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Stability of wheat genotypes for grain yield using the GGE Biplot methodology

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ABSTRACT

Wheat plays an important role in global agriculture, being one of the most widely cultivated cereals. Wheat cultivation in each region depends on the stability of grain yield in the given environment. The objective of this study was to identify the most productive and stable genotypes over three years of cultivation in the municipality of Frederico Westphalen, using GGE Biplot analysis. Twelve wheat genotypes were cultivated in a randomized complete block design, with three replicates over three years from 2019 to 2021. The experimental units consisted of six 4-meter rows, spaced 0.17 m apart. Grain yield was measured 3 meters from the four central rows. The data obtained was subjected to analysis of variance, which verified interactions between genotypes and years, and then performed GGE Biplot analysis. The grain yield of the wheat genotypes was influenced by the environmental conditions during the three years of cultivation. The genotypes UFSMFW 1-07 and USFMFW 1-04 were more productive in specific years, with the best performance for grain yield and stability being that of the genotype UFSMFW 1-08.

Keywords: *Triticum aestivum* L.; plant breeding; cereals.

INTRODUCTION

Wheat (*Triticum aestivum* L.) plays an important role in the global agricultural scenario, being one of the most cultivated cereals. Brazil produced approximately 8,1 million tons of wheat in the 2023 harvest. Wheat stands out in the south of Brazil, mainly in Paraná and Rio Grande do Sul, being the main winter crop. On the national scene, the cultivated area was 3,5 million hectares destined for cereal cultivation in the 2023 harvest, with the southern region responsible for more than 90% of the sown area.(1)

Wheat is used in human and animal nutrition, becoming a cereal of great importance for national and global agriculture. According to Sousa et al.,(2) wheat was one of the great pioneers when we talk about genetic improvement, which began in 1919, in the 70s that wheat research grew rapidly with the creation of research centers, such as, for example Embrapa. At that time, research and breeding companies incorporated genes that are related to plant size and photoperiod into the national wheat genome, thus obtaining plants of smaller stature and shorter flowering time, favoring the production system.

The cultivation of a given cultivar in a specific region is associated with its adaptability and stability in terms of grain yield.(3) If there is the possibility of genotype and environment interaction, their adaptability and stability must be evaluated. According to Branquinho et al.,(4) the interaction between genotype and environment is responsible for the response in the performance of genotypes under different environmental conditions, complicating the selection and launch of new cultivars.

Among the current methodologies that have adequately clarified the main effects (genotype and environment) and their interaction, two stand out: the additive main effects and multiplicative interaction model (AMMI) and the analysis of the main effects of genotype and genotype interaction and environment (GGE Biplot). These methodologies based on Biplot graphs can inform much of the variation in the data set regarding the relative importance of the genotype and its interaction with the environment.(5)

Testing genotypes in various environments helps in the selection of cultivars with broad adaptation and also adaptation in a specific environment.(6) Furthermore, the evaluation of genotypes in specific environments allows the indication of new cultivars that express their maximum grain yield potential.(7) Therefore, the objective of the work was to identify the most stable and promising genotypes for grain yield over three years of cultivation in the municipality of Frederico Westphalen, using the GGE Biplot.

MATERIAL AND METHODS

The experiment was conducted in the agricultural years 2019, 2020 and 2021, in the experimental area of the Federal University of Santa Maria Campus Frederico Westphalen, located at coordinates 27º23'50” S, 53º25'34” W, and with an altitude of approximately 480 meters. The site's soil is characterized as Dystrophic Red Oxisol.(8) The climate is classified as humid subtropical (Cfa) according to Köppen, with high mean annual precipitation, around 1,800 and 2,100 mm, well distributed throughout the year.(9)

Twelve treatments were evaluated, 10 wheat lines: UFSMFW 1-01, UFSMFW 1-02, UFSMFW 1-03, UFSMFW 1-04, UFSMFW 1-05, UFSMFW 1-06, UFSMFW 1-07, UFSMFW 1-08, UFSMFW 1-09 and UFSMFW 1-10 and two controls: Quartzo and Tbio Toruk.

The design used to conduct experiments was randomized blocks, with three replications. Each experimental unit was composed of 6 lines 4 meters long and spaced 0.17 m apart. The experiments were implemented using the direct sowing system on 06/05/2019, 05/29/2020 and 05/24/2021, with a seed density used of 330 suitable seeds per seeds per square meter.

