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DECOMPOSITION OF WHITE OAT PHENOTYPIC VARIABILITY BY ENVIRONMENTAL COVARIATES

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ABSTRACT

The study aims to quantify the effects of environmental variables on the interaction between genotypes x environments and to evaluate the sensitivity of white oat genotypes to grain yield in 10 years of cultivation. The experiment took place in the municipality of Augusto Pestana, Rio Grande do Sul State, Brazil. The experimental design used was in randomized blocks, being evaluated the grain yield of 26 white oat genotypes in 20 complex environments. Greater phenotypic stability was observed for the URS 21 genotype, by the AMMI and GGE methodologies. The URS Corona genotype showed general adaptation, high genetic value and predictable environmental variations by the GGE method and reaction norm. Higher minimum air temperature and lower medium temperature and relative air humidity enhance the productive performance of white oat genotypes. The genotypes URS 22, Fapa Slava, IPR Afrodite and Estampa express positive responses to the covariates temperature medium, maximum, minimum and relative air humidity, respectively. Relative humidity explains more than 50% of the biological variation of white oat genotypes.

Keywords: *Avena sativa* L, factor analysis, AMMI, GGE, reaction norm

INTRODUCTION

In the last four years, the Southern Region of Brazil revealed that white oats exhibited a linear increase of 7% in the sown area (CONAB, 2022). At the same time, it drives an increase in area by the strong demand for the cereal by the consumer market, due to its multifunctional aspects. Its main feature, which gives it this name, is the presence of bioactive compounds in the grains. With 5.5% of beta-glucan present in grains, a compound that acts to reduce blood cholesterol (VETVICKA et al., 2019). Associated with large-scale use in animal feed, this cereal has great

social, economic and agricultural importance, requiring the development of genotypes with greater productive performance.

The performance of a genotype, that is, the phenotypic manifestation is the result of its gene expression under the influence of the environment (TAIZ et al., 2017). When there is an evaluation of the genotypes in a series of environments, in addition to the genetic (G) and environmental (E) effects, there is an addition of the effects of the G x E interaction. The differential response of genotypes in different environments is the concept of this phenomenon. Thus, when identifying its significance in the model, it is possible to use methods that will allow the identification of genotypes with high predictability or stability, as well as specific or broad adaptability (CRUZ et al., 2012).

Some of the main methodologies currently used in the evaluation of genotypes for adaptability and stability are AMMI and GGE methods (CARVALHO et al., 2016; SZARESKI et al., 2018; SZARESKI et al., 2021; PEIXOTO et al., 2022; TOMAZ et al., 2022). While AMMI has in its mathematical model additive effects of genotypes and environments plus the multiplicative effects of the G x E interaction, the GGE expresses only the main effect of the genotype plus the G x E interaction. There is an impulse of growing use of these methodologies by the possibility of plotting the results on a Biplot chart and for the ease of interpreting the results (YAN et al., 2007).

These methodologies do not stratify the contribution of environmental variables in the decomposition of the variability resulting from and causing the G x E interaction. Understanding the effects of environmental variables minimizes doubts about the explanation of the interaction, and allows inferences to be made to the positioning of a cultivar not only by the mean phenotypic or genetic value per se, but rather, by the affinity of its performance with the meteorological elements that make up the ambientomics.

These environmental variables such as maximum, minimum and medium air temperature, relative air humidity and precipitation provide an opportunity to explain the phenotypic variation of the genotypes. This becomes possible through the application of reaction norm models with the addition of covariates, commonly observed in animal breeding (AMBROSINI et al., 2016; VELOSO et al., 2016). There are few studies that apply reaction norms (random regression) in plant breeding, which is conceptualized as the phenotypic expression of a genotype, considered in all environmental situations in which the genotype can survive (NICOGLOU, 2015). There was no portrait of these inferences for the *Avena sativa* species, which is a pioneering work of great

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importance as it portrays a decade of yield data based on consolidated meteorological variables. In this context, the present study aims to quantify the effects of environmental variables on the interaction between genotypes x environments and to evaluate the sensitivity of white oat genotypes to grain yield in 10 years of cultivation.

MATERIALS AND METHODS

The experiment took place in the municipality of Augusto Pestana - RS, located at latitude of 28º26'25'S and longitude of 54º00'07'W, with an altitude of 288 meters. The climate, according to the Köppen classification, is *Cfa* and the soil characterization is typical dystroferric Red Latosol. The use of the experimental design was randomized blocks, organized in a 26 factorial scheme white oat genotypes x 20 (complex environments). The white oat genotypes evaluated were: Barbarasul (G1), Brisasul (G2), Carlasul (G3), Chiarasul (G4), FAEM Dilmasul (G5), Fapa 2 (G6), URS Guapa (G7), IAC 7 (G8), IPR Afrodite (G9), FAPA Louise (G10), UPF 18 (G11), UPFA 22-Temprama (G12), UPFA Gaudéria (G13), UPFA Ouro (G14), URS-21 (G15), URS Charrua (G16), URS Corona (G17), URS Estampa (G18), URS Fapa Slava (G19), URS Guará (G20), URS Guria (G21), URS Penca (G22), URS Tarimba (G23), URS Taura (G24), URS Torena (G25), URS-22 Londrina (G26).

The environments were built by the effects of agricultural years (2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016 and 2017), in which two management scenarios were applied in each year contrasting absence (SF) and presence of the use of fungicides (CF), forming 20 environments complex: Env_1 (2008+CF), Env_2 (2009+CF), Env_3 (2010+CF), Env_4 (2011+CF), Env_5 (2012+CF), Env_6 (2013+CF), Env_7 (2014+CF), Env_8 (2015+CF), Env_9 (2016+CF), Env_10 (2017+CF), Env_11 (2008+SF), Env_12 (2009+SF), Env_13 (2010+SF), Env_14 (2011+SF), Env_15 (2012+SF), Env_16 (2013+SF), Env_17 (2014+SF), Env_18 (2015+SF), Env_19 (2016+SF) e Env_20 (2017+SF).

Sowings always took place in the first half of May in each environment. There was a use of density of 400 viable seeds per square meter with a base fertilization of 200 kg ha^{-1} of formulated fertilizer 03-15-10 (N-P-K). The experimental units consisted of five sowing rows, spaced at 20 cm, five meters long, totaling 5 m². In the development stage of four expanded leaves, 60 kg ha^{-1} of nitrogen had the application in topdressing. The harvest took place in the second half of October,

when there was the achievement of the grain yield (GY, kg ha^{-1}). The meteorological variables used in the present study were: maximum air temperature (Tmax, ºC), medium air temperature (Tmed, ºC), minimum air temperature (Tmin, ºC), relative humidity (RH, %) and precipitation rainfall (Prec, mm), obtained through the Nasa Power platform via R software, EnvRtype package (R CORE TEAM, 2022).

Grain yield data were submitted to the assumptions of error normality using the Shapiro Wilk test and homogeneity of residual variances using the Bartlett test. Variation factors were analyzed together to identify the interaction at 5% probability through the F test. Once the interaction between genotypes x environments was observed, the Additive Main Effects and Multiplicative Interaction (AMMI) method was applied. This model is given by:

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{n} \lambda_k \gamma_{ik} \alpha_{jk} + \rho_{ij} + \varepsilon_{ij}$$

Where: Y_{ij} is the average productivity of genotype i in environment j; μ: general average; g_i: genotype effect; e_j: effect of the environment; λ_k: is the singular value for the k-th axis of the principal component; γ_{ik}: is the i-th element of the k-th eigenvector of genotypes; α_{jk}: is the j-th element of the k-th eigenvector of environments; ρ_{ij}: is the additional error to be eliminated from the G x E interaction analysis; ε_{ij}: is the experimental error (DUARTE & VENCOVSKY, 1999).

