

New agricultural wheat frontier in Brazil: Envirotypes applied in the adaptability and stability of wheat genotypes in contrasting environments

Cleiton Renato Casagrande (✉ cleiton_casagrande@hotmail.com)

UFV: Universidade Federal de Vicosa <https://orcid.org/0000-0002-6396-3125>

Henrique Caletti Mezzomo

UFV: Universidade Federal de Vicosa

Crislene Vieira dos Santos

UFV: Universidade Federal de Vicosa

Diana Jhulia Palheta se Sousa

UFV: Universidade Federal de Vicosa

Celso Hideto Yamanaka

COOPADAP

Tiago Olivoto

UFSC: Universidade Federal de Santa Catarina

Kaio Olimpio das Graças Dias

UFV: Universidade Federal de Vicosa

Aluizio Borém

UFV: Universidade Federal de Vicosa

Maicon Nardino

UFV: Universidade Federal de Vicosa

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Abstract

Global climate changes can dramatically impact wheat production in Brazil's Cerrado biome, considered a new wheat farming frontier. Therefore, new approaches are needed to better understand the G×E interaction in environments with high climate variations. Here, we integrate envirotyping, adaptability, and stability techniques to better understand the G×E interaction and provide new insights for the recommendation of tropical wheat genotypes that can perform well in hotter and drier environments. Thirty-six wheat genotypes were evaluated for grain yield in eight field trials in 2018, 2019, and 2020 in the Brazilian Cerrado region. There is strong evidence that even in irrigated conditions, temperatures > 30 °C during the booting and heading/flowering stages dramatically reduce the grain yield. Two lines, VI14774 (GY = 3800 kg ha⁻¹), and VI14980 (GY = 4093 kg ha⁻¹) had better performance in the hotter environment (~ 22% and ~ 32% higher than the grand mean) and are potential germplasm sources for warmer environments at the booting and heading/flowering stages. Overall, this study provides new insights on how the environment typing can be useful to better understand the genotype-by-environment interaction and help to breed new climate-resilient wheat cultivars for the cerrado region. In this study, the REML/BLUP and GGE Biplot methods highly correlate in terms of genotype classification for selection and recommendation purposes. The genotypes VI 14127, VI 14197, VI 14026, and BRS 264 are the closest to a hypothetical ideal genotype.

Introduction

The per capita consumption of wheat flour in Brazil is 40.62 kg inhabitant⁻¹ year⁻¹ (USDA 2021). This figure is higher than that of traditional staple foods such as rice and beans, with 35.2 kg inhabitant⁻¹ year⁻¹ and 15.2 kg inhabitant⁻¹ year⁻¹, respectively (EMBRAPA 2020). Although Brazil is a major consumer of wheat, with an approximate consumption of 12 million tons (CONAB 2021), it is not self-sufficient and produces only 50% of the demand. Of the six million tons of wheat produced in Brazil, 86% are produced in the southern States of Brazil, such as Paraná and Rio Grande do Sul. However, Brazil has a high potential for expanding the cultivation of wheat, especially into regions of lower latitude, such as the Brazilian Cerrado (Casagrande et al. 2020; Mezzomo et al. 2021a; Pasinato et al. 2018).

Bornhofen et al. (2018) studied the genetic progress of wheat breeding programs in Brazil between 2004 and 2013 and found that the coldest and wettest regions of Brazil resulted in a genetic gain for grain yield of 115.53 kg ha⁻¹ year⁻¹ (3.14% year⁻¹), while in tropical, hot and dry regions the genetic gain was considerably lower: 61.59 kg ha⁻¹ year⁻¹ (1.68% year⁻¹). The lower performance in the Cerrado region can be explained by the presence of acidic soils with toxic aluminum (Boff et al. 2019), lower water availability (Pereira et al. 2019), high incidence of rice blast fungus (Goddard et al. 2020), and high temperatures that result in heat stress (Mezzomo et al. 2021b; Thungo et al. 2021). However, wheat production in this region has some economic advantages, such as greater proximity to the largest wheat consuming center in Brazil (the Southeast region), cultivation in the off-season, low relative humidity and low incidence of fungal diseases common to producing areas in the South region, which together lead to a high production potential and make it an alternative to produce high-tech wheat for the bakery industry (Pasinato et al. 2018; Oliveira et al. 2021).

The potential area for wheat production in Brazil is 7.27 million ha (Mingoti et al. 2014). As a result, the expansion and development of the national wheat chain, currently estimated at 2.6 million ha, could triple. However, this requires the development of new cultivars to increase productivity and contribute to a sustainable production (Johansson et al. 2020). It is necessary not only to develop new cultivars adapted to these environments, but also to identify already developed lines that are stable and adapted to this growing region. This task is not simple since there is an interaction between genotypes × environments (G × E), a complicating factor for breeders, especially of a complex nature, constituting a difficulty in the selection and recommendation of genotypes (Jarquin et al. 2017).

Several studies have reported a significant G × E interaction for grain yield of wheat (Beche et al., 2018; Mohammadi et al. 2018; Nehe et al. 2019; Rapp et al. 2018). This mainly occurs due to the differential response of a given genotype to a given environment in stimulated by both biotic, abiotic, or an interaction between them (Nardino et al. 2022a). For example, wheat

plants exposed to very high temperature, have accelerated senescence, decreased chlorophyll of leaves, lower CO₂ assimilation, and increased photorespiration (Nuttall et al. 2018). High temperatures (> 32°C) around anthesis can induce a non-recoverable reduction in yield by adversely affecting ovary development as well as pollen and floret viability (Pradhan et al. 2012). Therefore, even if the two environments are strictly similar (eg., in terms of soil fertility, average temperatures, and rainfall), extreme values can affect the plants differently, mainly depending on the crop stage they occur.

Reduced precipitation and increases in the maximum and minimum temperatures between 1961 and 2019 were recorded in the Cerrado (Hofmann et al. 2021), creating a cascade effect with a delay in the onset of the wet season and changes in important atmospheric parameters such as the reduction in relative humidity and evaporation and increase in the vapor pressure deficit (Marengo et al. 2022). The observational evidence of increasing climatic pressure in this area and unencouraging climate change projections (Reboita et al. 2022) put at risk the breeding efforts that generated wheat cultivars for this area and increase the challenges of breeding programs that aim to release new cultivars. Therefore, there is an urgent need to better understand the G×E interaction in this region, identifying climate-resilient genotypes that can perform well under warmer conditions. This can be one of the most effective ways for increasing wheat production in Brazil under new challenges from climate change.

Numerous methodologies are used with the objective of estimating the nature of G × E interactions, including parametric and non-parametric ones. These differ in terms of estimation concepts and procedures (Rad et al. 2013; Silva et al. 2012). However, a robust methodology is to use REML/BLUP mixed models (Restricted Maximum Likelihood/Best Unbiased Linear Predictor). The method proposed by Resende and Duarte (2007), which uses the harmonic mean of genotypic values (HMGV), allows selecting simultaneously for productivity and stability, in addition to adaptability, through the relative performance of the genotypic values of genotypes in environments. In other words, the model is based on the premise that the higher the HMGV of genotypic values in different environments, the lower the standard deviation of the genotypic behavior of genotypes in environments, crops, locations, or years of cultivation. This allows the expression of predicted genotypic values in proportion of a general mean of each environment in order to later obtain the mean value of this proportion in environments (Carvalho et al. 2016). Studies on wheat using this methodology are found in the literature, but there is a small number of environments considered (Machado e Silva et al. 2021).

Another tool is the model *genotype main effects + genotype environment interaction*, known as GGE Biplot (Yan et al. 2000). This model considers the additive effect of genotype with the multiplicative effect of the G × E interaction. This method, as well as the *additive main effects and multiplicative interaction* (AMMI), uses a biplot graphic representation of a data matrix. However, the AMMI compiles separately the main effects of G and E of the G × E interaction. According to Silva et al. (2012), the GGE Biplot model more effectively explores the G × E interaction, enabling a greater accuracy in the identification of mega-environments and the selection of stable genotypes adapted to specific environments and mega-environments. This becomes more evident in situations with a high number of genotypes and in highly contrasting environmental conditions, as that of this study.

Studies on adaptability and stability of wheat often combines different strategies such as harmonic mean of genotypic values (HMGV), Additive Main effects and Multiplicative Interaction (AMMI), and Genotype plus Genotype-Environment interaction (GGE) to identify stable genotypes and delineate mega-environments (Machado e Silva et al., 2021; Woyann et al. 2019; Verma and Singh 2021). Most of them, however, seem to not explore the climatic information in each environment. As previous studies have shown (Costa-Neto 2021a), environmental typing analysis (e.g., environmental covariables) can be an alternative to better understand the G×E interaction, mainly in a region/environment with high variations among the locations/seasons.

In this sense, the main goal of this study is to integrate envirotyping, adaptability, and stability techniques to better understand the G×E interaction and provide new insights for the recommendation of spring wheat genotypes in the new frontier of production in Brazil.

Material And Methods

Environments, Genotypes, and Experimental Design

From 2018 to 2020, eight field experiments were conducted in four different locations in the State of Minas Gerais, Brazil (Table 01). The trials were made from a partnership between the Federal University of Viçosa (UFV) and the Cooperativa Agropecuária do Alto Paranaíba (COOPADAP). In environment 6, there was inoculation with the fungus *Magnaporthe oryzae* pat. *Triticum*, which causes blast. This procedure was performed as described by Gomes et al. (2019).

Table 01
List of eight environments in the study and climatological and experimental variables during the trial period.