The base fertilization was carried out with N-P_2O_5-K_2O of the 09-25-15 formulation, following soil analysis and the nitrogen fertilization was supplemented in coverage, split 50% in the physiological double-ring stage and 50% in the terminal spikelet, as recommended for the culture. Phytosanitary management to control pests and diseases was carried out preventively. At maturation, 3 meters were harvested from the 4 central rows of each experimental unit, the plants were threshed and the grain mass per experimental unit and grain moisture were obtained, thus determining the grain yield (GRY) in kg ha^{-1}.

The meteorological data were collected from the automatic station in the municipality of Frederico Westphalen, state of Rio Grande do Sul (A854), the data refers to total biweekly precipitation, in the months of May, June, July, August, September and October, of the three years of cultivation (2019, 2020 and 2021), period in which the experiments were conducted, these data were presented in graphs.

To identify the presence of interaction between genotypes and years for all characteristics, joint analysis of variance and F test ($p < 0.05$) were performed, using the model statistics below, considering balanced data. $Y_{ijk} = \mu + G_i + A_j + GA_{ij} + B/A_{jk} + \epsilon_{ijk}$, where, Y_{ijk} is the observation obtained in the plot with *i-th* genotype in the *j-th* block, μ is general mean of the experiment, G_i is the effect of the *i-th* genotype considered fixed, A_j is the effect of the *j-th* year considered fixed, GA_{ij} is the effect of the *i-th* genotype interaction with the *j-th* year, B/A_{ik} effect of the *k-th* block within the *j-th* year, considered random and ϵ_{ij} random error effect.

From the observation of the interaction between genotypes and years, GGE Biplot analysis was performed to identify the ideal, most stable, and adapted genotypes, in addition to identifying the performance of the genotypes in each environment and selecting the best year for each genotype.

The GGE Biplot analysis was performed following the statistical model: $\varphi_{ij} = \widehat{Y}_{ij} - \mu - \beta_j = \sum_{k-1}^{p} \xi_{ik}^{*}\eta_{jk}^{*}$, where, φ_{ij} is the interaction effect between genotype *i* and year *j*; $\widehat{Y}_{ij}$ is the mean grain yield of genotype *i* in year *j*; μ is overall mean; β_j is the main effect of year *j*; $\xi_{ik}^{*} = \lambda_k^{\alpha}\xi_{ik}$; $\eta_{jk}^{*} = \lambda_k^{\alpha-1}\eta_{jk}$ where λ_k *k-th* is the eigenvalue of Singular Value Decomposition (SVD) (*k = 1, ...p*), with *p* ≤ min(e, g); α is singular value split factor for Principal Component (PC) *k*.(10) ξ_{ik}^{*} and η_{jk}^{*} are the PC *k* scores for genotype *i* and year *j*, respectively.

In the figures obtained, the notation Scaling = 1 (SD) indicates that the values are divided by the standard deviation of each environment, giving each environment similar importance. The Centering notation refers to the model used, where Centering = 2 indicates that it contains the GGE effect (genotype + genotype and environment interaction). Singular Value Partitioning (SVP), with SVP = 1, focusing on genotypic performance, used for the analysis of ideal genotypes, SVP = 2, focusing on the environment, used for environmental inferences and SVP = 3, with focus on genotype and environment interaction.(11)

Analysis of variance and GGE Biplot were applied to the data using R software, version 4.0.2(12), using the "metan" package.(13)

RESULTS AND DISCUSSION

The normality and homogeneity of the data were tested and considered adequate. The joint analysis of variation showed a significant effect for the years, genotypes and the interaction between genotypes and years (Table 1) for grain yield. The results showed that the genotypes present distinct responses over the years. The presence of interaction between genotypes and years enabled the application of GGE analysis and suggests the existence of mega-environments with distinct superior genotypes.(14)

For a new cultivar to be successful on the market, it depends on its agronomic performance and interaction with the growing environment.(15) The presence of interaction between genotypes and years makes cultivar selection and recommendation difficult.(16) In this sense, it is necessary to carry out more precise assessments to identify more adapted genotypes.(17)

Table 1. Summary of the analysis of variance for the grain yield characteristic of 12 wheat genotypes conducted in the Frederico Westphalen in the state of RS, in the years 2019, 2020 and 2021

Sources of variation	**Degrees of freedom**	**Mean square**
Bloco/Ambientes	6	67468.78
Genotypes (G)	11	473302.13*
Years (Y)	2	9668505.48*
G×Y	22	177628.93*
Error	66	41488.77
Total	107	
Mean grain yield (kg ha^{-1})		3884.73
Coefficient of variation (%)		5.24
Simple component of G×Y (%)		24.32
Complex component of G×Y (%)		75.68
Years	**Coefficient of variation (%)**	Mean grain yield (kg ha^{-1})
2019	4.92	3927.41
2020	6.46	3346.47
2021	4.58	4380.31

* Significant at 5% error probability.