The Genotype and Genotypes by Environments Interaction (GGE) method is supported by the model:

$$\bar{Y}_{ij} - \mu_j = \sum_{k=1}^{t} \lambda_1 \alpha_{i1} \gamma_{j1} + \lambda_2 \alpha_{i2} \gamma_{j2} + \varepsilon_{ij}$$

Where: $\bar{Y}_{ij}$: represents the average productivity of the i-th genotype in the j-th environment; μ_j: is the general average of genotypes in environment j; i=1, ..., g; j = 1, ... e, g and e being the numbers of genotypes and environments, respectively; t: is the number of main components used in the model; $\lambda_1 \alpha_{i1} \gamma_{j1}$: is the first principal component; $\lambda_2 \alpha_{i2} \gamma_{j2}$: is the second principal component; λ_1 e λ_2: are the eigenvalues associated with the first and second principal components, respectively; α_{i1} and α_{i2}: are the scores of the first and second principal components, respectively, of the e-th genotype; and γ_{j1} and γ_{j2}: are the scores of the first and second principal components,

respectively, for the jth environment; ε_{ij}: is the model error associated with the i-th genotype and j-th environment (YAN & KANG, 2003).

In order to select the meteorological covariates with the greatest contribution to the biological variance, factor analysis was applied through the model:

$$X_i = a_{i1}F_1 + a_{i2}F_2 + a_{i3}F_3 + \ldots a_{im}F_m + \varepsilon_i$$

On what: X_i: is the i-th score; a_{i1}, a_{i2}, a_{i3}, ..., a_{im}: are the factor loadings for the i-th test; F_1, F_2, ⋯, F_m refers to the j-th common factor; ε_i: refers to the error associated with a specific factor. The reaction norm was applied to understand the sensitivity of genotypes as a function of meteorological covariates selected by factor analysis. For this, the reaction norm model was used:

$$\{ge_{ij}\} = \sum_{t}^{T} \{\beta_{ti}\,\lambda_{tj} + ge_{(ij)}\}$$

On what: λ_{tj}: is the value of the t-th covariate in the j-th environment andβ_{ti}: is the coefficient of genotypic sensitivity or adaptability of the i-th genotype to the effect of the t-th environmental covariate (COSTA NETO et al., 2020; COSTA NETO et al., 2021).

Descriptive analysis of the genotype means in each environment had a performance, represented in a heat map. All analyzes were performed using the R software version 4.1.3 (R CORE TEAM, 2022), using the packages ggplot2, foreach, doParallel, gge, GGEBiplots, superheat, BGLR, devtools, FW e EnvRtype.

RESULTS AND DISCUSSION

The heat map allows the dynamic observation of the performance of genotypes, environments and G x E interaction in the expression of grain yield (Figure 1). It is observed that the green tones characterize the average tendencies of the dependent character. It is evident, specific manifestations maximized (yellow tones) or minimized (dark tones). In this order, the environments Env_9 (2016+CF), Env_17 (2014+SF) and Env_11 (2008+SF) tend to provide conditions for the high expression of grain yield for most genotypes. Levels with contrasting differential responses were observed, such as URS Corona grown in the Env_17 (2014+SF) environment (4,812.1 kg ha^{-1}) considered to have high productive performance, while the low grain yield was obtained by UPF 18 in the Env_2 (2009+CF) environment (385.3 kg ha^{-1}). In this sense,

it is inferred that the environments Env_14 (2011+SF) and Env_9 (2016+CF) strongly contribute to the manifestation of the interaction, since they are characterized by the limits of the lower and upper environmental index, respectively. The Fapa 2 and URS Corona genotypes show a high contribution to the G x E interaction.

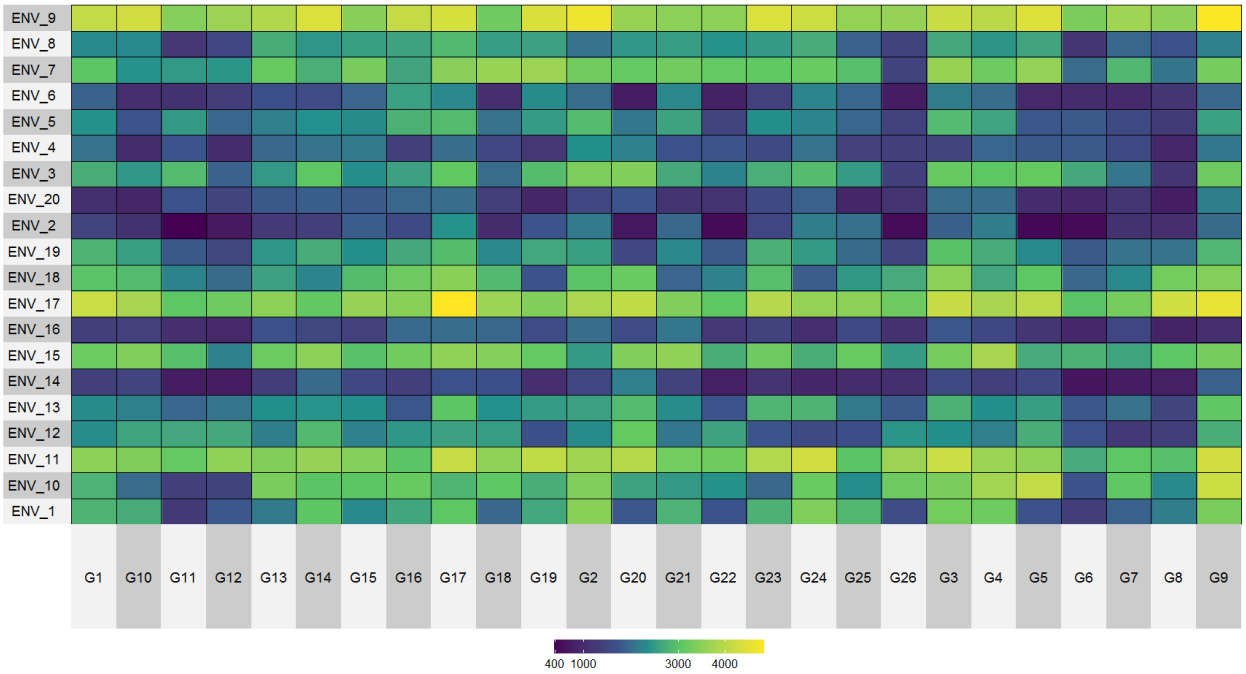

Figure 1. Heat map corresponding to the averages of grain yield (Kg ha^{-1}) of the 26 genotypes evaluated in 20 environments. Each color of the network represents an expression magnitude of the mean, with blue representing low average grain yield and yellow representing high average grain yield. Genotypes: Barbarasul (G1), Brisasul (G2), Carlasul (G3), Chiarasul (G4), FAEM Dilmasul (G5), Fapa 2 (G6), URS Guapa (G7), IAC 7 (G8), IPR Afrodite (G9), FAPA Louise (G10), UPF 18 (G11), UPFA 22-Temprama (G12), UPFA Gaudéria (G13), UPFA Ouro (G14), URS-21 (G15), URS Charrua (G16), URS Corona (G17), URS Estampa (G18), URS Fapa Slava (G19), URS Guará (G20), URS Guria (G21), URS Penca (G22), URS Tarimba (G23), URS Taura (G24), URS Torena (G25), URS-22 Londrina (G26). Environments: Env_1 (2008+CF), Env_2 (2009+CF), Env_3 (2010+CF), Env_4 (2011+CF), Env_5 (2012+CF), Env_6 (2013+CF), Env_7 (2014+CF), Env_8 (2015+CF), Env_9 (2016+CF), Env_10 (2017+CF), Env_11 (2008+SF), Env_12 (2009+SF), Env_13 (2010+SF), Env_14 (2011+SF), Env_15 (2012+SF), Env_16 (2013+SF), Env_17 (2014+SF), Env_18 (2015+SF), Env_19 (2016+SF) e Env_20 (2017+SF).