Environment	Year	Condition	Köppen	Sowing date	Trial period
1 Rio Paranaíba	2018	Irrigated	Aw	02/05/2018	May - August
2 Rio Paranaíba	2019	Irrigated	Aw	09/05/2019	May - August
3 Viçosa	2019	Irrigated	Cwa	10/06/2019	June - September
4 Viçosa	2020	Irrigated	Cwa	10/06/2020	June - September
5 Viçosa	2020	Dry	Cwa	16/06/2020	June - September
6 São Gotardo*	2020	Dry	Cwa	30/03/2020	April - July
7 São Gotardo	2020	Irrigated	Cwa	06/05/2020	May - August
8 Sete Lagoas	2020	Irrigated	Aw	16/07/2020	July - October
Environment	Altitude	Latitude	Longitude	Temp med (°C)	Relative humidity (%)
1 Rio Paranaíba	1,150 m	19°21'31"S	46°07'22"W	18.1	81.7
2 Rio Paranaíba	1,150 m	19°21'31"S	46°07'22"W	17.8	85.5
3 Viçosa	648 m	20°45'14"S	42°52'55"W	18.6	76.5
4 Viçosa	648 m	20°45'14"S	42°52'55"W	18.2	79.2
5 Viçosa	648 m	20°45'14"S	42°52'55"W	18.2	79.2
6 São Gotardo*	1,083 m	19°13'21"S	46°05'28"W	18.4	80.2
7 São Gotardo	1,083 m	19°13'21"S	46°05'28"W	18.7	82.3
8 Sete Lagoas	796 m	19°28'34"S	44°11'42"W	21.8	58.9
* Genotypes used in this environment were inoculated with blast.					

The treatments consisted of 31 lines from the UFV Wheat Improvement Program and five commercial cultivars from different breeders (Table 2). The treatments were arranged in a completely randomized blocks design with three replications. The plots consisted of five lines, five meters in length, spaced at 17 cm, in the trials of Rio Paranaíba and São Gotardo and 20 cm in the other environments. The population density was 350 seeds m⁻². For evaluation purposes, the three central lines were considered as the useful plot. The experimental management was carried out according to the technical recommendations for wheat cultivation in the Brazilian Cerrado (Technical information for wheat cultivation: EMBRAPA, 2020). Grain yield (GY) was determined in kg ha⁻¹, with correction for 13% moisture.

Table 02
Genealogy, breeding institution, and year of release of the commercial genotype or year of crossing for recombinant inbred lines (RILs) of the genotypes used in the trials.

	Class	Genotype	Genealogy	Developer	Year
G1	Cultivar	BRS 264	Buck Buck/Chiroca//Tui	Embrapa Trigo	2005
G2	Cultivar	CD 151	BRS 120/ORL 95282	Coodetec	2011
G3	Cultivar	ORS 1403	Inia Tijereta/Alcover//Abalone	OR Sementes	2014
G4	Cultivar	TBIO ATON	TBIO Mestre/Fuste//TBIO Mestre	Biotrigo Genética	2018
G5	Cultivar	TBIO DUQUE	Toruk#3/Celebra//Noble	Biotrigo Genética	2018
G6	RILs	VI 09004	Unknown	UFV	2009
G7	RILs	VI 09007	Unknown	UFV	2009
G8	RILs	VI 09031	Unknown	UFV	2009
G9	RILs	VI 09037	Unknown	UFV	2009
G10	RILs	VI 130679	Unknown	UFV	2013
G11	RILs	VI 130755	Unknown	UFV	2013
G12	RILs	VI 130758	Unknown	UFV	2013
G13	RILs	VI 131313	Unknown	UFV	2013
G14	RILs	VI 14001	Embrapa 42/ Pioneiro	UFV	2014
G15	RILs	VI 14022	BRS254/Aliança	UFV	2014
G16	RILs	VI 14026	BRS254/Aliança	UFV	2014
G17	RILs	VI 14050	IAC364/BRS207	UFV	2014
G18	RILs	VI 14055	IAC364/BRS207	UFV	2014
G19	RILs	VI 14088	IAC364/BRS207	UFV	2014
G20	RILs	VI 14118	IAC364/BRS207	UFV	2014
G21	RILs	VI 14127	BRS264/VI98053	UFV	2014
G22	RILs	VI 14194	BRS264/VI98053	UFV	2014
G23	RILs	VI 14197	BRS264/VI98053	UFV	2014
G24	RILs	VI 14204	BRS264/VI98053	UFV	2014
G25	RILs	VI 14208	BRS264/VI98053	UFV	2014
G26	RILs	VI 14214	BRS264/VI98053	UFV	2014
G27	RILs	VI 14239	IAC364/VI98053	UFV	2014
G28	RILs	VI 14327	Sel. Rec. 9–16	UFV	2014
G29	RILs	VI 14426	BRS264/BRS207	UFV	2014
G30	RILs	VI 14668	Unknown	UFV	2014
G31	RILs	VI 14708	Unknown	UFV	2014

	Class	Genotype	Genealogy	Developer	Year
G32	RILs	VI 14774	Unknown	UFV	2014
G33	RILs	VI 14867	Unknown	UFV	2014
G34	RILs	VI 14881	Unknown	UFV	2014
G35	RILs	VI 14950	Unknown	UFV	2014
G36	RILs	VI 14980	Unknown	UFV	2014

Environmental typing

For each location/season, we collected weather data on a daily basis using the R package EnvRtype (Costa-Neto et al. 2021a). EnvRtype is a very practical package to acquire and process weather data. Based on geographical coordinates (WGS84), plant date, and harvest date, the package collects and processes remote weather data from “NASA’s Prediction of Worldwide Energy Resources” (NASA POWER, <https://power.larc.nasa.gov/>). The following variables were gathered using the `get_wheater()` function: average air temperature (TMED, °C d⁻¹), minimum air temperature (TMIN, °C d⁻¹), and maximum air temperature (TMAX, °C d⁻¹), 2 m above the surface of the earth, rainfalls (RAINFALL, mm), wind speed at 2 meters (WS, km h⁻¹), and relative humidity (RH, %). Using the function `parm_temperature()`, `parm_atmospheric()`, and `parm_radiation()`, the following parameters were computed: thermal parameters: Growing Degree Day (GDD, °C d⁻¹, considering a base temperature of 5°C), daily temperature range (TRANGE, °C d⁻¹), effect of temperature on radiation use efficiency (FRUE, from 0 to 1); atmospheric parameters: potential evapotranspiration (ETP, mm d⁻¹), slope of saturation vapor pressure curve (SPV, Kpa °C d⁻¹), vapor-pressure deficit (VPD, kPa), and dewpoint temperature (TDEW, °C); and radiation parameter: extraterrestrial radiation (RTA, MJ m⁻² day⁻¹).

We used the function `W_matrix()` of the EnvRtype package (Costa-Neto et al., 2021a) to create a covariate matrix (**W**), as proposed by (Costa-Neto et al., 2021b). To better capture the temporal variation of the environmental information across crop development, the crop cycles were divided into five-time intervals: from 0 to 30 DAE (tillering); from 31 to 55 DAE (boosting); from 56 to 70 DAE (heading/flowering); from 71 to 94 DAE (kernel milk stage); and from 95 to 130 DAE (physiological maturity). These time intervals were defined based on agronomic knowledge of how wheat grows in the Brazilian Cerrado. For each variable–phenology combination, we calculated the first quartile (25%), median (50%), and third quartile (75%) of each combination of environmental variable × time interval across different environments. Therefore, each one of the 210 combinations of environmental variable × time interval × quantile has become an envirotypes descriptor of the environmental relatedness.

Using the **W** matrix, we calculated an enviromic kernel (equivalent to a genomic relationship), using the function `env_kernel()` of the EnvRtype package (Costa-Neto et al., 2021a). In order to identify mega-environments, a hierarchical clustering (average method) was applied to **W**, producing a heat map.

Statistical analysis

Deviance analysis and genetic parameters

The REML/BLUP methodology was used to estimate variance components and predict the effects of genotypic values and the G × E interaction. The model used was

$$y = Xr + Zg + Wge + e$$

where y is the vector of phenotypic data, r is the vector of repetition effects (assumed as a fixed effect), which includes all repetitions of all environments and encompasses the effect of environment and repetitions within environments plus the general average, g is the vector of genotypic effects (assumed to be random) ($g \sim N(0, \sigma_g^2)$), where σ_g^2 represents genotypic variance, ge is the vector of effects of the G \times E interaction (assumed to be random) ($ge \sim N(0, \sigma_{ge}^2)$), where σ_{ge}^2 is the variance of the G \times E interaction and e is the vector of errors or residuals (assumed to be random) ($e \sim N(0, \sigma_e^2)$), where σ_e^2 is the matrix of residual variance. The letters X, Z, and W mean the incidence matrices for the described effects.

The likelihood ratio test (LRT) was performed in order to test the random effects of the model through deviance analysis considering the complete model without the effect of genotype and G \times E interaction. Using the REML methodology, the variance components and genetic parameters were obtained: genetic variance (σ_g^2), variance of the G \times E interaction (σ_{ge}^2), residual variance (σ_e^2), phenotypic variance (σ_p^2), heritability of the mean of genotypes (\hat{h}_{mg}^2), selective accuracy (\hat{r}_{gg}), coefficient of determination of the G \times E interaction (R_{ge}^2), genotypic correlation of genotype performance across the evaluated environments (r_{ge}), genetic variation coefficient ($CV_{g\%}$), and environmental variation coefficient ($CV_{e\%}$), as follows:

a)

$$\hat{h}_{mg}^2 = \frac{\hat{\sigma}_g^2}{\left(\frac{\hat{\sigma}_g^2 + \hat{\sigma}_{ge}^2 + \hat{\sigma}_e^2}{E}\right)}, \text{ where E is the number of environments evaluated.}$$

$$\hat{r}_{gg} = \sqrt{\hat{h}_{mg}^2}$$

b)

$$R_{ge}^2 = \frac{\hat{\sigma}_{ge}^2}{\hat{\sigma}_{ge}^2 + \hat{\sigma}_g^2 + \hat{\sigma}_e^2} = \frac{\hat{\sigma}_{ge}^2}{\hat{\sigma}_p^2}$$

c)

$$r_{ge} = \frac{\hat{\sigma}_g^2}{\hat{\sigma}_g^2 + \hat{\sigma}_{ge}^2}$$

d)

$$CV_{g\%} = \left(\frac{\sqrt{\hat{\sigma}_g^2}}{\bar{\chi}}\right) \times 100, \text{ where } \bar{\chi} \text{ is the overall average (3,739.17 kg ha}^{-1}\text{)}$$

e)

$$CV_{e\%} = \left(\frac{\sqrt{\hat{\sigma}_e^2}}{\bar{\chi}}\right) \times 100$$

f)

The genotypic values free of the genotype \times environment interaction were obtained and given by the formula $\hat{\mu}_j + \hat{g}_i$, where $\hat{\mu}_j$ is the general mean of all environments and \hat{g}_i is the free genotypic effect of the G \times E interaction. For each

individual environment, the genotypic values were predicted using the formula $\hat{\mu}_j + \hat{g}_i + \hat{g}e_{ij}$, where $\hat{\mu}_j$ is the mean of the environment j , \hat{g}_i is the genotypic effect of the genotype i in the environment j , and $\hat{g}e_{ij}$ is the effect of the G × E interaction relative to the genotype i . For the eight environments considered in the study, an environmental stratification analysis was performed via least squares in order to identify groups of environments in which the G × E interaction is not significant. Furthermore, the G × E interaction was decomposed into its simple and complex parts using two methodologies: Robertson (1959) and Cruz and Castoldi (1991).