The oscillation of the genotypes' response to the years of cultivation can be observed in general in Figure 1. The highest grain yields were obtained in 2021 and 2019, respectively (Table 1). The year 2021 was the most favorable for grain yield, presenting the highest means, higher than the general mean for the years. On the other hand, 2019 was an intermediate year between the three test years, even so it presented grain yield means higher than the general mean. The year 2020 was the least favorable for grain yield, with means lower than the general mean.

The low volume of accumulated precipitation for the period from the second half of August to the second half of October in 2020 (Figure 2) ended up harming grain filling. In 2019, we can note that the crop development period was dry, with no precipitation occurring in the first half of June, affecting crop establishment. The year 2021 was marked by a dry period, followed by another very rainy one, extreme conditions that harmed the development of the genotypes. According to Oteros et al.,(18) phenological stages are influenced by the environment, mainly soil water concentration and ambient temperature. When these are not suitable for the plants, they cause distinct physiological responses, which can alter the classification in relation to the best genotypes.

In general, the UFSMFW genotypes presented grain yield potential close to that of the control cultivars (Figure 1). The UFSMFW 1-01 genotype was highlighted, presenting the highest mean for grain yield in 2021, surpassing the control cultivars Tbio Toruk and Quartzo. In this harvest there was a drier period ranging from the first half of July to the second half of August, but rain that occurred in the first half of September provided better grain filling and consequently greater grain yield in the general mean of the genotypes.

In 2019, the best genotypes were UFSMFW 1-04 and UFSMFW 1-07, also surpassing the control cultivars Tbio Toruk and Quartzo. The year 2020 had very atypical weather conditions, it was the worst year in relation to the performance of the genotypes, with the genotype UFSMFW 1-06 standing out in grain yield, also with grain yield higher than the control cultivars. The period of water scarcity from the second half of July 2020 affected the reproductive phase and consequently grain yield (Figure 2).

In general, if we consider the three years of cultivation (2019, 2020 and 2021), the performance of the UFSMFW genotypes for grain yield was evident, where these, in most cases, were superior to the controls (Figure 1). Although they behave differently in different years, some genotypes have greater productive stability in all years while others do not. UFSMFW 1-01 was highly productive in 2021, but in 2020 it presented the worst grain yield, while UFSSMFW 1-07 maintained a certain productive stability in all the years the trials were conducted.

In studies with wheat cultivation, researchers have already observed that the cultivation environment is an important factor in contributing to production instability.(16) In this study, each year of cultivation was considered an environment, thus the Techniques for evaluating genotype