The individual residual variances of each environment provided the conjugation in a single analysis of variance through the manifestation of the *Cocchhan* test below magnitude seven. Thus, the joint ANOVA showed a significant effect of the interaction between genotypes x environments for grain yield (Table 1). In this context, it was possible to apply the AMMI method, in order to represent its main and multiplicative effects through main components (PC_1 and PC_2). $AMMI_1$ and $AMMI_2$ models were used, with principal components evidencing the explanation of 42.90% of the variation in the sum of squares of the genotypes x environments interaction (SQ_{GxE}), with PC_1

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responsible for 27.30% and PC_2 15.60%. This great variability and the difficulty in having a high representation in the vertex are due to the nature of the grain yield characteristic, which definition is by a large set of genes that interact with each other and result in low heritability, as well as genotypic correlations of the genotype performance with complex nature (YOKOMIZO et al., 2013).

Regarding the explanation of the SQ_{GxE} through the main components, Oliveira et al. (2003) point out that the maximum explanation of this sum of squares should not be sought, as they capture a greater percentage of the standard fraction of the G x E interaction. While the accumulation of components reduces the standard fraction and increases the effects of errors in the experimental conditions (CARVALHO et al., 2016). Although the selection of a few components does not exhibit a high explanation of the original SQ_{GxE} portion, it tends to capture a higher percentage of pattern and minimum noise (OLIVEIRA et al., 2003). In this sense, it has an understanding that 42.9% of the SQ_{GxE} have relevant information to infer about the behavior of the genotypes in the various environments tested. Two components are satisfactory for maximizing the chosen model and supported by consolidated works by Oliveira et al. (2003), Melo et al. (2018), Sing et al. (2019) and Szareski et al. (2021), who use 40 to 60% of explainability.

Table 1. Joint analysis of variance and splitting of interaction effects on interaction components for AMMI analysis.

Source	Df	Sum Sq	Mean Sq	Fvalue	Pr(>F)	Proportion	Accumulated
Env (E)	19	913070547.00	48056344.58	131.76	0.00E+00	-	-
Rep (Env)	40	14589392.70	364734.82	4.05	4.05E-15	-	-
Gen (G)	25	170812388.80	6832495.55	75.88	7.62E-211	-	-
G x E	475	218057053.90	459067.48	5.10	5.57E-104	-	-
PC_1	43	59422221.10	1381912.12	15.35	0.00E+00	27.30	27.30
PC_2	41	34099401.70	831692.72	9.24	0.00E+00	15.60	42.90
Residue	1000	90044572.80	90044.57	-	-	-	-
Total	2034.00	1624619240.20	798731.19	-	-	-	-

Significant at 5% probability. Env: Environments; Rep: Repetition; Gen: Genotype; PC1: first main component; PC2: second main component.

For AMMI1, the genotypes FAEM Dilmasul and URS Guará contributed enormously to the effects of the G x E interaction, obtaining PC_1 scores above 20 (Figure 2A). Stability or predictability of the phenotypic response above the general average of grain yield has the base to IPR Afrodite genotype. On the other hand, only environment Env_9 (2016+CF) is considered as a cause of stability and high grain yield, a fact that is not attributed to environments Env_14 (2011+SF), Env_2 (2009+CF), Env_16 (2013+SF), Env_20 (2017+SF) and Env_4 (2011+CF), considered undesirable with low character average.

Through $AMMI_2$, considered a complement to the manifestation of the explanation of the total variation of the interaction, it was evidenced that Env_11 (2008+SF) and Env_8 (2015+CF) environments are considered stable, but with contrasting performance in terms of grain yield (Figure 2B). Smaller deviations contributing to the G x E interaction were obtained using the URS21 and UPFA Gaudéria genotypes, with high magnitude additions for grain yield. It can be seen that stable genotypes may not reflect high grain yield, on the other hand, unstable genotypes may have high deviations and their performance may be far from the general average. Duarte and Vencovski (1999) report that these genotypes should not be discarded, since they may exhibit specific adaptability to environments with intrinsic characteristics. Therefore, specific adaptability was found for URS Guará, UPF 18, UPFA 22 Temprana, Fapa 2, URS Penca and UPFA Ouro under the conditions of Env_12 (2009+SF), Env_3 (2010+CF), Env_16 (2013+SF), Env_20 (2017+SF), Env_4 (2011+CF), Env_15 (2012+SF) and Env_13 (2010+SF).

For the GGE inferences using the mean x stability (Figure 3A), it allows comparing the stability and grain yield of the genotypes between environments and the formation of the mega-environment (YAN et al., 2007). The arrow on the abscissa axis called the mean environmental axis (RAD et al., 2013) indicates the main effect of genotypes on grain yield. Higher yields are inferred for IPR Afrodite, URS Corona and Carlasul. The proximity of the genotypes to the origin of the medium axis of the environment indicates greater stability (OLADOSU et al., 2017), which characterizes that URS21 has high stability. However, URS Guará and FAEM Dilmasul are considered unstable, but with high productivity. Under these conditions, the genotypes Carlasul and URS Corona were considered major contributors to the G x E interaction.

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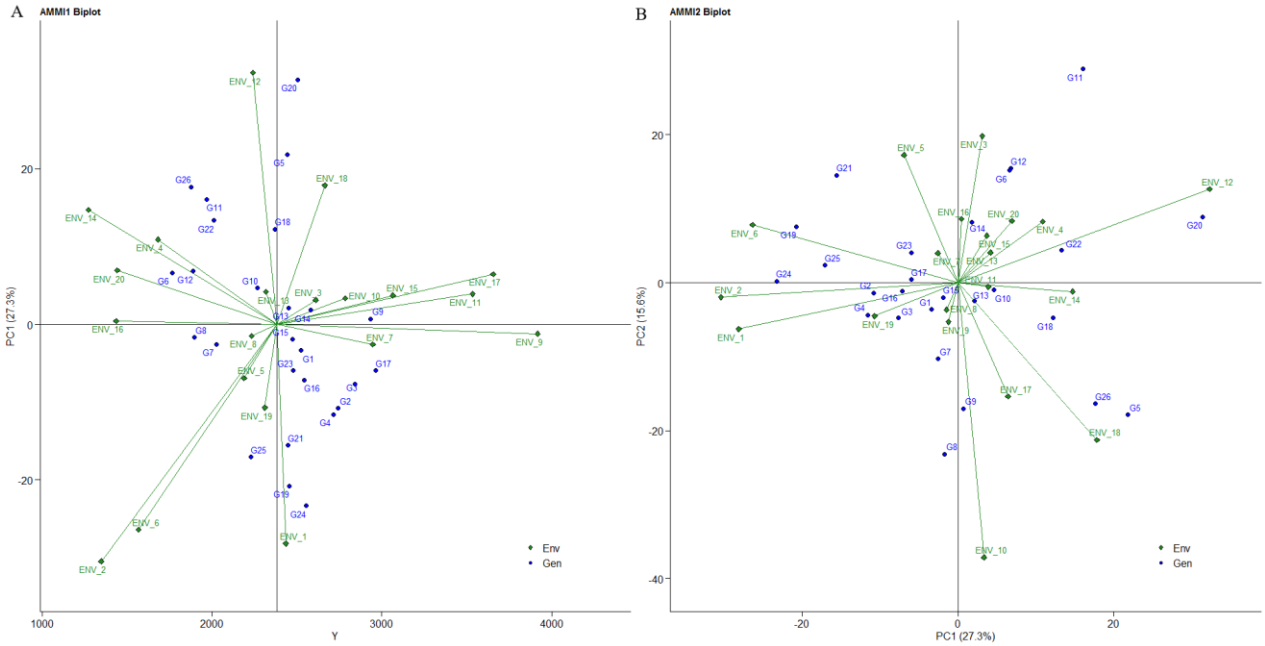

Figure 2. AMMI biplot analysis for grain yield (kg ha^{-1}) for 26 white oat genotypes (G) evaluated in 20 growing environments (E). Genotypes: Barbarasul (G1), Brisasul (G2), Carlasul (G3), Chiarasul (G4), FAEM Dilmasul (G5), Fapa 2 (G6), URS Guapa (G7), IAC 7 (G8), IPR Afrodite (G9), FAPA Louise (G10), UPF 18 (G11), UPFA 22-Temprama (G12), UPFA Gaudéria (G13), UPFA Ouro (G14), URS-21 (G15), URS Charrua (G16), URS Corona (G17), URS Estampa (G18), URS Fapa Slava (G19), URS Guará (G20), URS Guria (G21), URS Penca (G22), URS Tarimba (G23), URS Taura (G24), URS Torena (G25), URS-22 Londrina (G26). Environments: Env_1 (2008+CF), Env_2 (2009+CF), Env_3 (2010+CF), Env_4 (2011+CF), Env_5 (2012+CF), Env_6 (2013+CF), Env_7 (2014+CF), Env_8 (2015+CF), Env_9 (2016+CF), Env_10 (2017+CF), Env_11 (2008+SF), Env_12 (2009+SF), Env_13 (2010+SF), Env_14 (2011+SF), Env_15 (2012+SF), Env_16 (2013+SF), Env_17 (2014+SF), Env_18 (2015+SF), Env_19 (2016+SF) e Env_20 (2017+SF).