Stability analysis

For the stability and adaptability analysis, the model 54 (Stability, Adaptability and Productivity) of the Selegen software (Resende 2016) was used, which corresponds to the design of complete blocks in various environments with one information per plot. The concept of stability is based on the harmonic mean of genotypic values (HMGV). The concept of adaptability refers to the relative performance of genotypic values (RPGV). Thus, the conception of the analysis by stable, adaptable, and productive genotypes occurs through the analysis of the harmonic mean of the relative performance of genotypic values (HMRPGV), which considers both information together.

$$HMGV = \frac{E}{\sum_{j=1}^E \left(\frac{1}{GV_{ij}} \right)}, \text{ where } E \text{ is the number of environments } (E = 8), \text{ where the genotype } i \text{ was evaluated, } GV_{ij} \text{ is}$$

the genotypic value of genotype i in the environment j , expressed in relation to the mean of that environment.

a)

$$RPGV = \frac{1}{E} \times \frac{\sum_{j=1}^E GV_{ij}}{\hat{\mu}_j}, \text{ where } \hat{\mu}_j \text{ is the mean grain yield of the wheat genotypes in the environment } j.$$

b)

$$HMRPGV = \frac{E}{\left(\sum_{j=1}^E \times 1 \right) / GV_{ij}}$$

c)

The genotypic adaptability (PRGV) and the simultaneous stability and adaptability (HMRPGV) are multiplied by the general mean of the environments, PRVG* $\hat{\mu}$ and HMRPVG* $\hat{\mu}$, respectively.

To account for the mean performance and stability of genotypes, we also computed the WAASBY index, which allows weighting between the mean performance Y and stability (WAASB). This index was computed considering an weight of 65 for mean performance and 35 for stability (Olivoto et al. 2019).

Graphical approach

The GGE Biplot method was constructed using the information on the genotypic values of each genotype. This method is based on a graphical visualization of the data matrix, which considers the main effect of each genotype together with the effect of the G × E interaction. This methodology was described by Yan et al. (2000) and consists of:

$$Y_{ij} - \mu - B_j = \lambda_1 \xi_{1i} \eta_{1j} + \lambda_2 \xi_{2i} \eta_{2j} + \epsilon_{ij}$$

where Y_{ij} is the predicted genotypic value for the GY of genotype i in the environment j , μ is the overall mean, B_j is the effect of the environment j . λ_1 and λ_2 are Eigenvalues associated with PC1 and PC2, ξ_{1i} and ξ_{2i} are the scores for the PC1 and PC2 axes for the genotype i , η_{1j} and η_{2j} are the scores for the PC1 and PC2 axes for genotype the j . ϵ_{ij} is the error

associated with the two-dimensional model, that is, the percentage of $G + G + E$ effects not explained by the first two PCs. These analyses were processed using the Metan package in the R software (Olivoto and Lúcio, 2020).

Relationships between mean performance, stability, and climate variables

We used the WAASB index (Olivoto et al. 2019) for each environment to quantify the genotypic variation within each environment. Environments with higher WAASB are considered more discriminative, i.e., the variation among genotypes is assumed to be higher in such an environment. To study the relationships between environmental variables and how they could be related to mean performance and stability, we conducted a Principal Component Analysis with a two-way table containing the environmental variables, the WAASB index, and the average grain yield for each environment. The biplot was produced using the function `fviz_pca_biplot()` of the R package `factoextra` (Kassambara and Mundt 2020) in order to show the relationships between studied traits.

Finally, to better understand the distribution of the maximum temperature across the crop cycle in each environment, we used the function `env_typing()` of the `EnvRtype` package (Costa-Neto et al. 2021a) to create a plot with the relative frequency of occurrence. Therefore, it was possible to compare how environments (and mega-environments) are similar or not related to this environmental covariable.

Results And Discussion

Envirotyping

From the environmental covariates we performed the similarity analysis considering 14 enviromic kernels (Fig. 01), where we can visualize the formation of four groups (mega-environments), which we worked on individually. In the similarity analysis, we visualize that environments E6 (São Gotardo* - dry) and E8 (Sete Lagoas) are contrasting in relation to the other environments that did not group with any other environment, where such environments represent a mega-environment. On the other hand, environments E3 (Viçosa irrigated 2019), E4 (Viçosa irrigated 2020) and E5 (Viçosa dry 2020) have greater similarity for the environmental covariates analyzed, indicating that the relative performance of genotypes in a same city did not change as a function of the water regime. This indicates that the variance components of the $G \times E$ interaction between these environments are not significant.

The environment E1 (Rio Paranaíba - irrigated 2018), E2 (Rio Paranaíba - Irrigated 2019) and E7 (São Gotardo irrigated 2020) have greater similarity, these environments formed another subgroup, possibly explained by the proximity between the three environments.

Figure 02 shows the biplot for the Principal Component Analysis between environmental variables, grain yield, and genotypic variation in the environments. The two principal component axes explained 88.6% of the total variation. There was a positive correlation between TMED, TMAX, SPV, and ETP, and a negative correlation of these climate variables with RH.

The PCA scores suggest that E3, E4, E5, and E8 were mainly characterized as having a higher TMD, TMAX, TMIN, a lower RH, and consequently a higher VPD, which is the difference (deficit) between the volume of moisture in the air and how much moisture the air can hold when it is saturated. The VPD can be then used as an accurate indicator of current air evaporative capacity. The combination of higher temperatures with high VPD resulted in higher rates of ETP observed for E4, E5, and E8. Therefore, it can be concluded that in warmer environments, the loss of water by evapotranspiration is greater than in cooler environments. This is supported by the positive association between ETP and environment temperatures (mean, minimum, and maximum).

The positive association of TMAX, TRANGE, and VPD and the negative association of RH with WAASB suggest that these environmental variables play a key role in the manifestation of genotypic variation in each environment. Therefore, good prospects for the selection of climate-resilient wheat genotypes for the Cerrado are expected.

Figure 03 shows the distribution of the maximum air temperature within each mega environment. It is observed that maximum temperature ($TMAX \text{ } ^\circ\text{C d}^{-1}$) showed a variable distribution, especially in mega environment four, which showed low average grain yield values (see the distribution for other variables in Supplementary material S1).

Investigating the maximum air temperature in each of the five development stages (tillering, booting, final flowering, kernel milk stage and physiological maturity) it was observed that the higher temperatures of the E8 (Fig. 03) were mainly observed during booting, heading/flowering, and kernel milk stage with temperatures between 29 and 39°C during more than 75% of the days in these stages. On the other hand, environment E1 (Rio Paranaíba -irrigated), in which the wheat genotypes showed the highest BLUP for grain yield, we were able to analyze in the workflow that the relative frequency of maximum air temperature in the development stages was reduced, which contributed to the excellent results obtained in this environment. Similar results for grain yield and maximum air temperature, we can observe for environments E3 (Viçosa irrigated 2019), E4 (Viçosa irrigated 2020) and E7 (São Gotardo irrigated).

Wheat is cereal of the most important food crops worldwide in terms of production and human nutrition. Brazil is a major consumer of wheat, with an approximate consumption of 12 million tons (Conab 2021), it is not self-sufficient and produces only 50% of the demand. Brazil has a high potential for expanding the cultivation of wheat, especially into regions of lower latitude, such as the Brazilian Cerrado (Casagrande et al. 2020). However, in the Brazilian Cerrado we need to develop and release cultivars with tolerance to heat, once those high temperatures same that for short periods have the potential to significantly reduce grain production (Nuttall et al. 2018). In the research by Hofmann et al. (2021) the importance and potential of the Brazilian Cerrado is highlighted with a prediction of maximum air temperature for 2050. The authors highlighted an increase in maximum temperature of 4.0, 3.4, 4.4, and 6.0 °C in the months of July, August, September and October, respectively. During these months, the wheat crop will be in full development in the field in this region. In parallel, the increase in maximum air temperature, the study also indicates a ~ 15% decrease in relative humidity.

Of the eight environments evaluated, in three (E6, E8 and E5) the wheat genotypes showed grain yields below the general average of the other environments, where E8 and E5 were environments with maximum air temperatures greater than 29°C at critical development stages, such as heading/flowering. The high temperature at anthesis or after anthesis decreased chlorophyll content, individual grain weight and grain yield of wheat (Pradham et al. 2012). High temperature stress decreases chlorophyll content as a result of damaged thylakoid membranes or lipid peroxidation of chloroplast membranes (Ristic et al. 2007; Djanaguiraman et al. 2010).

With these data, we understand that the development cycle of the genotypes was accelerated in this environment, which reduces the time for the accumulation of photo-assimilated reserves in the stalk and leaves that would be translocated to the grain later. High temperature, especially above 34°C at flowering, as we observed, increases flower sterility in the spikelets, reducing the number of grains per spike and thus grain yield. Once, that reduced grain number may only be partially compensated by increased grain filling due to proportionally greater allocation of assimilate to the remaining kernels (Jenner et al. 1991; Nuttall et al. 2018). At growth stage (double ridge), high temperature adversely affects spikelet formation (Shpiler and Blum 1986), at meiosis decreases grain number per spike by inducing ovule and pollen sterility and anther indehiscence (Prasad et al 2008a), at anthesis, stress decreases the grain number by adversely affecting ovarian development, pollen germination and pollen tube growth (Prasad et al. 2008b) At grain filling period, high temperature decreases leaf chlorophyll content and accelerates senescence (Zhao et al. 2007), leading to a shorter grain filling duration with an ultimate decrease in individual grain weight and yield (Pradhan et al 2012).