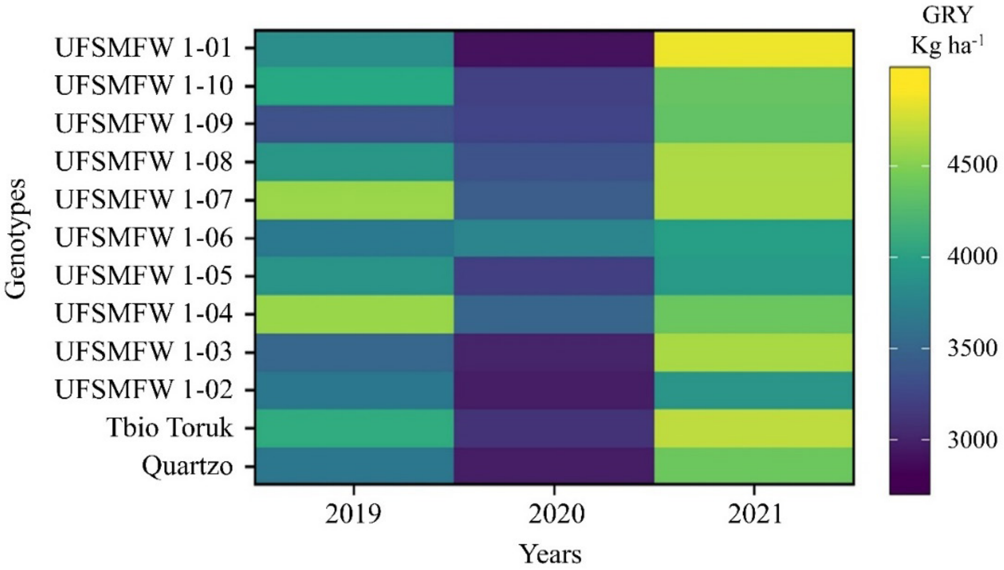

Figure 1. Overview of the interaction between genotypes (12 genotypes) and years (2019, 2020 and 2021) for grain yield (GRY).

and environment interactions allowed the identification of the most adapted and stable genotypes for the municipality of Frederico Westphalen/RS. The recommendation of these genotypes for other locations requires testing, as a new cultivar must be developed and tested in specific cultivation environments.

The GGE analysis revealed that the first two main components (PC1 and PC2) justified a total of 88.71% of the total variation (PC1 62.89% and PC2 25.82%) for the grain yield trait. The first principal component (PC1) is represented on the projection of the genotype is from the origin (0) on the Y axis, it means that it is more stable.(11)

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Therefore, some genotypes stood out with the highest grain yields, namely UFSMFW 1-07, UFSMFW 1-04 and UFSMFW 1-08 (Figure 3a). When the production stability of these genotypes was analyzed, it was observed that UFSMFW 1-07 and UFSMFW 1-04 were unstable while UFSMFW 1-08 was stable, leading to the conclusion of adaptation to specific environmental conditions. The genotypes UFSMFW 1-08, and UFSMFW 1-06, UFSMFW 1-10 and Quartzo proved to be the most stable genotypes to environmental variations in the 3 years of cultivation.

Visualizing the "who-won-where" pattern for multi-environment analyses is crucial for defining different mega-environments in a region. In this work, the possibility of mega-environments occurring indicates similarity between years. A mega-environment is defined as a group of environments that consistently share 1 or more identical genotypes.(10) The best way to observe patterns of genotype and environment interaction is through visualization in a Biplot. Figure 3b shows the formation of 7 different sectors for grain yield. The years 2019 and 2020 were grouped in the same sector, revealing themselves as a mega-environment that shares the UFSMFW 1-04 and UFSMFW 1-07 genotypes as the most productive. The genotypes at the vertices of the polygon in each sector have the highest grain productivity in the years in which they fall within these same sectors.(20) The year 2021 was isolated in one sector and comprised 1 vertex, containing the UFSMFW 1-01 genotype, which is the most productive in this environment.

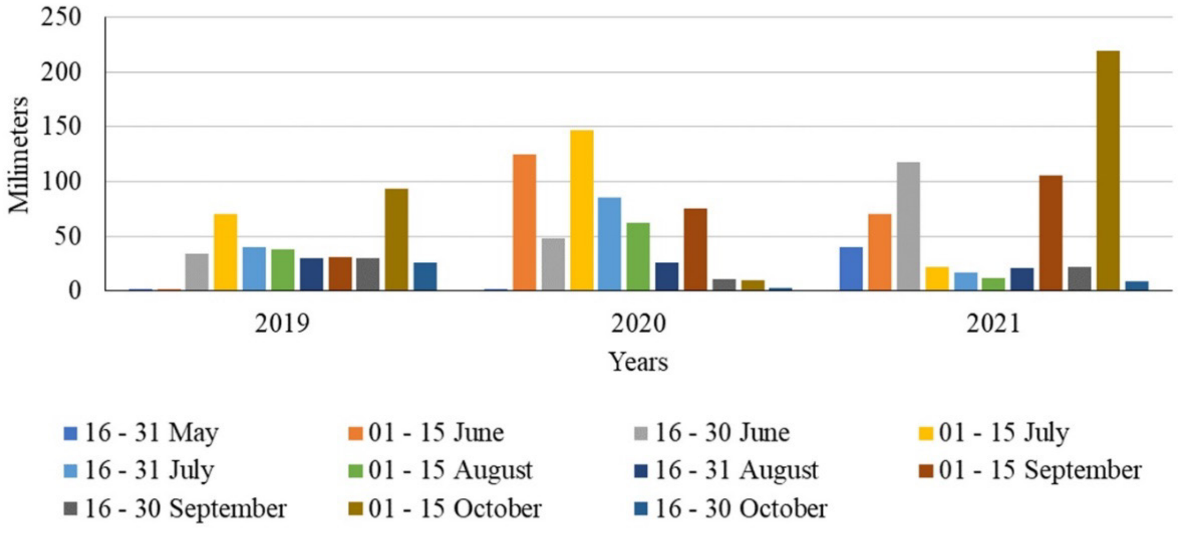

Figure 2. Accumulated biweekly precipitation, covering the months of May to October, in the years 2019, 2020 and 2021, in the Frederico Westphalen in the state of RS.

