STRATEGIC POSITIONING OF THE NUTRITIONAL PROFILE OF WHEAT GRAINS BASED ON GENETIC PARAMETERS †

[POSICIONAMIENTO ESTRATÉGICO DEL PERFIL NUTRICIONAL DE LOS GRANOS DE TRIGO EN BASE A PARÁMETROS GENÉTICOS]

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SUMMARY

Background. Wheat is a staple food crop and easily accessible to the population, so the biofortification of wheat grains is substantial to mitigate malnutrition. **Objective.** To evidence and select wheat genotypes based on nutritional multi-characters of grains based on genetic parameters. **Methodology.** Experiments were carried out in the 2019 agricultural season in five wheat areas of the state of Rio Grande do Sul, in two sowing seasons, in the municipalities of Cachoeira do Sul, Cruz Alta, Santo Augusto, São Gabriel and Vacaria. The experimental design was randomized blocks, organized in a factorial scheme with 10 cultivation environments (5 sites by two sowing dates) and 30 genotypes, with three replications. To carry out the selection of genotypes, the WAASB, AMMI, GGE and BLUP methodologies were applied. **Results.** In terms of lipids and fibers, three mega environments were formed, highlighting the genotypes BRS 327, CD 1550, Ametista, CD 1303 and BRS 331, respectively. For mineral material, there was the formation of two mega environments and the genotypes that stood out were Quartz and Tbio Toruk, while for carbohydrate there was the formation of a mega environment and the genotype that stood out was CD 1550. The Tbio Mestre and LG Prisma genotypes were the ideal genotypes, with high performance in the Cachoeira do Sul environment – Sowing 2nd fortnight. Tbio Iguaçú expressed high levels of lipids in Santo Augusto – Seeding 1st fortnight, São Gabriel – Seeding 2nd fortnight and Vacaria – Seeding 2nd fortnight. ORS 1405 and Tbio Iguaçú expressed high levels of carbohydrates in the Vacaria - Seeding 2nd fortnight environment. Heritabilities without interaction effects were high, which characterizes high genotypic additive variance. **Implications.** The current results indicate that there is genetic variability, making it possible to select genotypes with greater expression of nutrients in the grains. **Conclusion.** The TBio Mestre, CD 1440, LG Prisma and Marfim genotypes expressed greater performance and stability of the evaluated traits.

Key words: *Triticum aestivum*; genotype selection; WAASB; GGE; BLUP; AMMI.

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RESUMEN

Antecedentes. El trigo es un cultivo alimentario básico y de fácil acceso para la población, por lo que la biofortificación de los granos de trigo es sustancial para mitigar la desnutrición. **Objetivo.** Evidenciar y seleccionar genotipos de trigo con base en multicaracteres nutricionales de granos con base en parámetros genéticos. **Metodologia.** Se realizaron experimentos en la campaña agrícola de 2019 en cinco áreas trigueras del estado de Rio Grande do Sul, en dos temporadas de siembra, en los municipios de Cachoeira do Sul, Cruz Alta, Santo Augusto, São Gabriel y Vacaria. El diseño experimental fue bloques al azar, organizados en esquema factorial con 10 ambientes de cultivo (5 sitios por dos fechas de siembra) y 30 genotipos, con tres repeticiones. Para realizar la selección de genotipos se aplicaron las metodologías WAASB, AMMI, GGE y BLUP. **Resultados.** En cuanto a lípidos y fibras, se formaron tres mega ambientes, destacándose los genotipos BRS 327, CD 1550, Ametista, CD 1303 y BRS 331, respectivamente. Para material mineral se presentó la formación de dos mega ambientes y los genotipos que sobresalieron fueron Quartz y Tbio Toruk, mientras que para carbohidrato se presentó la formación de un mega ambiente y el genotipo que sobresalió fue CD 1550. El Tbio Mestre y LG Los genotipos Prisma fueron los genotipos ideales, con alto rendimiento en el ambiente de Cachoeira do Sul – Siembra 2ª quincena. Tbio Iguaçú expresó altos niveles de lípidos en Santo Augusto – Siembra 1ª quincena, São Gabriel – Siembra 2ª quincena y Vacaria – Siembra 2ª quincena. ORS 1405 y Tbio Iguaçú expresaron altos niveles de carbohidratos en el ambiente Vacaria - Siembra 2ª quincena. Las heredabilidades sin efectos de interacción fueron altas, lo que caracteriza una alta varianza aditiva genotípica. **Implicaciones**. Los resultados actuales indican que existe variabilidad genética, lo que permite seleccionar genotipos con mayor expresión de nutrientes en los granos. **Conclusión.** Los genotipos TBio Mestre, CD 1440, LG Prisma y Marfim expresaron mayor rendimiento y estabilidad de las características evaluadas.