Based on these results we can also highlight the huge importance of considering the application of envirotyping in understanding the GxE interaction (Heinemann et al. 2022), for deciphering environmental impacts of covariable climates

on wheat genotypes. Wheat genotypes vary significantly in their sensitivity to high temperature, where many studies have showed significant differences in the response in heat tolerance (Pradhan et al. 2012; Farooq et al. 2011; Stone and Nicolas 1998). Thus, considering the impact that maximum air temperature has on the wheat crop and that the expansion area in Brazil will have an increase in maximum temperature, we need to select wheat genotypes that are resilient to these environmental conditions. Currently, a first step can be taken by analyzing the genetic variability of germplasm and recommending wheat genotypes that are more resilient to higher temperature environments.

Deviance analysis

According to the restricted maximum likelihood test (LRT) shown in Table 03, there is a significant effect of genotype and $G \times E$ interaction for the character GY ($p < 0.01$). The genetic variability of the conjoint analysis is the arithmetic mean of genotypic variance components of individual analyses minus the interaction (Cruz et al. 2012). In view of this, the practice of selection based on an average of the environments is not effective and appropriate. Therefore, it is necessary to use methods that capitalize on the effects of the $G \times E$ interaction in order to maximize gains for a series of environments. Other recent studies on wheat have also reported a significant effect of the $G \times E$ interaction for GY (Lozada et al. 2020; Sehgal et al. 2020; Szareski et al. 2021).

Table 03

Likelihood ratio test, variance components, and genetic parameters of 36 tropical wheat genotypes as for grain yield (GY) in eight environments evaluated in the 2018, 2019, and 2020 crop seasons in the Brazilian Cerrado.

Effect	Deviance	LRT		Variance Component
Genotype	11,973.71	8.56	**	$\hat{\sigma}_g^2$ 33,357.93
G × E interaction	12,015.05	49.90	**	$\hat{\sigma}_{ge}^2$ 140,613.16
Residue	-	-		$\hat{\sigma}_e^2$ 387,595.02
Complete model	11,965.15	-		$\hat{\sigma}_p^2$ 561,566.11
Genetic Parameters				
Heritability of mean genotype (\hat{h}_{mg}^2)				0.50
Selective accuracy (SA)				0.71
Coefficient of determination of interaction G × E (R_{ge}^2)				0.25
Genotypic correlation of performance in environments ($\hat{\sigma}_{ge}$)				0.19
Genetic variation coefficient (VCg, %)				4.88
Experimental variation coefficient VCe, %)				16.65
Mean (kg ha ⁻¹)				3,739.17
$**\chi_{1\%}^2 = 6.63$ $*\chi_{5\%}^2 = 3.84$				

The variance component $\hat{\sigma}_p^2$ presented a greater contribution of components due to the effects of the G × E interaction ($\hat{\sigma}_{ge}^2$) and the environment ($\hat{\sigma}_e^2$) in relation to the genotypic component ($\hat{\sigma}_g^2$). This situation is quite common for complex characters, such as GY, as it has a strong environmental influence and is governed by many genes. The genetic parameters \hat{h}_{mg}^2 and the selective accuracy were 0.50 and 0.71, respectively. Casagrande et al. (2020) reported estimates similar as these for GY upon studying the diversity of a panel of wheat genotypes using REML/BLUP. According to Resende and Duarte (2007), selective accuracy estimates greater than 0.70 indicate a high experimental precision in the selection of genotypes. The CVe estimate was 16.65%, corroborating the parameter of accuracy and study of Nardino et al. (2022b) considering the variable GY in wheat.

The CVg/CVe ratio was lower than the unit, suggesting difficulties in multi-environment selection. The R_{ge}^2 and $\hat{\sigma}_{ge}$, which Table 03 shows, were low: 0.25 and 0.19, respectively. Low estimates for these parameters derive from the presence of a complex G × E interaction, which indicates an inconsistency in genotype superiority with variation across environments (Cruz et al. 2012).

Nature of genotype-environment interaction

Figure 04 shows the percentage of G × E interaction of the complex part. A high predominance of the complex part over the simple part is attested by estimates higher than 50% in both methodologies. In the comparison between the pairs of environments, there is a lack of correlation between the best genotypes of each environment. The lowest estimates are from the E1 × E6 environments in both methodologies. These environments are those with the highest and lowest means, respectively. These results indicate that there is a trend towards less change in the ranking of genotypes between these environments.

Genotypic mean performance

The BLUPs represented in Table 04 refer to the mean genotypic value in the various environments and capitalizes the average interaction with all evaluated environments. There is a high environmental variability according to the estimates of the genotypes evaluated. The environment with the highest average was E1, in Rio Paranaíba 2018, followed by the environments E3 and E7, Viçosa 2019 and São Gotardo 2020, with mean yields per environment of 5,029.03, 4,292.80, and 4,265.80 kg ha⁻¹, respectively. These environments, classified as favorable environments or with high technology, if compared to the national average of wheat productivity in Brazil in 2020 (2,663 kg ha⁻¹), are 1.89 (E1), 1.61 (E3), and 1.60 (E7) times superior. It is important to point out that the Brazilian average of wheat productivity mainly reflects the South region, which historically cultivates wheat. In view of this, it is possible to verify a high potential of these cultivation environments for the cultivation of wheat in warmer regions.

Table 04

Best linear unbiased predictor (BLUP) for 36 tropical wheat genotypes in eight environments considering G x E interaction as evaluated in the 2018, 2019, and 2020 crop seasons in the Brazilian Cerrado.

Genotypes	$\mu + g_i + (ge)_{ij}$								Mean $\mu + g_i$
	Environments								
	E1 ^{a*}	E2 ^{bd}	E3 ^b	E4 ^b	E5 ^b	E6 ^c	E7 ^{cd}	E8 ^e	
BRS 264	5282.23	4375.40	4594.23	4309.59	4281.84	1388.56	4780.20	3097.16	3918.94
CD 151	5133.16	3981.86	3926.71	3794.05	3484.88	1319.71	4620.75	2623.31	3654.93
ORS 1403	4766.96	3736.36	4220.72	3889.71	3180.30	1257.97	4654.84	2338.53	3586.24
TBIO ATON	5245.11	4194.03	4931.53	4342.03	3907.79	1403.87	4381.30	3334.58	3888.73
TBIO DUQUE	4721.24	4002.78	4320.12	4029.86	3515.71	1194.67	4173.36	2472.32	3617.74
VI 09004	5405.13	3823.78	4219.48	4673.11	3945.29	1567.34	4064.07	4068.09	3890.86
VI 09007	5306.46	4077.72	4036.95	4251.37	3699.00	1348.74	3712.14	2862.33	3688.52
VI 09031	5113.06	3957.37	4254.31	4028.08	3583.42	1515.56	3624.16	2929.14	3664.81
VI 09037	5349.56	4144.17	3984.18	3818.95	3395.13	1322.17	4082.31	3068.60	3677.91
VI 130679	4898.96	3482.30	4240.45	4341.23	3503.98	1290.43	4090.40	2681.78	3625.88
VI 130755	4621.50	3607.51	4299.76	3979.09	3228.69	1536.86	4279.23	2956.01	3624.17
VI 130758	4420.23	3883.09	4110.79	3996.55	3162.77	1465.33	4025.40	2914.98	3580.82
VI 131313	4638.85	3365.61	4406.71	3928.31	3836.29	1027.85	4130.87	3607.03	3659.61
VI 14001	4767.34	3882.66	4113.74	4005.18	3987.86	1274.39	4414.19	3260.62	3722.19
VI 14022	5795.32	3893.18	3657.15	3906.81	3444.77	1409.05	4351.73	2821.19	3687.25
VI 14026	5587.80	4356.68	4478.56	4073.46	3590.93	1644.69	4746.96	3500.30	3908.31
VI 14050	5138.20	3740.85	4237.25	4146.22	3727.61	1120.71	3846.74	2737.49	3639.43
VI 14055	5317.19	3807.28	4461.51	4550.30	3900.65	1305.89	4654.96	3781.99	3891.97
VI 14088	4424.98	3853.66	4527.73	4318.06	3484.28	1447.72	4055.07	3289.19	3697.20
VI 14118	5104.55	4268.61	4110.80	4387.65	3901.30	1460.54	4242.79	3212.28	3802.63
VI 14127	5706.27	4364.26	4603.74	4747.49	3915.44	1740.92	4482.76	3393.77	3988.15
VI 14194	5676.27	4162.07	4961.24	4398.18	3427.17	1629.55	4427.03	2851.64	3871.78
VI 14197	5884.07	4282.66	4379.20	4424.87	3995.84	1551.62	4602.84	3402.94	3952.90
VI 14204	5459.91	3703.28	4151.58	4351.95	3572.02	1646.64	4380.79	2555.84	3731.69
VI 14208	5005.01	3947.98	4307.44	4315.33	3684.80	1439.66	4344.18	2242.44	3687.88
VI 14214	5060.30	4182.44	4368.34	4813.63	3932.94	1467.10	4521.61	2750.58	3836.07

* Environments followed by the same letter show non-significant G x E interaction components at 5% probability by F test.

