied by the general average (HMRPGV * GY). The most productive, adapted, and stable line in the three environments was VI 14194. Of the two commercial cultivars evaluated in this study, only BRS 264 was in the group of lines with the highest values for HMGV, PRGVG * GY, and HMRPGV * GY simultaneously. This cultivar presented GY only lesser than the lines VI 14194, VI 14026, VI 14127, and VI 14197. These estimates suggest the high productive potential of these lines combined with the high adaptability and stability of production, allowing their recommendation for cultivation in the Central and South-Central regions of Brazil.

The analysis of genotypic stability based on HMGV is related to the dynamic concept of stability since it is associated with grain productivity. Thus, lines with high HMGV values are productive and stable in different environments. The selection based on HMGV*GY takes into account the average yield and the adaptability of the lines. In this sense, the best lines are the most productive and best able to respond to variations in the environment. The joint analysis of these factors given by HMRPGV * GY allows the selection considering mean performance, stability, and adaptability simultaneously (Woyann et al., 2019).

The REML/BLUP methodology is advantageous because it allows the interpretation of genotypic values already penalized or capitalized by the adaptability and stability estimates. However, this method does not allow the analysis of the relative performance of lines in specific environments, which limits the identification and selection of potential lines with adaptability and / or stability restricted to certain environments (Resende, 2007).

- *Lin and Binns*

Through the methodology of Lin and Binns (1988) modified by Carneiro (1998) it is possible to observe the averages of productivity, the values of general Pi, favorable Pi,

and unfavorable Pi of the 28 lines in the three environments (Figure 1b).

Considering the general Pi it is observed that the first five lines (VI 14194, VI 14026, VI 14127, VI 14197 and BRS 264) with the lowest values, that is, the most adapted and stable, are also the ones with the best performance by the methodology HMRPGV, therefore, there is an agreement between these two methods in the identification of superior lines. Paula et al. (2014) also reported similarities between these two methods when studying the adaptability and stability of 15 sugarcane clones in nine environments in the state of Minas Gerais.

Genotype VI 14194 showed the lowest overall Pi value. It should be noticed that, in addition to presenting the best performance in terms of adaptability and general stability, the VI 14194 strain obtained the highest average productivity (5098.99 kg ha^{-1}), which allows it to be characterized as an ideal genotype since its high productive performance is consistent in heterogeneous environments.

The lines VI 141045 and VI 14194, with average productivity of 4614.62 kg ha^{-1} and 5098.99 kg ha^{-1} respectively, had the lowest Pi values in favorable environments, which indicate a good capacity of these lines to respond positively to improvements in environmental conditions. The lines VI 14026 and VI 14194 with average productivity of 4891.43 kg ha^{-1} and 5098.99 kg ha^{-1} respectively, had the lowest Pi values in unfavorable environments, which reveal their low sensitivity to the adversities of the environment, reflecting a high productive stability (Cruz et al., 2012).

- *AMMI analysis*

The PC1 and PC2 main components explained 74.10 and 25.90% of the total variation ($p < 0.05$) (Table 1). Figure 1c shows the behavior of the lines as a function of the environments through the biplot. The closer the lines are to the origin of the biplot, the greater the stability. Lines located in the same quadrant of a specific environment, on the other hand, are more adapted to this environment (Veenstra et al., 2019).

AMMI analysis allows the visualization of mega environments, which makes it possible to identify lines with good performance and adapted to specific environments. Figure 1c shows the formation of three environments. In environment 1 are the lines that showed above-average productivity, showing adaptability to this specific environment, with the lines VI 14197, VI 141045 and VI 14158 having the best performance. According to Paderewski et al. (2016) the existence of lines with specific adaptability allows the subdivision of the cultivation region or breeding program into two or more mega environments, thus enabling the exploitation of adaptive advantages and commercial recommendation.

Environments 2 and 3 group the lines that had a below-average performance. The lines distributed in these environments could not be selected even if they had high adaptability and stability, since their productive performance is not satisfactory. It is also observed that environment 2 was the one that least contributed to the effects of GEI captured by PC1 (Figure 1c). However, the low productive performance of these lines limits the recommendation for cultivation.

The selection of the best lines must be carried out based on the productivity estimates, as well as on the broad adaptability (Gauch, 2013). In this sense, the highly productive and broadly adapted lines were VI 14194, VI 14026, VI 14127, BRS 264, and VI 09004. Singh et al. (2019), investigating the GEI in wheat lines, also used the AMMI methodology to select highly productive and stable lines in different environments.

• *GGE Biplot*

The total variation explained by the two main components corresponds to 86% (Figure 2). According to Yan et al., (2000) the first component (PC1) indicates the degree of adaptability of the lines, being highly correlated with grain yield. The second main component (PC2) is related to genotypic stability.