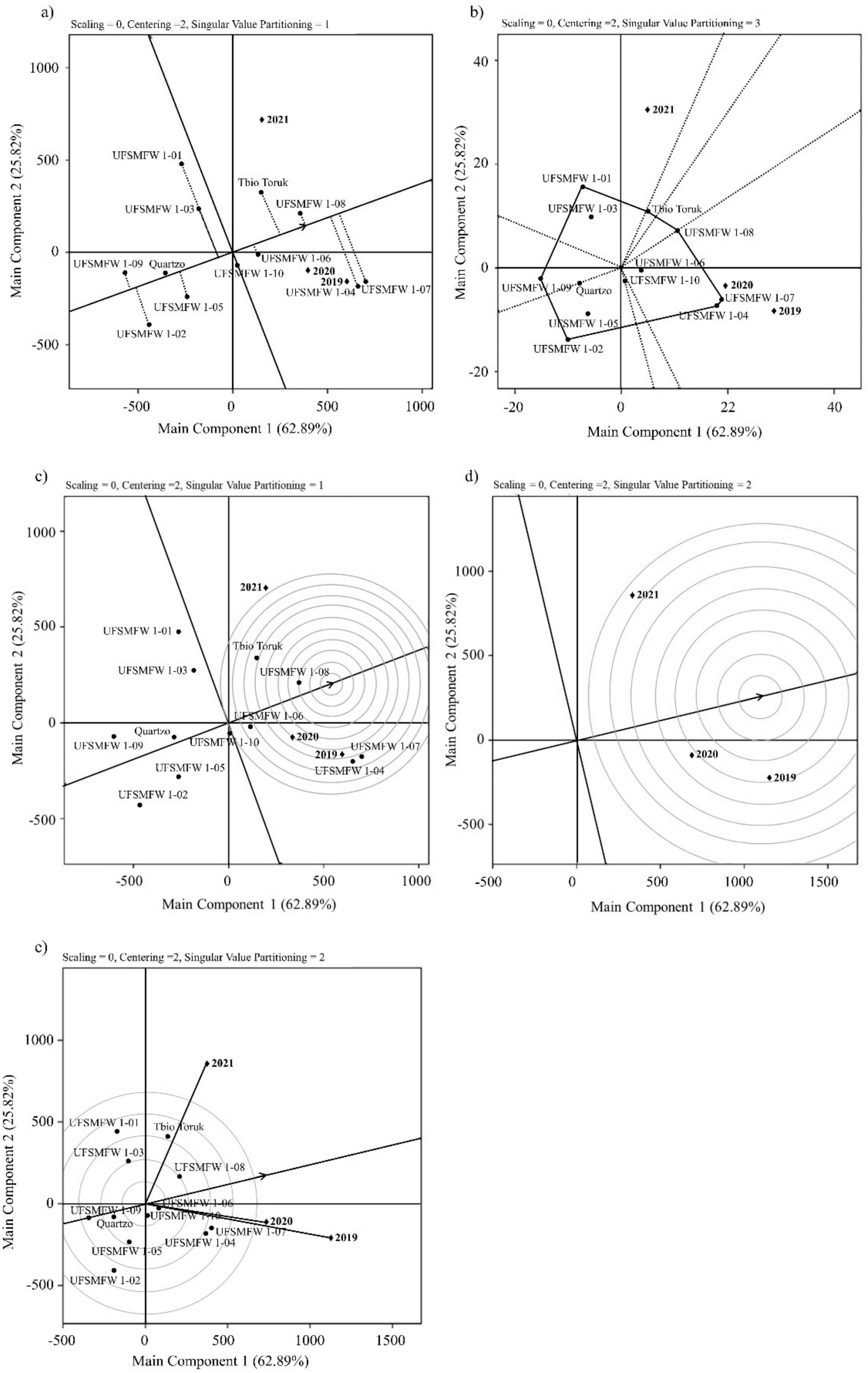

Figure 3. GGE Biplot in mean performance patterns vs. stability (a) and who-won-where (b), GGE Biplot representing the ideal genotypes (c) and environments (d), GGE Biplot representing discriminative and representative environments (e), for grain yield, evaluated in 12 wheat genotypes cultivated in the years 2019, 2020 and 2021.