Palabras clave: *Triticum aestivum*; selección de genotipos; WAASB; GGE; BLUP; AMMI.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the widely cultivated winter cereals, due to its use mainly in human and animal food. In the 2021 harvest, the sown area of wheat in Brazil was 2.73 million hectares with a production of 7.67 million tons of grain (Conab, 2022). The grain consists of 8.9 g of proteins and 2.1 g of lipids, in addition to fiber, mineral material and carbohydrates. Evaluations of nutritional contents are important because of their influence in the industrial quality of wheat, for example, the total protein, about 80% to 90% is represented by gluten protein, responsible for gliadin and glutenin chains which provide good extensibility and elasticity, respectively (Chiang *et al*., 2006).

Agricultural production is influenced by several factors, such as edaphoclimatic variations of environment, characteristics of the genotypes used and the relationship between genotypes x environments (G x E) (Szareski *et al*., 2019). These factors determine the phenotypic expression of the individual, so it is necessary to use parameters that show how much of phenotype expression comes from genetic variation (Carvalho *et al*., 2019). Thus, heritability (H^2) becomes the tool that allows this measurement, in addition to determining the experimental precision (Carvalho *et al*., 2016). This parameter is classified as high ($H^2 > 0.70$), medium ($0.30 > H^2 < 0.70$) and low ($H^2 < 0.30$) (Hallauer and Miranda, 1988).

Studies conducted by Carvalho *et al*. (2019) with dual-purpose wheat found that main ear and tiller length have intermediate heritability. Also, according to the same authors, crude protein and mineral material showed low magnitudes of heritability, indicating a strong influence of the cultivation environment. Understanding the magnitude of the genetic effects of a trait is substantial to promote advances in genetic improvement through indirect selection. To estimate factors responsible for the phenotypic variation of the character of interest, a study is carried out to define the phenotypic stability and adaptability of the genotype to favorable and unfavorable environments and the definition of macro environments (Szareski *et al*., 2017). In order to estimate superior genotypes and crop environments, several biometric tools are available, and it is necessary to use methods that represent the effects of genotypes x environments interaction (Szareski *et al*., 2019). On this occasion, using Additive and Multiplicative Main Effects Models (AMMI) it is possible to acquire estimates related to the variation of factors and the magnitude of the character of interest through a biplot graphic (Zobel, 1988). Another model used is the one that considers the main effects of the genotype and method of interaction of genotypes with environments (GGE) that allows combining effects related to genotypes, cultivation environments and G x E interaction, thus presenting genotypes and environments with high performance (Yan, 2000).

For the positioning of genotypes, due to different environments, adaptability and phenotypic stability models can be used through Restricted Maximum Likelihood and Best Unbiased Linear Predictor, which allows for visualizing the genetic contribution of the genotypes performance and providing greater precision of estimates and predictions. Thus, the objective of this work was to evidence and select wheat genotypes based on nutritional multi-characters of grains based on genetic parameters.