Figure 2a shows the formation of six different sectors; this is an efficient tool for analyzing the performance of lines in mega environments. The three environments were distributed in the two sectors at the bottom of the biplot. The Rio Paranaíba 2018 and Rio Paranaíba 2019 environments grouped into the same mega environment and share lines with above-average grain yield, which reveals homogeneity between these environments. According to Mushay et al. (2020), in these cir-
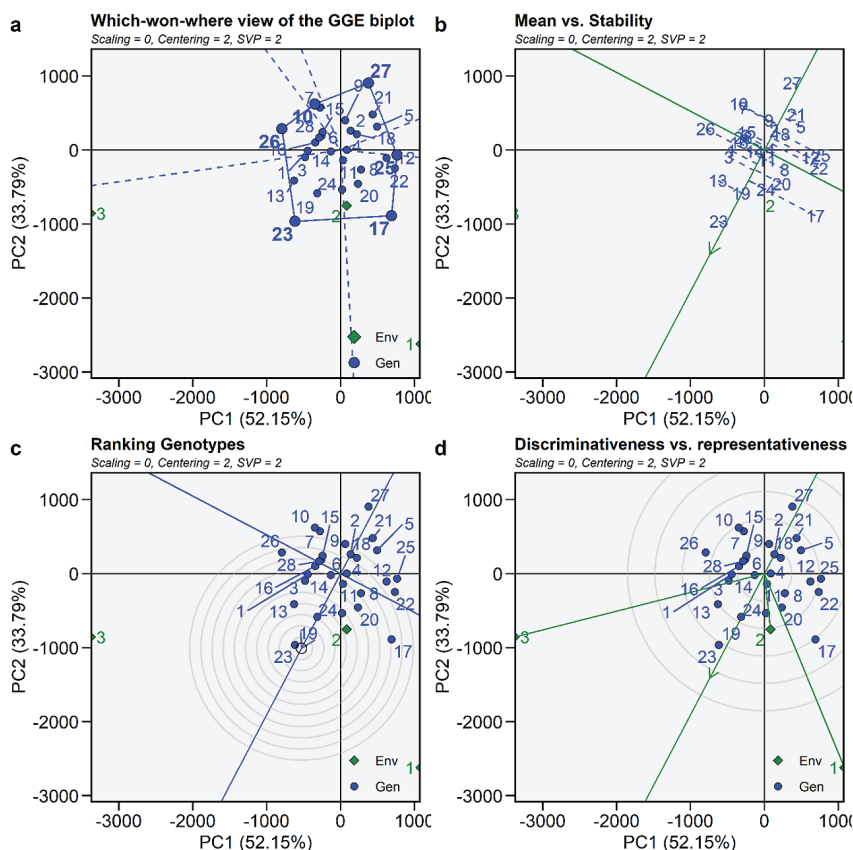

Fig. 2. Which-won-where pattern (A), stability (B), ideal genotype (C) and ideal environment (D) obtained by the GGE biplot method for grain productivity (kg ha^{-1}) of 28 tropical wheat lines evaluated in three environments in the State of Minas Gerais in 2018 and 2019.
Lines: 1 = BRS 264; 2 = CD 151; 3 = VI 09004; 4 = VI 09007; 5 = VI 09023; 6 = VI 09031; 7 = VI 09037; 8 = VI 09039; 9 = VI 130535; 10 = VI 130679; 11 = VI 14017; 12 = VI 14022; 13 = VI 14026; 14 = VI 14048; 15 = VI 14050; 16 = VI 14055; 17 = VI 141045; 18 = VI 14114; 19 = VI 14127; 20 = VI 14158; 21 = VI 14166; 22 = VI 14171; 23 = VI 14194; 24 = VI 14197; 25 = VI 14204; 26 = VI 14208; 27 = VI 14286 e 28 = VI 14327. Environments: 1 = Rio Paranaíba 2018; 2 = Rio Paranaíba 2019 e 3 = Viçosa 2019

cumstances, environments have similar power to discriminate lines. This similarity between the two environments can be explained by the fact that the tests were conducted in the same location, with variation only between the years of evaluation.

According to Bányai et al. (2020), stability analysis based on biplots is used not only to group environments based on the similarity of their effects on yield components but also to identify lines with superior performance and stability in one or more groups of environments. Thus, the genotype VI 141045 is the vertex genotype of the sector in which the Rio Paranaíba 2018 and 2019 environments are located. This means that this genotype was the one with the best performance in these two environments. Similar to the AMMI methodology, the genotype VI 141045 could be recommended for the municipality of Rio Paranaíba with specific adaptability in mind. It is worth mentioning that this line presented the lowest Pi value for favorable environment by the Lin & Binns (1988) methodology, which indicates that the municipality of Rio Paranaíba offers favorable conditions for the response of this genotype. The VI 14194 lines had the best performance in Viçosa 2019. In the sectors corresponding to the upper part of the biplot are the lines that have not had satisfactory productive performance throughout the environments by the GGE biplot method.