The fact that 2021 is isolated from the others can be explained by the higher grain yield means in this year, while in 2019 and 2020 the means were lower (Table 1). Also, the similarity between the two years, as observed by(21) in wheat, can be explained by the fact that the tests were carried out in the same location, with only variation between the years of evaluation. The year effect is more important in multi-year analysis, with high performance over the years being a desirable characteristic in a genotype.(21)

At the vertices where no year was understood, there are genotypes that did not have satisfactory productive performance in all years using the GGE Biplot method. To be considered ideal, a genotype must present high productive performance associated with high stability.(22) In GGE Biplot analysis, this "ideal genotype" is defined by the longest vector in PC1 (yield), without projections in PC2 (instability), which means being closest to the smallest central concentric circle.(17) By looking at the concentric circles along the arrowhead, we can classify the lines according to their inclusion in the circles and their distance from the arrowhead.

None of the tested genotypes proved to be the ideal genotype (Figure 3c). Although its existence is only symbolic, it serves as a reference in the evaluation of the others.(23) However, the genotype closest to the ideal was UFSMFW 1-08, which can be compared with the other genotypes. The genotype classification in the Biplot is as follows: UFSMFW 1-08 > UFSMFW 1-07 > UFSMFW 1-04 > Tbio Toruk > UFSMFW 1-06 > UFSMFW 1-10 > UFSMFW 1-03 > UFSMFW 1-01 > UFSMFW 1-05 > Quartz > UFSMFW 1-02 > UFSMFW 1-09.

The years are classified in Figure 3d, with the ideal year represented by the circle at the tip of the arrow. The year closest to the ideal is 2019 and the years 2020 and 2021 proved to be further from the ideal environment.

Environments that are distinct are fundamental in a breeding program to detect and select stable and adapted genotypes.(24) The Biplot of the "discriminant x representative" pattern aims to evaluate a test year and identify, in this case, the ideal years of cultivation to efficiently select superior genotypes for a mega-environment. An ideal test environment should discriminate against the best genotypes and be representative of all test years.(25)

The longer the vector length of a test site, the greater its ability to discriminate genotypes.(26) For grain yield (Figure 3e), the years 2019 and 2021 were the most discriminating, presenting the longest vector, superior to that of the genotypes, allowing us to differentiate the behavior of the genotypes. Years with short vectors are less important in discriminating against genotypes and should not be used as a test year.(27)

The Biplot pattern represents the environment, that is, which years represent the others. The smaller the angle of the location vector in relation to the axis of the single arrow representing the average environment coordinate, the greater the year's representativeness in relation to the other years evaluated. In Figure 3e, 2020 was the most representative year, corresponding to the average of the years.

Discriminating and representative years are important in indicating cultivars with broad adaptation, while discriminating but not representative environments help in discarding unstable genotypes.(15)

CONCLUSIONS

The grain yield of wheat genotypes was highly influenced by climatic conditions throughout the three years of cultivation. The genotypes UFSMFW 1-07 and USFMFW 1-04 were the most productive in specific environments and the best performance in terms of stability and grain yield was from the genotype UFSMFW 1-08.

DATA AVAILABILITY

The dataset is available upon request from the corresponding author, Volmir Sergio Marchioro. The data is not publicly available because they contain information on promising wheat lines.

AUTHOR CONTRIBUTIONS

Conceptualization: Luís Antônio Klein, Ricardo Reffatti Bastiani, Volmir Sergio Marchioro.

Data curation: Luís Antônio Klein, Volmir Sergio Marchioro.

Investigation: Ketlyn Mäger Kittlaus, Marlon Ribeiro Feldens, Ricardo Reffatti Bastiani, Évelyn Clarissa Mühl Ignacio.

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Validation: Luís Antônio Klein, Volmir Sergio Marchioro.

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Writing – review & editing: Luís Antônio Klein, Volmir Sergio Marchioro.

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