Genotypes	$\mu + g_i + (ge)_{ij}$								Mean $\mu + g_i$
	Environments								
	E1 ^{a*}	E2 ^{bd}	E3 ^b	E4 ^b	E5 ^b	E6 ^c	E7 ^{cd}	E8 ^e	
VI 14239	4509.86	3706.07	3816.21	3738.57	3646.55	1090.03	3869.91	2648.90	3502.80
VI 14327	5206.94	3838.80	4342.12	4467.27	3680.39	1304.04	4322.40	3075.91	3765.74
VI 14426	4814.14	3970.33	3994.47	3881.57	3657.52	1469.28	4270.01	2844.01	3656.32
VI 14668	5227.38	3898.25	4148.27	4154.12	3817.16	1671.45	4182.97	3525.37	3797.43
VI 14708	4962.56	3870.11	4414.74	4199.28	3464.51	1191.21	4292.40	3077.76	3703.08
VI 14774	4384.20	4211.41	4495.34	4339.31	3882.48	1745.95	4368.15	3800.89	3846.77
VI 14867	4420.44	4165.90	4756.99	4198.06	3345.16	1515.56	4374.17	3551.35	3773.08
VI 14881	4626.01	3964.26	4359.08	4332.43	3526.44	1232.24	3906.15	2712.93	3636.52
VI 14950	4482.00	3748.62	3625.09	3651.65	3269.52	1178.56	3753.46	3359.90	3506.29
VI 14980	4581.94	4252.46	4684.44	4616.68	3972.25	1448.69	4538.37	4093.31	3925.40
Mean	5029.03	3964.00	4292.80	4205.56	3654.24	1406.24	4265.80	3095.68	3739.17
* Environments followed by the same letter show non-significant G x E interaction components at 5% probability by F test.									

The least productive environment was the E6, São Gotardo 2020, a rainfed environment with sowing before the end of the rainy season and with pressure by disease (blast inoculation). Grain yield in this environment was 1,406.24 kg ha⁻¹. The second lowest productive average was in Sete Lagoas 2020 (E8), followed by Viçosa 2020 (E5). Among the three most unfavorable environments, two are environments with rainfed cultivation (E5 and E6). These results corroborate those Pereira et al. (2019) described. The authors concluded that there is a need for a greater drought tolerance in wheat to unlock the production potential of the Brazilian Cerrado.

Another unfavorable environment was E8, characterized as the environment with the highest average temperature during the cultivation period (21.8 °C) and the lowest relative humidity (58.9%) among all environments evaluated (Table 01). Leaf respiration is highly associated with higher air temperature in wheat and inversely proportional to yield, especially during the grain filling phase, with negative correlation estimates between 0.50 and 0.85 (Pinto et al., 2017). Heat tolerance in wheat is a polygenic trait difficult to quantify, and there are still no effective methods for selecting parents that are heat-tolerant and few molecular markers are used for the selection of this trait (Ni et al., 2018; Zhongfu et al. 2018). However, this characteristic, coupled with tolerance to water deficit, are essential factors for the advancement of wheat in Brazil, especially for lower regions in the Southeast and Midwest regions and in the North and Northeast States in general.

The environmental stratification grouped the environments E2, E3, E4, and E5. This indicates that the variance components of the G x E interaction between these environments are not significant. The three environments in Viçosa, together with the Rio Paranaíba 2019 environment, established a mega-environment (b). The environments E6 and E7, rainfed and irrigated, of São Gotardo established another subgroup (c), indicating that the relative performance of genotypes in a same city did not change as a function of the water regime. The environments irrigated Rio Paranaíba (2020) and irrigated São Gotardo (2019) formed another subgroup, possibly explained by the proximity between the two environments. The environments E1

and E8, with lower and higher average air temperature, did not group with any other with non-significant $G \times E$ interaction. They are thus independent environments.

Among the ten most productive genotypes in the E1 environment, the most favorable environment in this study, six are among the group of the ten most productive genotypes in the E8, with artificial inoculation of blast, namely: VI 14127, VI 14204, VI 14026, VI 14194, VI 09004, and VI 14197. These results suggest the classification of these strains as an ideal genotype due to the high performance of these materials in favorable as well as in unfavorable environments. The VI 14127 genotype was present in the selection of the ten most productive genotypes in all evaluated environments. Other published studies have also reported a high performance of this genotype (Machado e Silva et al. 2021). Figure 02 shows the relationship between climate variables, environments, and grain yield.

Table 05 shows the results of stability (HMGV), adaptability (RPGV), stability, and adaptability. The HMGV results indicate that the most productive and stable genotypes were VI 14127, VI 14774, VI 14026, VI 14197, and VI 09004. The HMGV analysis simultaneously brings together a selection based on two concepts: productivity and stability. Productivity is the result of an ordering of genotypes based on their genotypic values (BLUP), and stability is calculated through the standard deviation of the genotype behavior in the environments evaluated. The smaller the standard deviation, the greater the harmonic mean of genotypes. The genotypes VI 14980 and BRS 264, the 3rd and 4th most productive genotypes based on environment means (Table 04), are not among the five genotypes with the highest estimate of HMGV. These results indicate that, despite being productive when the average across environments is analyzed, they present little predictable behaviors.

Table 05

Genotypic stability (HMGV), genotypic adaptability (RPGV), simultaneous genotypic adaptability and stability (HMRPGV), genotypic value multiplying adaptability (RPGV* μ), and genotypic value penalized by instability and multiplied by adaptability (HMRPGV* μ) for 36 tropical wheat genotypes as for grain yield (GY) in eight environments evaluated in the 2018, 2019, and 2020 crop seasons in the Brazilian Cerrado.

Line	HMGV	Line	RPGV	RPGV* μ	Line	HMRPGV	HMRPGV* μ
VI 14127	3670.10	VI 14127	1.1117	4156.81	VI 14127	1.1092	4147.30
VI 14774	3570.17	VI 14197	1.0872	4065.32	VI 14197	1.0857	4059.75
VI 14026	3539.64	VI 14980	1.0845	4055.24	VI 14980	1.0747	4018.48
VI 14197	3534.09	VI 14026	1.0772	4027.91	VI 14026	1.0729	4011.71
VI 09004	3507.41	VI 09004	1.0743	4017.05	VI 09004	1.0640	3978.65
VI 14980	3493.21	VI 14774	1.0711	4005.12	BRS 264	1.0629	3974.48
VI 14668	3459.32	BRS 264	1.0662	3986.57	VI 14774	1.0596	3961.97
VI 14194	3437.34	TBIO ATON	1.0568	3951.45	TBIO ATON	1.0552	3945.41
BRS 264	3399.40	VI 14055	1.0560	3948.58	VI 14055	1.0496	3924.61
TBIO ATON	3391.96	VI 14194	1.0545	3942.86	VI 14194	1.0474	3916.27
VI 14867	3356.20	VI 14668	1.0412	3893.19	VI 14668	1.0359	3873.43
VI 14118	3348.19	VI 14214	1.0364	3875.43	VI 14214	1.0317	3857.54
VI 14214	3341.72	VI 14118	1.0289	3847.26	VI 14118	1.0276	3842.32
VI 14055	3338.90	VI 14867	1.0253	3833.60	VI 14867	1.0177	3805.48
VI 14204	3291.34	VI 14204	1.0029	3749.85	VI 14327	1.0009	3742.40
VI 14088	3243.72	VI 14327	1.0024	3747.99	VI 14204	0.9933	3714.16
VI 09031	3215.70	VI 14088	0.9912	3706.27	VI 14088	0.9876	3692.79
VI 14327	3197.80	VI 14001	0.9905	3703.50	VI 14001	0.9870	3690.73
VI 14426	3190.58	VI 09031	0.9773	3654.11	VI 09031	0.9733	3639.15
VI 130755	3187.44	VI 09007	0.9752	3646.32	VI 09007	0.9716	3633.07
VI 14001	3163.61	VI 14208	0.9744	3643.62	VI 14426	0.9703	3628.11
VI 14022	3145.82	VI 14022	0.9739	3641.74	VI 14708	0.9701	3627.43
VI 09007	3140.78	VI 14708	0.9732	3638.97	VI 09037	0.9675	3617.54
VI 14208	3126.08	VI 14426	0.9722	3635.29	VI 14022	0.9670	3615.95
VI 09037	3121.60	VI 09037	0.9704	3628.36	VI 14208	0.9626	3599.26
VI 130758	3116.07	VI 130755	0.9639	3604.21	VI 130755	0.9600	3589.65
CD 151	3069.25	CD 151	0.9581	3582.51	CD 151	0.9530	3563.51
VI 14708	3064.48	VI 131313	0.9558	3573.88	VI 14881	0.9464	3538.71
VI 130679	3035.88	VI 14881	0.9499	3551.69	VI 130679	0.9439	3529.26
VI 14881	3020.73	VI 130679	0.9468	3540.24	VI 130758	0.9421	3522.56

Line	HMGV	Line	RPGV	RPGV* μ	Line	HMRPGV	HMRPGV* μ
TBIO DUQUE	2955.48	VI 130758	0.9449	3533.15	VI 131313	0.9392	3511.69
ORS 1403	2937.66	VI 14050	0.9427	3524.85	VI 14050	0.9367	3502.45
VI 14050	2935.84	TBIO DUQUE	0.9377	3506.30	TBIO DUQUE	0.9320	3484.96
VI 131313	2912.19	ORS 1403	0.9263	3463.43	ORS 1403	0.9173	3429.93
VI 14950	2900.67	VI 14950	0.9060	3387.55	VI 14950	0.9005	3367.07
VI 14239	2808.35	VI 14239	0.8932	3339.80	VI 14239	0.8891	3324.56

Genotypic adaptability (RPGV) is expressed as the mean value of the proportion of predicted genotypic values in relation to the general mean of each environment. In this sense, the most adapted genotypes were those with the highest estimate of HMGV, plus the genotype VI 14980. The genotype VI 14980 had previously the 6th highest value of HMGV. The HMRPGV, which combines the concepts of productivity, stability and adaptability, classifies the genotypes exactly in the same way as the RPGV statistic informs. According to this method, the most productive, stable, and adapted genotypes are VI 14127, followed by the genotypes VI 14197, VI 14980, VI 14026, and VI 09004. No commercial genotype was among the top five for each parameter evaluated. The best commercial genotype was the BRS 264, with HMRPVG * μ 3,974.48 kg ha⁻¹. This method is very similar to the classical method proposed by Linn and Binns (1988), but in a genotypic and not in a phenotypic context.

Other authors have already reported the use of this method for soybean (Gonçalves et al. 2020), cotton (Peixoto et al. 2020), and other oilseed species that produce biodiesel (Alves et al. 2018). For wheat, there is only one study in the literature (Machado e Silva et al. 2021); however, only three environments were used in it.