Figure 2b allows visualizing the lines regarding productive performance and stability. The straight line with an arrow that passes through the origin of the biplot, called Average Environment Coordination (AEC), points to the lines with the best productive performance. The genotype line perpendicular to the AEC axis represents performance variability in terms of stability. Thus, the increasing order of genotype productivity starts from the bottom diagonal of the biplot. The lines VI 14194, VI 14026, VI 14127, VI 141045, and VI 14197 were the most productive according to the GGE biplot methodology. In addition to presenting above-average productivity, the lines VI 14194, VI 14127, and VI 14197 demonstrated high production stability considering the three environments.

A genotype can only be considered ideal when it has high productive performance associated with high stability. Similar to the HMRPGV, Lin & Binns (1988) and AMMI methodologies, the lines VI 14194 and VI 14127 can be considered ideotypes by GGE biplot analysis, which justifies their recommendation considering broad adaptability and production stability (Figure 2c). Kendal & Sener (2015) also selected wheat lines with satisfactory stability associated with high productivity and grain quality using the GGE biplot methodology. According to Paderewski et al. (2016) the existence of lines with high productivity, wide adaptability, and production stability is beneficial for breeding programs

due to the reduction of costs with multi-environment tests. Besides, these cultivars can be recommended for more than one growing region.

Figure 2d made it possible to identify ideal test environments for recommending lines adapted to mega environments. Thus, it was observed that Rio Paranaíba 2018 and Viçosa 2019 were more discriminating compared to Rio Paranaíba 2019. On the other hand, Rio Paranaíba 2019 was more representative. Mushay et al. (2020) pointed out that ideal environments for the selection of lines must be discriminating and representative at the same time. Test environments that are discriminating, but not representative, can be used to select lines adapted to specific environments. Representative and homogeneous environments are ideal for the selection of broadly adapted lines (Bányai et al., 2020).

- *Join methods review*

There was a general agreement among the methodologies, identifying VI 14194, VI 14127, VI 14026, and BRS 264 as highly productive, broadly adapted, and stable lines. In terms of adaptability and stability for specific environments, the VI 141045 line was more productive and adapted to the municipality of Rio Paranaíba according to the AMMI and GGE biplot methodologies. Through the Lin & Binns (1988) methodology, modified by Carneiro (1998), it is possible to infer that the municipality of Rio Paranaíba offers adequate conditions for the expression of the productive potential of genotype VI 141045. The AMMI method was not able to identify lines with productivity above-average and with adaptability and production stability for the municipality of Viçosa-MG. In contrast, the GGE Biplot method pointed out the VI 14194 line as being productive, with adaptability and stability for this location.

Conclusion

The lines VI 14194, VI 14127, VI 14026, and BRS 264 have the potential for selection in the tropical region of Central Brazil, whose objective is high productivity, broad adaptability, and production stability.

The VI 141045 genotype demonstrated high productive performance and specific adaptability and production stability for the Alto Paranaíba region.

The lines VI 14026 and VI 14194 had higher productivity and adaptability to unfavorable environments.

Modern methods such as HMRPGV can be used to select productive, adaptable, and stable lines due to the ease of interpretation of the results. Classic methods (Lin and Binns, AMMI, and GGE Biplot) should be used when the goal is to select superior lines in specific environments.

References

Bányai, J., Kiss, T., Gizaw, S. A., Mayer, M., Spitkó, T., Tóth, V., Kuti, C., Mészáros, K., Láng, L., Karsai, I. & Vida, G. (2020). Identification of superior spring durum wheat lines under irrigated and rain-fed conditions. *Cereal Research Communications*, *48*, 355-364.

Carneiro, P. C. S. (1998). New methodologies for analyzing adaptability and behavior stability. Tese, Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.

CONAB (2021). Monthly wheat history. https://www.conab.gov.br/info-agro/analises-do-mercado-agropecuario-e-extrativista/analises-do-mercado/historico-mensal-de-trigo (accessed 19th feb 2021)

Cruz, C. D. (2016). Genes Software – extended and integrated with the R, Matlab and Selegen. *Acta Scientarum*, *38 (4),* 547-552.

Cruz, C. D. & Castoldi, F. L. (1991). Simple and complex decomposition in parts of the genotypes × environments interaction. *Revista Ceres*, *38 (219),* 422430.