Environments that express unique information must be identified, as they do not provide unique information about genotypes. Discarding some similar environments can reduce driving costs and maximize test efficiency. In Figure 3B, the environments Env_5 (2012+CF) and Env_19 (2016+SF) reliably express this correlation and classification of genotypes (YAN et al., 2007). According to Yan et al. (2007), the environment vector discriminates the environment through standardized data (Scalling = 0). Thus, it is possible to identify environments that contribute significantly with information about the genotypes, simply by long vectors in the Biplot. It can be seen that Env_12 (2009+SF), Env_10 (2017+CF) and Env_2 (2009+CF) environments are discriminating. However, their vectors form large angles with the abscissa axis and are not recommended for use in the selection of superior genotypes. Env_7 (2014+CF), Env_8 (2015+CF) and Env_9 (2016+CF) environments are considered the most discriminating and representative for

the selection of superior genotypes with long vectors and minimum angles in relation to the abscissa.

Short vectors close to the data origin are reflected for the environments Env_15 (2012+SF) and Env_16 (2013+SF) are similar with low contribution between the variability of the genotypes. The environments Env_3 (2010+CF), Env_11 (2008+SF), Env_13 (2010+SF), Env_20 (2017+SF) and Env_17 (2014+SF) are representative and trainers of the mega-environment considered and obtained by smaller angles between their vectors.

The genotype classification (Figure 3C) allows identifying the best performance of URS Corona, FAEM Carlasul genotype due to the proximity to the arrow in the concentric circle, resulting in greater phenotypic stability or predictability. This classification indicates that these genotypes are ideal in all evaluated environments, considered promising. Figure 3D represents the ranking of the ideal environments for the selection of superior genotypes that should present long vectors, small angles with the abscissa and close to the center of the concentric circle. In this sense, Env_7 (2014+CF) and Env_8 (2015+CF) environments were considered ideal for the selection of genotypes aimed at grain yield.

Based on information from 26 genotypes cultivated in 20 environments, the GGE method inferred the division of eight sections (Figure 3E). The genotypes URS Taura and URS Fapa Slava expressed the highest grain yield and were highly stable mainly in Env_2 (2009+CF) and Env_6 (2013+CF) environments. On the other hand, the genotypes URS Corona and IPR Afrodite exhibited the best performance in the section formed by the largest number of environments. However, the genotypes located at the vertex of the polygon in a section without an environmental indicator, results in URS-22 Londrina, Fapa 2 and URS Torena presenting low performance (OLADOSU et al., 2017). These results can be used to understand the performance relationships of the genotypes interrelated with the meteorological variables, allowing the phenotypic decomposition of the differential effects of the genotype x environment interaction.

The genetic values derived from grain yield allow inferring the stability of the genotypes (Figure 4). The residual variance indicates the stability of the genotypes, since high residual variances reveal high oscillations in the performance of the genotypes in different environments. Genotypes with breeding values of 1.200 kg ha^{-1}, 2.600 kg ha^{-1}, 400 kg ha^{-1} and 3.500 kg ha^{-1} are considered unstable due to high residual variance, in contrast, breeding values of 1.900 kg ha^{-1}, 1.850 kg ha^{-1}, 2.000 kg ha^{-1} and 2.050 kg ha^{-1} may show less instability.

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The identification of the quadrants revealed that quadrant I contains the unstable genotypes with genetic value lower than the general average of the experiment, with decreasing instability for UPF 18, IAC 7, URS-22 Londrina and URS Estampa. In relation to quadrant II referring to the genotypes URS Guará, URS Taura, FAEM Dilmasul, URS Fapa Slava and URS Charrua were defined as having superior breeding value and low stability, breeding values below the general average and high stability are obtained through UPFA 22 -Temprana, FAPA Louise, URS Torena, URS Penca, Fapa 2 and URS Guapa, located in the third quadrant. The genotypes within the fourth quadrant express genetic values above the general average and present high stability, being genotypes more suitable for selection and close to the ideal genotype proposed by Yan and Kang (2003). In this classification, the URS Corona genotype can be considered as the one with the highest average genetic value and high stability, however, the Fapa 2 and URS Guará genotypes exhibit the lowest average genetic value and stability.

The slopes of the reaction norm for the genetic responsiveness of genotypes, that is, the ability to respond to favorable environmental conditions, ranged from 0.74 to 1.33 (Figure 5). Low slope coefficient indicates a low genotypic responsiveness to improved environmental conditions and, if combined with a low average genetic value, it is considered an undesirable genotype. Falconer (1990) describes that the slope of the reaction norm is closely associated with the G x E interaction and represents the environmental sensitivity of the genotypes in the reaction to the environment. Felipe et al. (2012) report that there is a tendency for the slope of the line, which represents the sensitivity of individuals to the environment, to be more positive as the intercept value (average genetic value) increases. In other words, it means that there is a tendency for genotypes with higher productive performance to exhibit a better response to favorable environments.