The first two principal components (PC1 and PC2) in the GGE Biplot analysis encompassed approximately 70% of the total variation (64.75%) present in the environments (Fig. 05A). Other authors, in a similar study with 50 wheat genotypes and nine environments, observed an explanation between PC1 and PC2 of 50%. According to Yan et al. (2000), PC1 indicates the degree of adaptability of the genotypes; it is correlated with the performance *per se* in each environment. PC2 indicates the degree of stability of each genotype. In this type of analysis, the cosine of the angle between two environments corresponds to the genetic correlation between them. There is a high negative genetic correlation between the environments E1 and E8. The high discordance between the performance of genotypes in these environments can be explained by the agroclimatic differences existing between them (Table 01).

The comparison between mean and stability (Fig. 05B) considers the continuous green line with the arrow, called “*average-environment axis*” (AEA), classifying the genotypes with the highest average performance across the environments; the line perpendicular to the AEA indicates a greater environmental productivity variability (less stability) in any direction, such that the longer the dotted green line, the less stable the genotype (Yan and Tinker 2006). Based on these concepts, the sister lines G21 (VI 14127) and G23 (VI 14197) present genetic superiority in relation to the others. In addition, other genotypes show high stability and productivity: G1 (BRS 264), G16 (VI 14026), G18 (VI 14055), and G4 (TBIO ATON). The closer to the X axis (green line with arrow to the left), the greater the stability. In this case, the most stable genotypes are G27 (VI 14239), G34 (VI 14881), and G31 (VI 14708). However, these genotypes have a low grain yield in most environments. In general, the less productive a genotype is, the more stable it tends to be, as it consistently underperforms in many environments. The G36 (VI 14980) presented the greatest distance, evidencing a low estimate of prediction of productive behavior, which is different from the previous HMRPGV analysis.

The genotypes derived from cultivar BRS 264 (G21, G22 and G23) in its *pedigree* are among the best results for stability. Other studies have already reported the high productivity, adaptability, and stability of this genotype under Brazilian Cerrado

conditions (Albrecht et al., 2007). This cultivar occupies 70% of the cultivated area in the Cerrado of Brazil and the world record for daily productivity: $9,630 \text{ kg ha}^{-1}$, that is, $80.9 \text{ kg ha}^{-1} \text{ day}^{-1}$. Based on this, it is suggested that stability and adaptability are complex traits and are confused with grain yield. Their inheritance should be better investigated to optimize the selection of this trait in wheat breeding programs.

Based on the graphic representation *Which-won-Where* (Fig. 05C), the genotypes G21, G23, G22, G15, G3, G27, G35, G32, and G36 are the furthest from the Biplot origin and have a better performance in one or more environments. Therefore, these genotypes delimit the area of the polygon. The blue dotted lines leaving the center of the Biplot (0,0) delimit the diagram in nine different sectors, with the formation of three distinct mega-environments (ME). The first mega-environment (ME1) is composed of only E1, the second mega-environment (ME2) is composed of the environments E2, E3, E4, E5, E6 and E7, and the third mega-environment (ME3) is composed of the E8 environment. Each mega-environment can be defined as a group of environments where one or more genotypes show a high adaptability, similar to what occurs in environmental stratification analyses. The three mega environments formed by the GGE Biplot analysis corroborate the results obtained in the environmental stratification analysis due to the formation of subgroups with a non-significant $G \times E$ interaction. G22 showed high adaptability to ME1, G21 and G23 showed better performance in ME2, while the genotypes G36 and G32 showed high adaptability to ME3. The genotypes present in sectors where there is no environment were not responsive to any environment studied.

ME1 and ME3 were more discriminative, while ME2 was more representative (Fig. 05D), especially the E6, a rainfed environment with blast inoculation. Mushayi et al. (2020) report that ideal environments for selection must be discriminatory and representative; however, no ME in this study was classified as ideal (Fig. 05E). Discriminatory but not representative environments can be used to select genotypes adapted to specific environments. Representative and homogeneous environments are ideal for the selection of widely adapted lines (Bányai et al., 2020). A genotype is considered ideal when high productive performance is linked to high stability. The genotypes closer to the center of the concentric circles are the most desirable and present a behavior close to that of the ideal genotype ideotype (Fig. 05F). In this study, the genotypes G21, G23, G16, G1, G4, and G22 are the closest to a hypothetical ideal genotype according to the GGE Biplot methodology. These results corroborate those found through the WAASBY index (Fig. 06).

Conclusions

The genotypes VI 14127, VI14197, VI14026, and BRS 264 were selected simultaneously by the HMRPGV and GGE Biplot method as highly productive, adaptable, and stable, being promising genotypes to be cultivated in the cerrado region. The environmental typing contributed to a better understanding of genotypic performance across contrasting environments. The grain yield was negatively correlated with the temperature at the dewpoint and relative humidity. The environment with a lower yield had natural rainfall and mild temperatures. Surprisingly, the environment with higher natural rainfall precipitation that received irrigation was the second less productive. There is strong evidence that the high temperatures ($> 30 \text{ }^\circ\text{C}$) during 75% of the days during boosting stage and during the entire stage of heading/flowering were the main limiting climate factor in this environment. Within that environment, VI14774 and VI14980 strains showed better performance ($\text{GY} > 3800 \text{ kg ha}^{-1}$) and are potential germplasm sources for high-temperature environments at the boosting and heading/flowering stages. Overall, this study provides new insights on how the environment typing can be useful to better understand the genotype-by-environment interaction and help to breed new climate-resilient wheat cultivars for the cerrado region. The joint use of HMRPGV and GGE Biplot methodologies is highly promising in exploring the $G \times E$ interaction, especially in situations with contrasting environments.

Declarations

Acknowledgments

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The authors declare that they have no conflict of interest.

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Figures

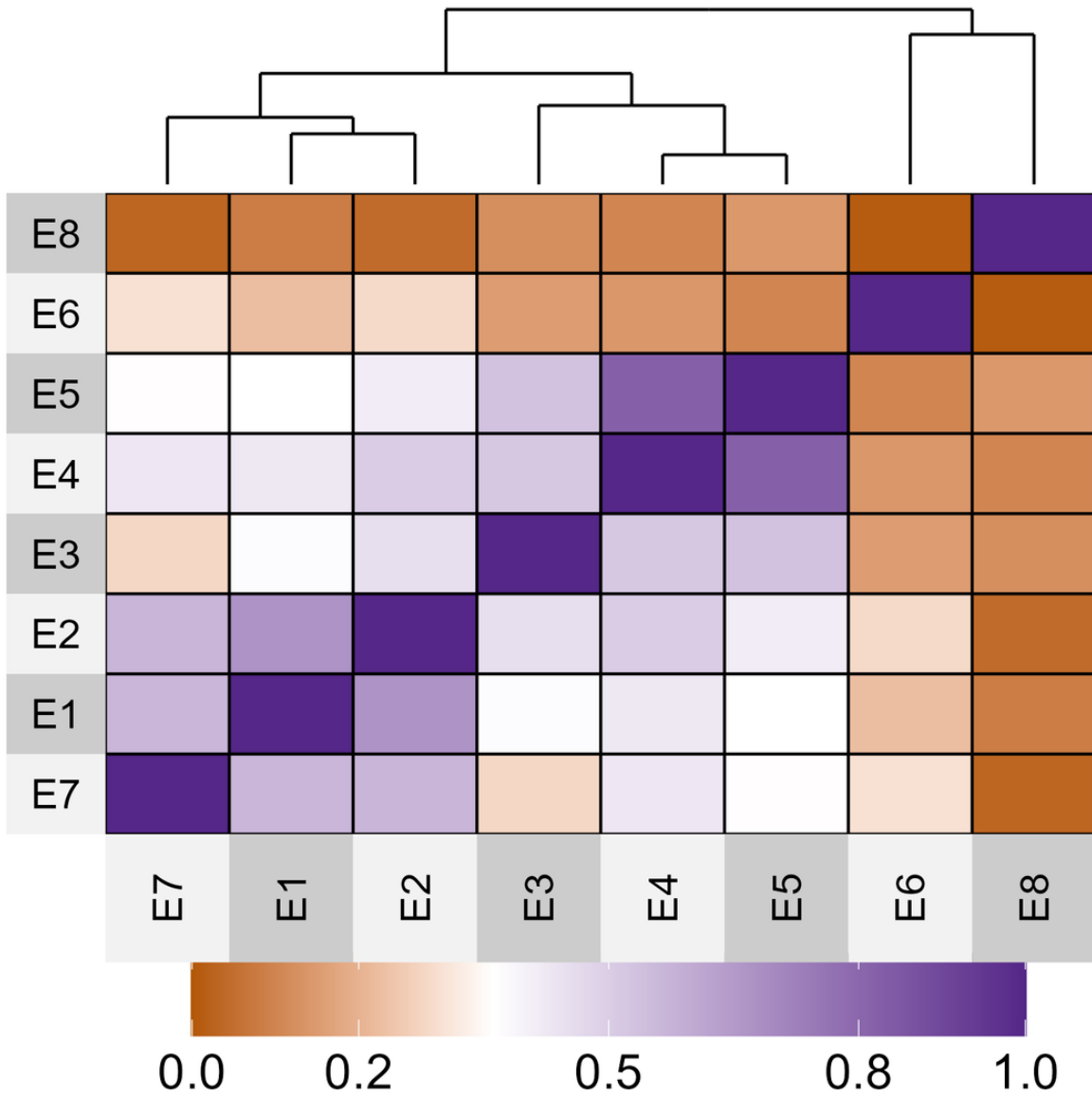


Figure 1

Nonlinear enviromic kernels (Gaussian) based on 14 environmental covariates over eight tropical wheat environments (E1, E2, E3, E4, E5, E6, E7 and E8) shown in Table 1.