Cruz, C. D., Regazzi, A. J. & Carneiro, P. C. S. (2012). Biometric models applied to genetic improvement. UFV, Viçosa, Minas Gerais, Brazil.

EMBRAPA (2018). Technical information for wheat and triticale. http://ainfo.cnptia.embrapa.br/digital/bistream/item/196239/1/ID44570-2018InfTecTrigoTriticale2019.pdf (accessed 30th May 2020).

Gauch, Jr., H. G. (2013). A simple protocol for AMMI analysis of yield trials. *Crop Science*, *53 (5),* 1860-1869.

Gauch, H. G. & Zobel, R. W. (1996). AMMI analysis in yield trials. In: Kang, M. S., Gauch, H. G., *Genotype by environment interaction*, CRC Press, New York, 1-40.

Kendal, E. & Sener O. (2015). Examination of genotype × environment interactions by GGE biplot analysis in spring durum wheat. *Indian Journal of Genetics*, *75 (3),* 341-348.

Lin, C. S. & Binns, M. R. (1988). A superiority measure of cultivar performance for cultivar x location data. *Canadian Journal of Plant Science*, *68 (3),* 193-198.

Mushayi, M., Shimelis, H., Derera, J., Shayanowako, A. I. T. & Mathew, I. (2020). Multi-environmental evaluation of maize hybrids developed from tropical and temperate lines. *Euphytica*, *216 (84),* 1-14.

Olivoto, T. & Lúcio, A. D. (2020). Metan: An R package for multi-environment trial analysis. *Methos Ecol. Evol.*, *11, (6),* 783-789.

Paderewski, J., Gauch Jr, H. G., Madry, W. & Gacek, E. (2016). AMMI analysis of four-way genotype × location × management × year data from a wheat trial in Poland. *Crop Science*, *56 (5),* 2157-2164.

Paula, T. O. M., Marinho, C. D., Souza, V., Barbosa, M. H. P., Peternelli, L. A., Kimbeng, C. A. & Zhou, M. M. (2014). Relationships between methods of variety adaptability and stability in sugarcane. *Genetics and Molecular Research*, *13 (2),* 4216-4225.

Piepho, H. P., Williams, E. R. & Maddlen, L. V. (2012). The use of two-way linear mixed models in multitreatment meta-analysis. *Biometrics*, *68 (4),* 1269-1277.

R Core Team (2018). R: a language and environment for statistical computing. Vienna.

Resende, M. D. V. (2007). Mathematics and statistics in the analysis of experiments and in genetic improvement. Colombo, Paraná, (Br).

Resende, M. D. V. (2016). Software Selegen-REML/BLUP: a useful tool for plant breeding. *Crop Breeding and Applied Biotechnology*, *16 (4),* 330-339.

Resende, M. D. V. & Duarte, J. B. (2007). Precision and quality control in cultivar evaluation experiments. *Pesquisa Agropecuária Tropical*, *37 (3),* 182-194.

Santos, A., Ceccon, G., Teodoro, P. E., Correa, A. M., Alvarez, R. D. C. F., Silva, J. F. & Alves, V. B. (2016). Adaptability and stability of erect cowpea lines via REML/BLUP and GGE Biplot. *Bragantia*, *75 (3),* 299-306.

Shukla, S., Mishra, B. K., Mishra, R., Siddiqui, A., Pandey, R. & Rastogi, A. (2015). Comparative study for stability and adaptability through different models in developed high the baine lines of opium poppy (*Papaver somniferum* L.). *Industrial Crops and Products*, *74*, 875-886.

Singh, C., Gupta, A., Gupta, V., Kumar, P., Sendhil R., Tyagi, B. S., Singh, G., Chatrath, R. & Singh, G. P. (2019). Genotype × environment interaction analysis of multi-environment wheat trials in India using AMMI and GGE biplot models. *Crop Breeding and Applied Biotechnology*, *19 (3),* 309-318.

Veenstra, L. D., Santantonio, N., Jannink, J. L. & Scorells, M. E. (2019). Influence of genotype and environment on wheat grain fructan content. *Crop Science*, *59 (1),* 190-198.

Woyann, L. G., Zdziarski, A. D., Baretta, D., Meira, D., Dallacorte, L. V. & Benin, G. (2019). Selection of high-yielding, adapted and stable wheat lines in preliminary trials. *Crop Breeding and Applied Biotechnology*, *19 (4),* 412-419.

Yan, W., Hunt, L. A., Sheng, Q. & Szlavnics, Z. (2000). Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Science*, *40* (3), 597-605.

Zobel, R. W., Wright, M. J. & Gauch, Jr., H. G. (1988). Statistical analysis of a yield trial. *Agronomy Journal*, *80 (3),* 388-393.