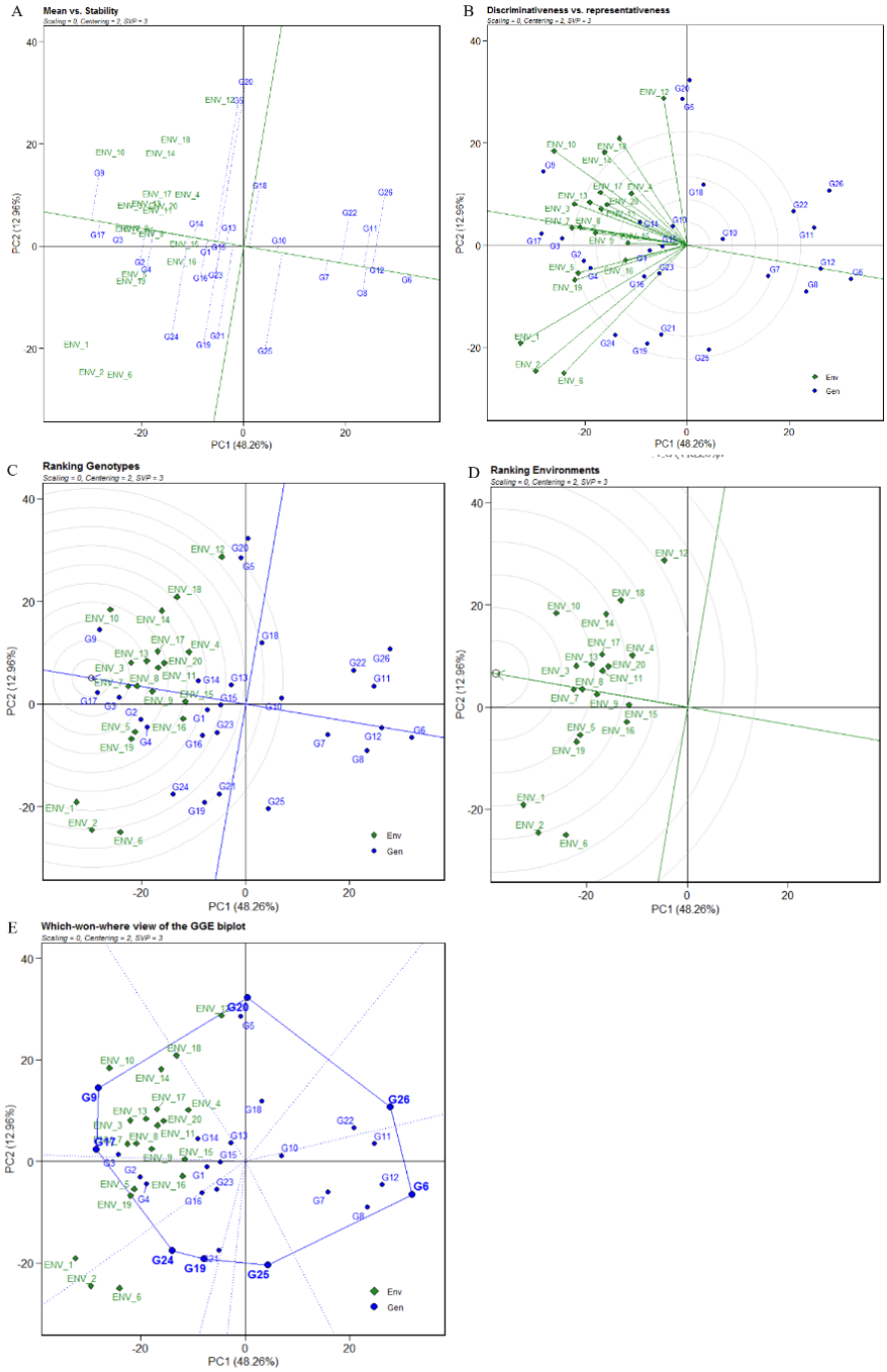

Figure 3. GGE biplot for grain yield (kg ha^{-1}) for 26 white oat genotypes (G) evaluated in 20 growing environments (E). Genotypes: Barbarasul (G1), Brisasul (G2), Carlasul (G3), Chiarasul (G4), FAEM Dilmasul (G5), Fapa 2 (G6), URS Guapa (G7), IAC 7 (G8), IPR Afrodite (G9), FAPA Louise (G10), UPF 18 (G11), UPFA 22-Temprama (G12), UPFA Gaudéria (G13), UPFA Ouro (G14), URS-21 (G15), URS Charrua (G16), URS Corona (G17), URS Estampa (G18), URS Fapa Slava (G19), URS Guará (G20), URS Guria (G21), URS Penca (G22), URS Tarimba (G23), URS Taura (G24), URS Torena (G25), URS-22 Londrina (G26). Environments: Env_1 (2008+CF), Env_2 (2009+CF), Env_3 (2010+CF), Env_4 (2011+CF), Env_5 (2012+CF), Env_6 (2013+CF), Env_7 (2014+CF), Env_8 (2015+CF), Env_9 (2016+CF), Env_10 (2017+CF), Env_11 (2008+SF), Env_12 (2009+SF), Env_13 (2010+SF), Env_14 (2011+SF), Env_15 (2012+SF), Env_16 (2013+SF), Env_17 (2014+SF), Env_18 (2015+SF), Env_19 (2016+SF) e Env_20 (2017+SF).

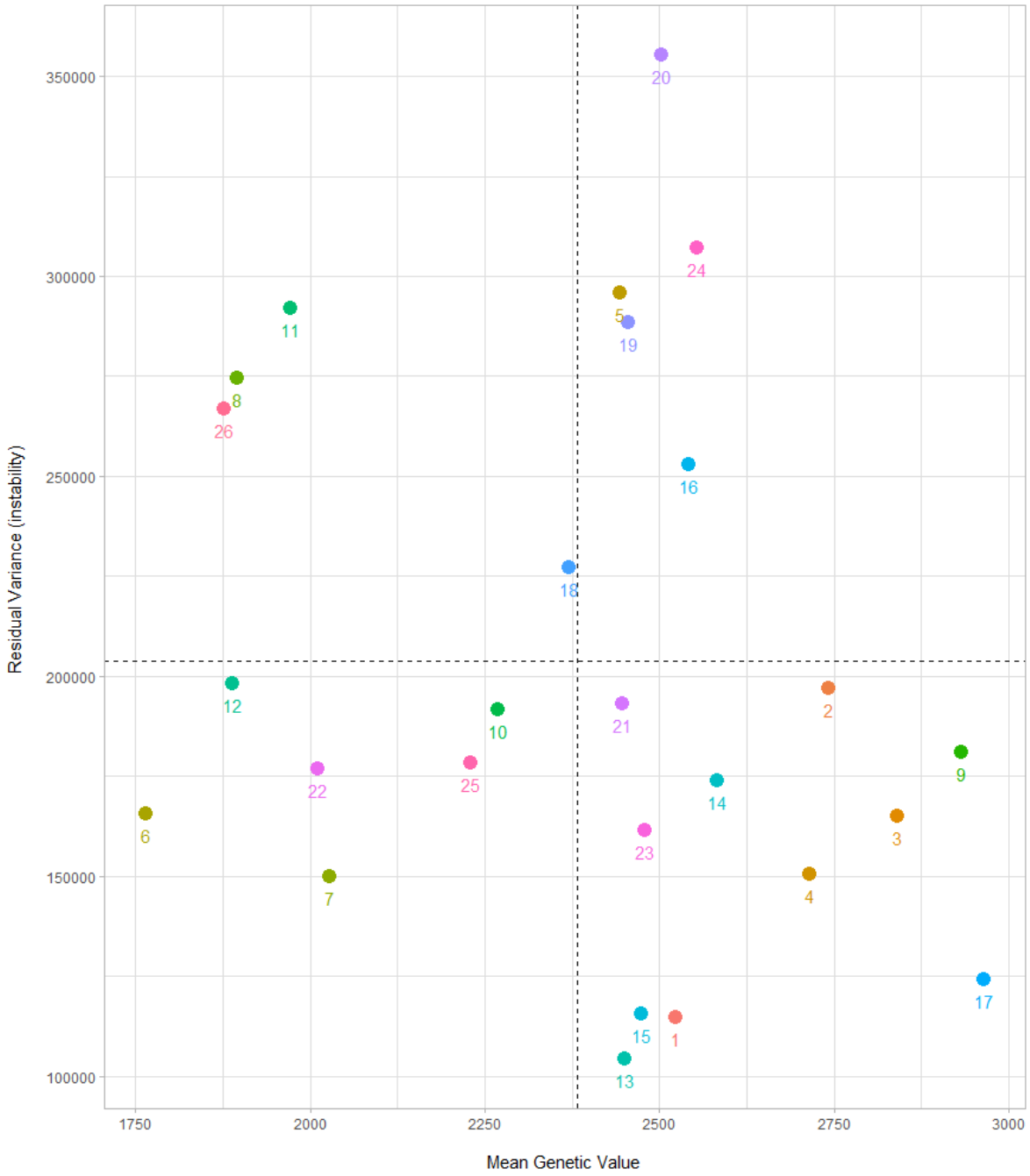

Figure 4. Reaction norm of mean breeding values of grain yield (Kg ha^{-1}) and residual variance (instability) for 26 white oat genotypes (G) evaluated in 20 growing environments (E). Genotypes: Barbarasul (1), Brisasul (2), Carlasul (3), Chiarasul (4), FAEM Dilmasul (5), Fapa 2 (6), URS Guapa (7), IAC 7 (8), IPR Afrodite (9), FAPA Louise (10), UPF 18 (11), UPFA 22-Temprama (12), UPFA Gaudéria (13), UPFA Ouro (14), URS-21 (15), URS Charrua (16), URS Corona (17), URS Estampa (18), URS Fapa Slava (19), URS Guará (20), URS Guria (21), URS Penca (22), URS Tarimba (23), URS Taura (24), URS Torena (25), URS-22 Londrina (26).