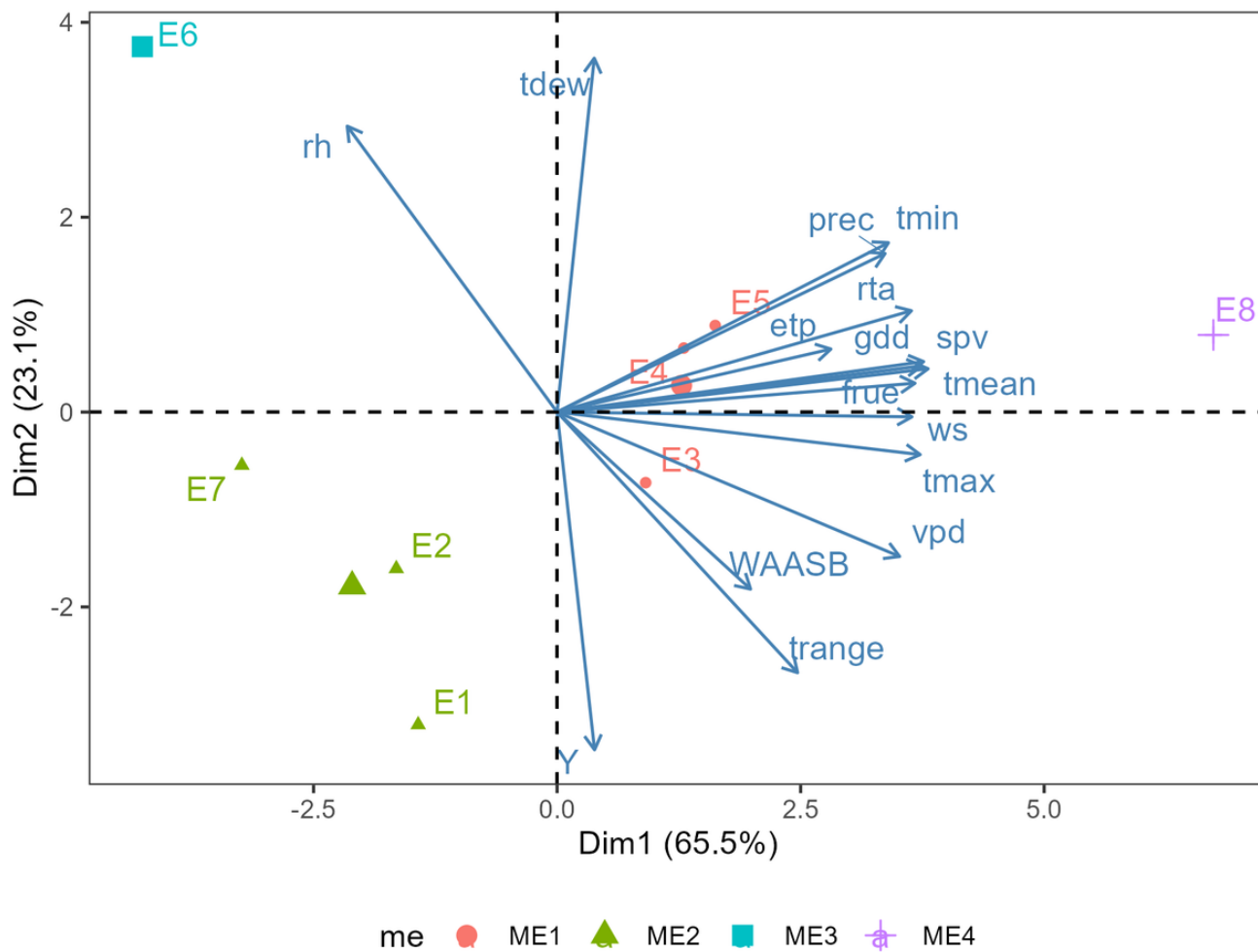


Figure 2

Principal Component Analysis with a two-way table containing the environmental variables, the WAASB index, and the average grain yield for each environment/season for 36 tropical wheat genotypes in eight environments considering G x E interaction as evaluated in the 2018, 2019, and 2020 crops seasons in the Brazilian Cerrado.

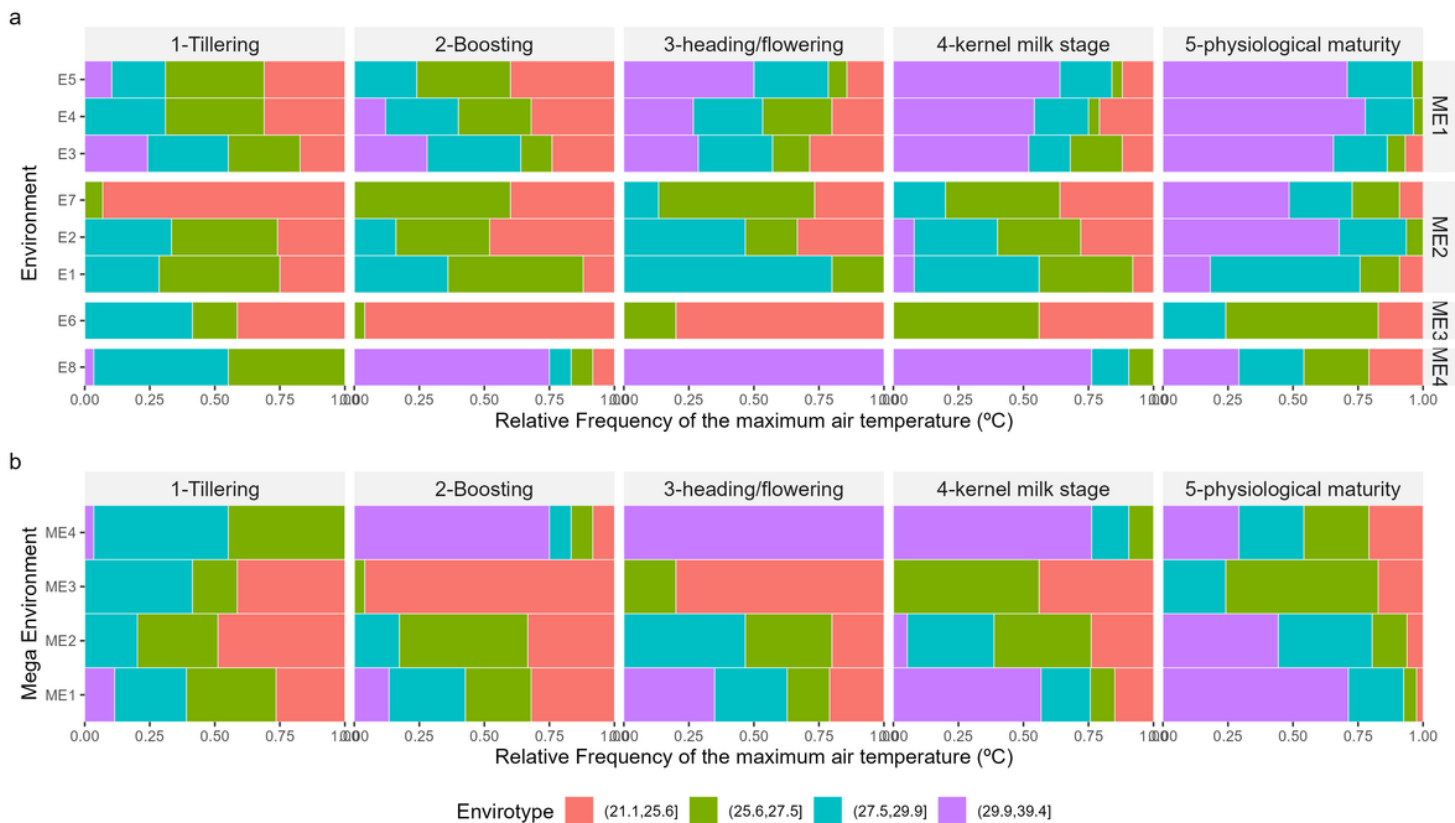


Figure 3

Workflow for a scale envirotyping analysis for maximum air temperature (TMAX, °C d⁻¹) effects variable at 8 environmental level and 4 Mega Environment at 5 development stages (tillering, boosting, flowering final, kernel milk stage and physiological maturity) in wheat (total 112 ECs).