Similarly, to the interpretation of this coefficient, Cruz et al. (2012) describe that genotypes with angular coefficients equal to 1 reflect general adaptability to environments, while coefficients greater than 1 or less than 1 indicate genotypes with specific adaptation to favorable and unfavorable environments, respectively. Given this information, it is clear that the URS Corona genotype exhibits a high average genetic value and a slope coefficient close to 1, revealing its positive response for all environments. The IPR Afrodite genotype can be positioned for favorable environments, as it has a slope coefficient greater than 1 with high genetic value. Coefficient lower than 1 and genetic value higher than the general average is presented by the Brisasul genotype, indicating that it is promising in unfavorable environments. At the extremes in relation to abscissa, the FAEM Dilmasul and URS Guria genotypes show high adaptation to favorable and unfavorable environments, respectively, with genetic values above the general average. Interpretations can also be performed using the quadrants.

The reaction norm of the slope of the genetic responsiveness and residual variance indicates that the genotypes located in quadrant I and II and away from the abscissa express low stability as the genotypes URS Guará, URS Taura, UPF 18 and URS Fapa Slava (Figure 6). Whereas genotypes in quadrants III and IV away from the abscissa are the most stable. Genotypes in quadrant I and III have the capacity for genetic response to unfavorable environments, while in quadrants II and IV they express a positive response to favorable environments, the further away from the ordinate.

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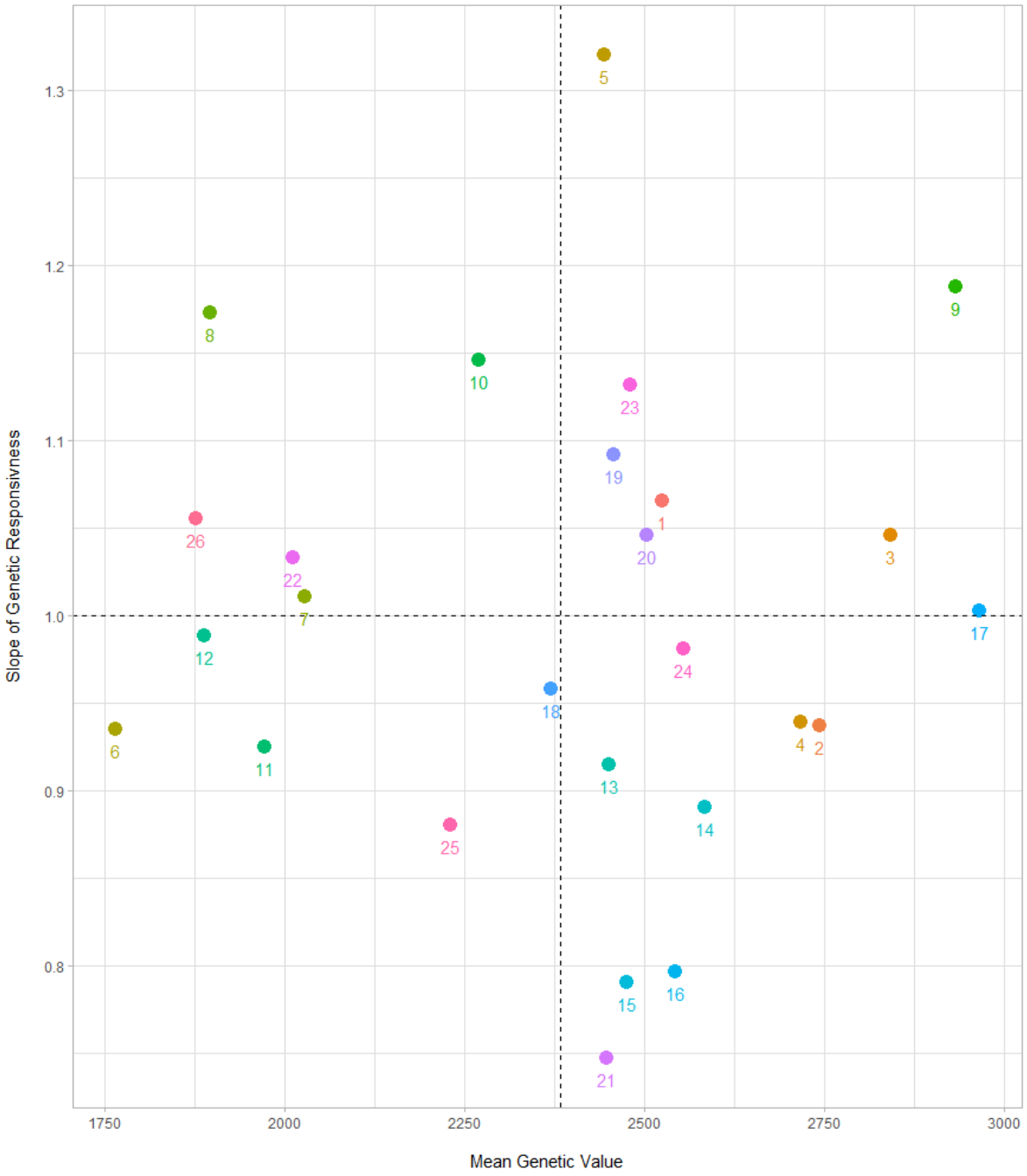

Figure 5. Reaction norm of mean breeding values of grain yield (Kg ha^{-1}) and slope of genetic responsiveness for 26 white oat genotypes (G) evaluated in 20 growing environments (E). Genotypes: Barbarasul (1), Brisasul (2), Carlasul (3), Chiarasul (4), FAEM Dilmasul (5), Fapa 2 (6), URS Guapa (7), IAC 7 (8), IPR Afrodite (9), FAPA Louise (10), UPF 18 (11), UPFA 22-Temprama (12), UPFA Gaudéria (13), UPFA Ouro (14), URS-21 (15), URS Charrua (16), URS Corona (17), URS Estampa (18), URS Fapa Slava (19), URS Guará (20), URS Guria (21), URS Penca (22), URS Tarimba (23), URS Taura (24), URS Torena (25), URS-22 Londrina (26).

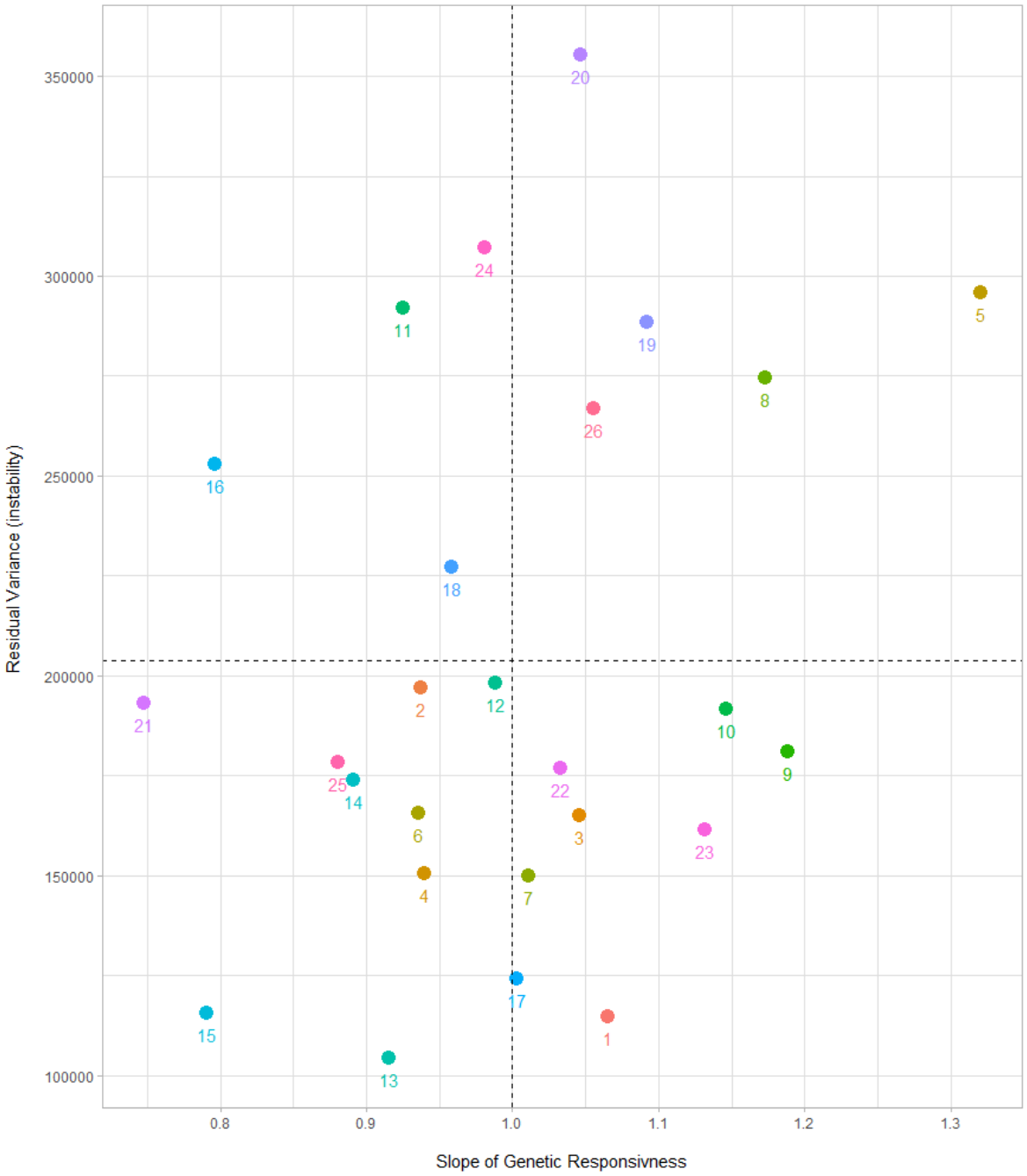

Figure 6. Reaction norm of residual variance (instability) and slope of genetic responsiveness for 26 white oat genotypes (G) evaluated in 20 growing environments (E). Genotypes: Barbarasul (G1), Brisasul (G2), Carlasul (G3), Chiarasul (G4), FAEM Dilmasul (G5), Fapa 2 (G6), URS Guapa (G7), IAC 7 (G8), IPR Afrodite (G9), FAPA Louise (G10), UPF 18 (G11), UPFA 22-Temprama (G12), UPFA Gaudéria (G13), UPFA Ouro (G14), URS-21 (G15), URS Charrua (G16), URS Corona (G17), URS Estampa (G18), URS Fapa Slava (G19), URS Guará (G20), URS Guria (G21), URS Penca (G22), URS Tarimba (G23), URS Taura (G24), URS Torena (G25), URS-22 Londrina (G26).

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Therefore, a broad genetic response capacity and high stability of the URS Corona genotype are observed. Thus, regardless of the evaluated environment, this genotype exhibits a positive response capacity to the improvement of the environment associated with predictability and high genotypic value for grain yield. The Barbarasul and UPFA Gaudéria genotypes are promising genotypes, since they are the most stable, with average genetic values above the general average and genetic responsiveness to favorable and unfavorable environments, respectively.

It is observed that more than 50% of the biological variance is associated with relative humidity, which is common in all genotypes (Figure 7). This indicates the power of explanation of this variable, as well as its importance in the genotype x environment interaction. Thus, it can be interpreted as responsible for the greater contribution of environmental effects on the phenotypic expression of the evaluated white oat genotypes.

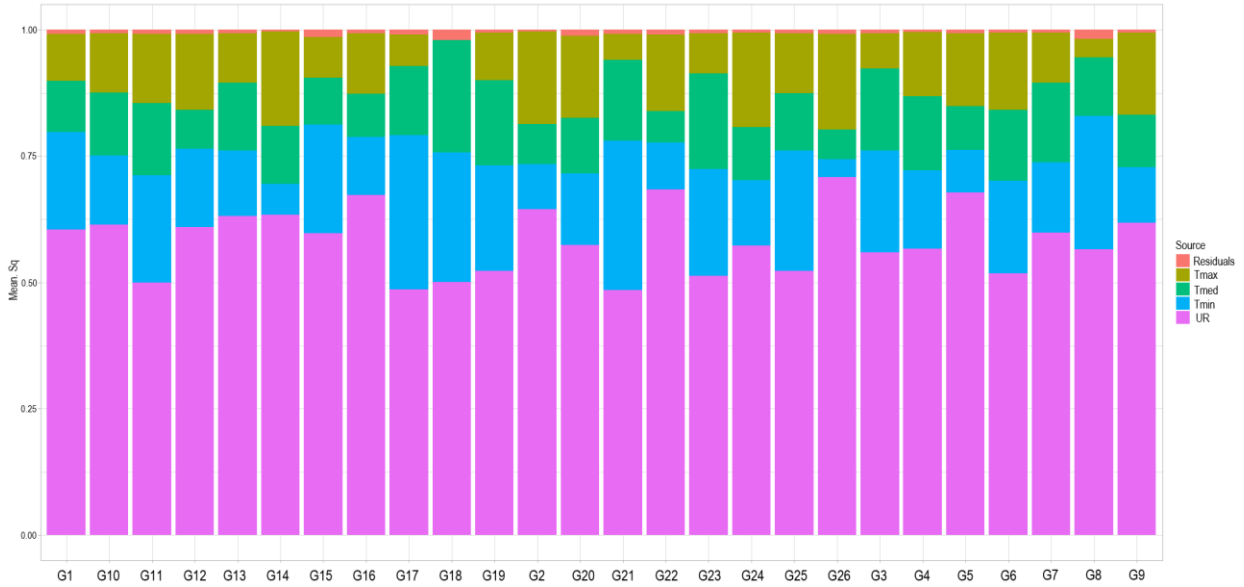

Figure 7. Biological decomposition of variance in meteorological covariates: maximum air temperature (Tmax, ºC), medium air temperature (Tmed, ºC), minimum air temperature (Tmin, ºC), relative air humidity (RH, %) for 26 genotypes of white oat (G) evaluated in 20 growing environments (E). Genotypes: Barbarasul (G1), Brisasul (G2), Carlasul (G3), Chiarasul (G4), FAEM Dilmasul (G5), Fapa 2 (G6), URS Guapa (G7), IAC 7 (G8), IPR Afrodite (G9), FAPA Louise (G10), UPF 18 (G11), UPFA 22-Temprama (G12), UPFA Gaudéria (G13), UPFA Ouro (G14), URS-21 (G15), URS Charrua (G16), URS Corona (G17), URS Estampa (G18), URS Fapa Slava (G19), URS Guará (G20), URS Guria (G21), URS Penca (G22), URS Tarimba (G23), URS Taura (G24), URS Torena (G25), URS-22 Londrina (G26).

The minimum air temperature explained 2 to 10% of the biological variation, varying according to the genotypes. Lower values of explanation are observed for the medium and

maximum air temperature, both have similarities in the percentage of explanation. Temperatures have a similar effect on the biological expression of the genotypes, this is because both are correlated with each other, that is, when there are high maximum temperatures there is also a strong tendency for the minimum temperature to also increase. It is observed that the model residual is extremely low, indicating a good reliability of the total explanation of the biological variation of the genotypes.

Genotypes located below the abscissa show negative regression or slope coefficients, indicating greater sensitivity to the environmental variable, in other words, a reduction in genetic value + intercept the greater the variable's units are (Figure 8). On the other hand, genetic values + intercept are potentiated when the genotypes are above the abscissa, indicating positive slope coefficients, that is, the genotype response tends to be greater than the measure at each increase of one unit of the environmental variable. In this sense, we look for genotypes that have high genetic value + intercept and low negative sensitivity to environmental variables.