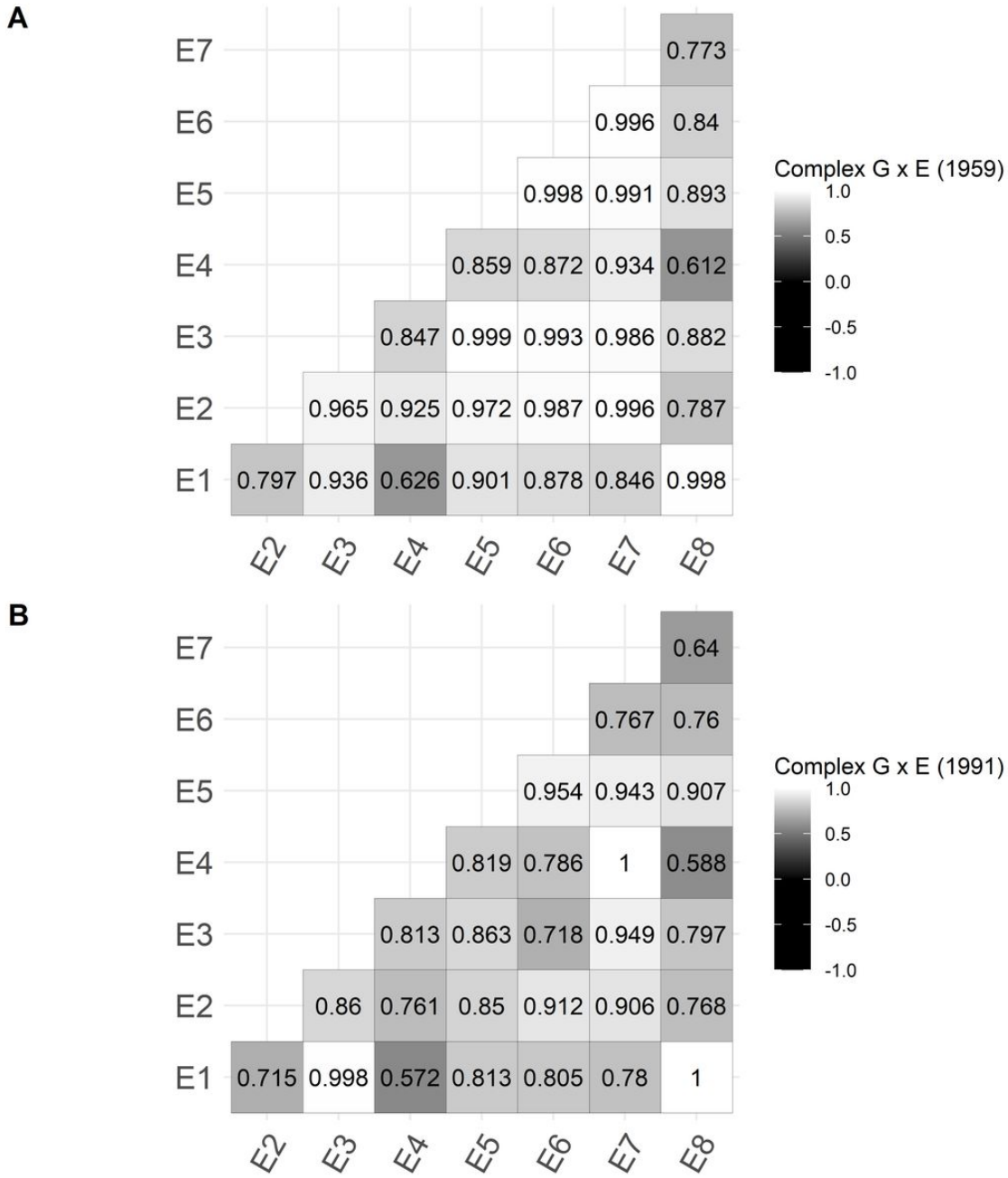


Figure 4

Percentage of $G \times E$ interaction of the complex part according to (A) Robertson (1959) and (B) Cruz and Castoldi (1991).

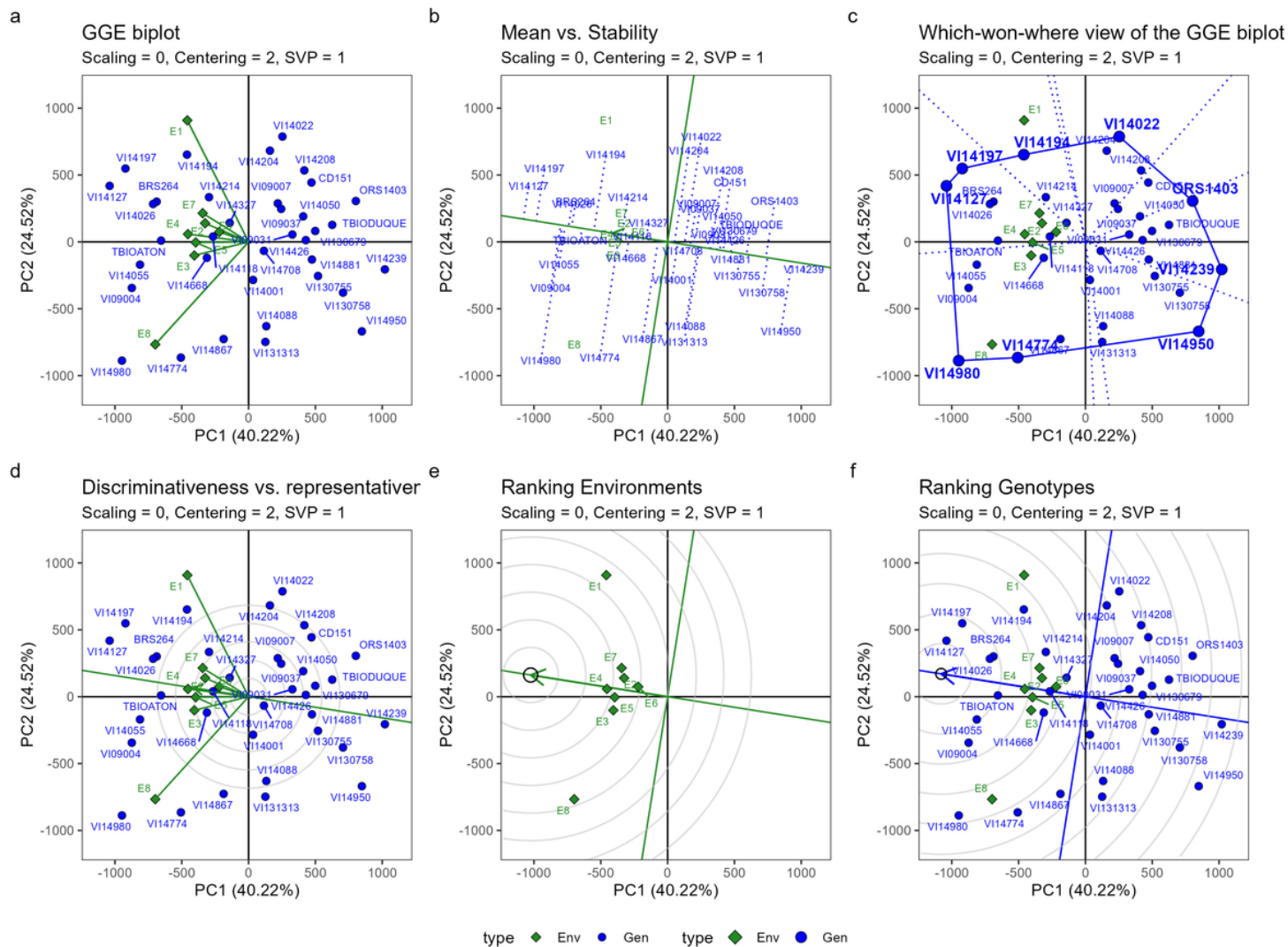


Figure 5

GGE Biplot graph (A), stability (B), polygon (C), environment discrimination (D), ideal environment (E), and ideal genotype (F) obtained by the GGE Biplot method considering the first two principal components (PC1 and PC2) for 36 tropical wheat genotypes as for grain yield (GY) in eight environments evaluated in the 2018, 2019, and 2020 crop seasons in the Brazilian Cerrado.

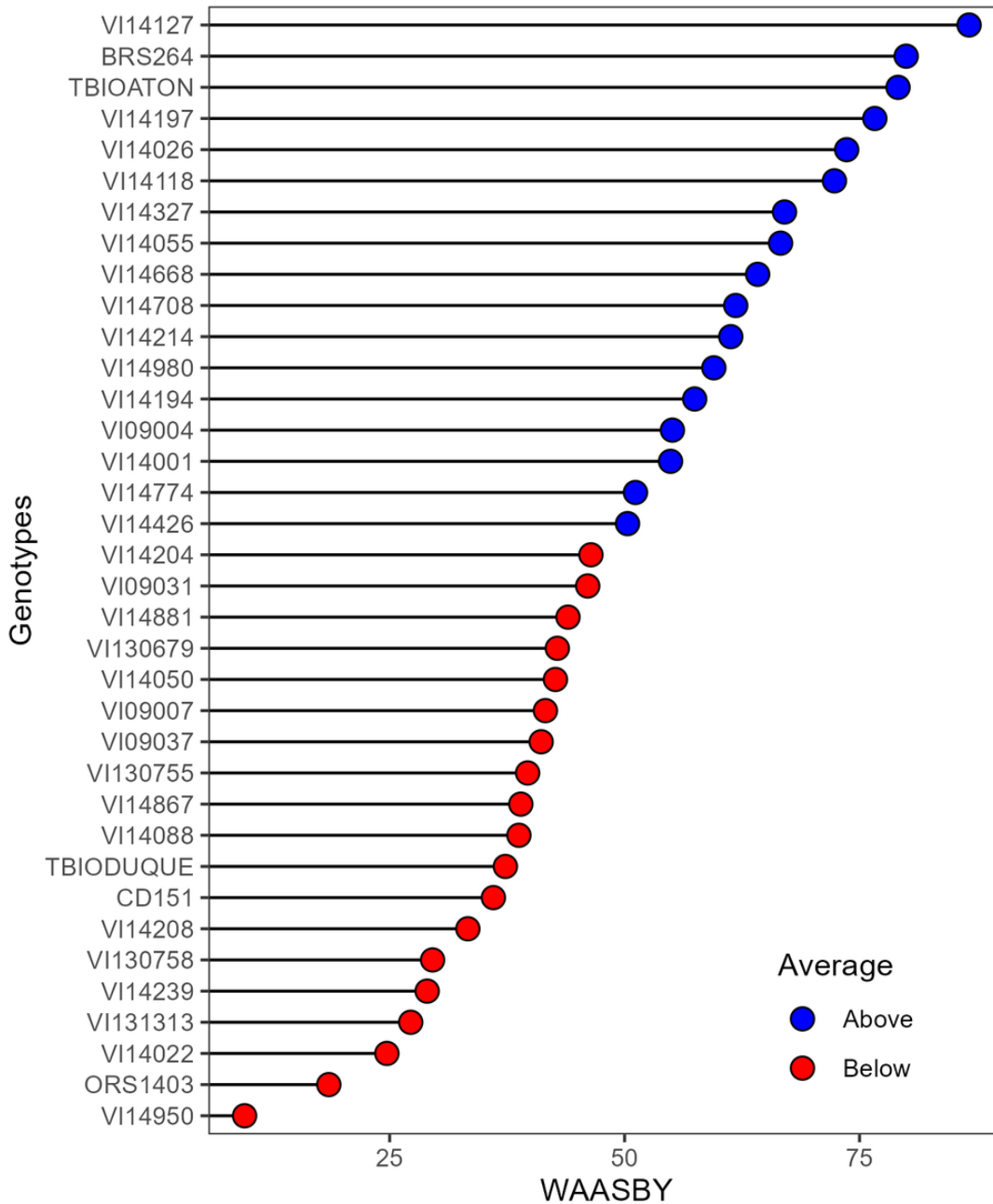


Figure 6

Estimated values of weighted average of stability (WAASB) and mean performance (Y) (WAASBY) for 36 tropical wheat genotypes as for grain yield (GY) in eight environments evaluated in the 2018, 2019, and 2020 crop seasons in the Brazilian Cerrado.

Supplementary Files

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