Figure 8. Responsiveness stratified by meteorological variables: maximum air temperature (Tmax, ºC), medium air temperature (Tmed, ºC), minimum air temperature (Tmin, ºC), and relative air humidity (RH, %) for 26 oat genotypes white (G) evaluated in 20 growing environments (E). Genotypes: Barbarasul (G1), Brisasul (G2), Carlasul (G3), Chiarasul (G4), FAEM Dilmasul (G5), Fapa 2 (G6), URS Guapa (G7), IAC 7 (G8), IPR Afrodite (G9), FAPA Louise (G10), UPF 18 (G11), UPFA 22-Temprama (G12), UPFA Gaudéria (G13), UPFA Ouro (G14), URS-21 (G15), URS Charrua (G16), URS Corona (G17), URS Estampa (G18), URS Fapa Slava (G19), URS Guará (G20), URS Guria (G21), URS Penca (G22), URS Tarimba (G23), URS Taura (G24), URS Torena (G25), URS-22 Londrina (G26).

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Thus, for example, in the variable mean air temperature, all genotypes have negative sensitivity, as they have negative slope coefficients. It can be inferred that, as the medium temperature increases, there is a reduction in the genetic values + intercept of all evaluated genotypes. However, there is a difference in the sensitivity of the genotypes to medium temperature, such as URS-22 Londrina genotype, that exhibits the lowest sensitivity to the environmental variable, because it exhibits the lowest slope coefficient, while URS Fapa Slava is the most sensitive. In this sense, it can be inferred that this genotype will exhibit the lowest sensitivity, compared to the other genotypes, if positioned in environments where the medium air temperature, in the wheat growing and development season, tends to be high. However, it can be seen that this genotype does not exhibit the highest genetic value + intercept. This trait of high genetic value is expressed by the IPR Afrodite genotype regardless of the environmental variable.

Sensitivity differences between the genotypes, of lesser magnitude, are also observed for the maximum air temperature. Higher slope coefficients are evidenced in the genotypes URS Fapa Slava, URS Corona, URS Torena, UPF 18 and Fapa 2. This indicates that as the maximum air temperature increases, there is a small increase in the performance of the genotype mediated by the environmental variable. The opposite occurs in the most sensitive genotypes with negative slope coefficients.

The minimum air temperature enhances the performance of the genotypes, as they all exhibit positive slope coefficients. This indicates that the genotypes express superior performances when exposed to environments of higher minimum temperatures. The URS Fapa Slava genotype has the highest positive sensitivity to this variable, enhancing productive performance by increasing the minimum air temperature. The IPR Afrodite genotype has the highest genetic value + intercept and is the third in positive response to this variable, so it can be considered the most suitable genotype for environments with higher minimum temperatures.

High levels of relative humidity are associated with higher incidences of diseases in white oat crops. For this reason, the slope coefficient was negative in all genotypes for relative air humidity. Thus, it can be inferred that oat grain yield is maximized in low relative humidity environments. The differences in sensitivity of the genotypes were of low magnitude compared to the other variables. The FAEM Dilmasul genotype was the most negatively sensitive and URS Estampa and URS-21 the most responsive to low relative humidity. Therefore, it can be understood that grain yield is maximized in environments of higher minimum air temperature with medium

temperature and low relative air humidity. The maximum air temperature exhibits divergences between the sensitivity of the genotypes, where some exhibit positive and others negative responses.

The genotypes are ordered, in Table 2, according to the general average sensitivity to environmental variables, referring to the average genetic values + intercept and the slope coefficients. It can be noticed positive coefficients for minimum temperature and negative for medium temperature and relative humidity for all genotypes. While it has changes in the sign of the genotype coefficients for the maximum air temperature. The coefficients ranged from -140.92 to -42.39, -10.76 to 31.62, 60.63 to 132.64 and -39.06 to -15.14 for medium, maximum, minimum temperature and relative humidity of air, respectively. It is observed that the IPR Afrodite genotype, although it has one of the most negative coefficients for medium temperature and air humidity, its genetic value + intercept is the highest and, associated with positive minimum and maximum air temperature coefficients, tends to be the most productive genotype in the different environmental variations. This response can be evidenced by simulating values for the environmental variables and their respective coefficients.

The results obtained by AMMI and GGE analysis show that, for greater precision in positioning and reduction of errors attributed to the interaction between genotypes x environments, the breeder must use the methodologies together. The use of the reaction norm model provides an understanding of the responsiveness of genotypes to environments together with the average genetic values. Inferring the responsiveness of genotypes on meteorological covariates, with consolidated data from 10 years of experiment, demonstrates new approaches that can be used to model the phenotypic and genetic expression resulting from the G x E interaction. The information obtained is relevant for decision making of breeders and companies to choose genotypes based on meteorological, phenotypic and genetic information. Avoiding the inappropriate cultivation of genotypes that do not express satisfactory performance in the production system, for the enhancement of grain productivity.

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Table 2. Genetic values + intercept (mean) and regression or slope coefficients of environmental variables of 26 white oat genotypes.

Genotypes	Mean	Tmed	Tmax	Tmin	RH
Barbarasul	4874.74	-102.13	14.57	99.44	-26.01
FAPA Louise	5173.69	-103.8	11.18	108.94	-32.82
UPF 18	4067.18	-121.6	31.62	104.87	-24.48
UPF 22-Temprama	4265.17	-100.41	17.47	93.2	-26.61
UPFA Gaudéria	4612.27	-69.06	3.26	78.11	-24.27
UPFA Ouro	5713.12	-75.11	2.24	89.15	-36.16
URS-21	3855.38	-63.25	9.32	60.63	-15.14
URS Charrua	4793.05	-66.99	1.73	74.76	-24.87
URS Corona	4806.62	-117.96	26.91	103.85	-20.64
URS Estampa	3795.92	-55.34	-2.93	70.14	-15.17
URS Fapa Slava	5212.98	-140.92	28.87	132.64	-31.75
Brisasul	6023.66	-99.24	9.53	103.33	-37.13
URS Guará	4686.81	-92.9	18.29	86.7	-25.1
URS Guria	4118.67	-102.53	21.85	93.28	-18.8
URS Penca	4456.84	-68.43	1.72	75.11	-27.02
URS Tarimba	4940.73	-124.74	24.36	120.14	-28.4
URS Taura	5381.07	-119.56	25.36	109.42	-32.73
URS Torena	4358.33	-123.78	29.91	106.69	-24.22
URS-22 Londrina	4644.69	-42.39	-10.76	61.76	-30.89
Carlasul	5259.04	-108.01	15.58	109.08	-27.2
Chiarasul	5276.73	-108.64	19.05	106.35	-29.58
FAEM Dilmasul	5942.81	-89.18	-1.17	104.98	-39.06
Fapa 2	4042.42	-120.44	30.11	106.02	-26.68
URS Guapa	4546.34	-88.62	8.22	96.75	-28.66
IAC 7	3787.5	-92.52	12	91.16	-20.46
IPR Afrodite	6259.65	-113.51	14.57	115.7	-37.93

Maximum air temperature (Tmax, ºC), Medium air temperature (Tmed, ºC), Minimum air temperature (Tmin, ºC), Relative humidity (RH, %).

CONCLUSION

Greater phenotypic stability is observed for the URS 21 genotype, by the AMMI and GGE methodologies.

The URS Corona genotype showed general adaptation, high genetic value and predictable environmental variations by the GGE method and reaction norm.

Higher minimum air temperature and lower medium temperature and relative air humidity enhance the productive performance of white oat genotypes. The genotypes URS 22, Fapa Slava,

IPR Afrodite and Estampa express positive responses to the covariates temperature medium, maximum, minimum and relative air humidity, respectively. Relative humidity explains more than 50% of the biological variation of white oat genotypes.

The simultaneous use of reaction norms with biometric models promotes better information for genotype selection.

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