MATERIALS AND METHODS

Experiments were carried out during the 2019 agricultural season in five wheat regions in the state of Rio Grande do Sul (Figure 1), in two sowing seasons, in the municipalities of Cachoeira do Sul, Cruz Alta, Santo Augusto, São Gabriel and Vacaria. The experimental design was randomized blocks, organized in a factorial scheme with 10 cultivation environments and 30 genotypes (Table 1), in three replications.

The experimental units consisted of five rows of plants spaced by 0.20 meters with five meters in length. Sowing was carried out in the first and second half of May 2019 for all cultivation environments. The population density used was 330 viable seeds per square meter, the population density used was 330 viable seeds per square meter, adjusted according to the seed germination rate. The nutritional management was based on 250 kg ha^{-1} of NPK (08-25-20) at sowing, with 50 kg ha^{1} of nitrogen in coverage (Urea: 46 % nitrogen) applied in the full tillering stage. Weeds, insect pests and diseases were controlled in order to minimize biotic effects in the experiment. Contents of proteins (PTN, %), lipids (LIP, %), fiber (FIB, %), mineral material (MM, %), and carbohydrates (CHO, %) were evaluated. Grain yield (GY, kg. ha^{-1}) was measured by harvesting the useful area of each experimental unit, which was 5.0 m^{2}, and then the seed mass was adjusted to 13% moisture and to kg ha^{-1}.

Table 1. Geographic information, altitude, soil type, genotypes used and growing environments for the 2019 crop.

Cultivation Environments (E) and Genotypes (G)	Growing environment (1)		Coordinate	Altitude (m)	Soil (2)
	Municipality of RS	Sowing time in May 2019			
E1	Cachoeira do Sul	1st fortnight	30º17'52"S, 52º57'54"W	113	Eutrophic Haplic Planosol (Alfisol)
E2	Cruz Alta	1st fortnight	28º38'19"S, 53º36'23"W	452	Dystrophic Red Latosol (Oxisol)
E3	Santo Augusto	1st fortnight	27º54'47"S, 53º49'04"W	503	Dystroferric Red Latosol (Oxisol)
E4	São Gabriel	1st fortnight	30º20'09"S, 54º10'21"W	159	Eutrophic Haplic Planosol (Alfisol)
E5	Vacaria	1st fortnight	28º30'44"S, 50º56'02"W	971	Latosol Bruno (Oxisol)
E6	Cachoeira do Sul	2nd fortnight	30º17'52"S, 52º57'54"W	113	Eutrophic Haplic Planosol (Alfisol)
E7	Cruz Alta	2nd fortnight	28º38'19"S, 53º36'23"W	452	Dystrophic Red Latosol (Oxisol)
E8	Santo Augusto	2nd fortnight	27º54'47"S, 53º49'04"W	503	Dystroferric Red Latosol (Oxisol)
E9	São Gabriel	2nd fortnight	30º20'09"S, 54º10'21"W	159	Eutrophic Haplic Planosol (Alfisol)
E10	Vacaria	2nd fortnight	28º30'44"S, 50º56'02"W	971	Latosol Bruno (Oxisol)
			Genotypes		
G1	Ametista	G11	Esporão	G21	ORS 1405
G2	BRS 327	G12	Estrela Átria	G22	ORS 25
G3	BRS 331	G13	FPS Certero	G23	Quartzo
G4	BRS Parrudo	G14	Jadeíte 11	G24	Tbio Iguaçú
G5	CD 1104	G15	LG Cromo	G25	Tbio Mestre
G6	CD 1303	G16	LG ORO	G26	Tbio Sintonia
G7	CD 1440	G17	LG Prisma	G27	Tbio Sinuelo
G8	CD 1550	G18	LG Supra	G28	Tbio Sossego
G9	CD 1705	G19	Marfim	G29	Tbio Tibagi
G10	Celebra	G20	Mirante	G30	Tbio Toruk

(1) RS, state of Rio Grande do Sul, Brazil. (2) Source: Santos *et al*. (2013) and Streck *et al*. (2008).

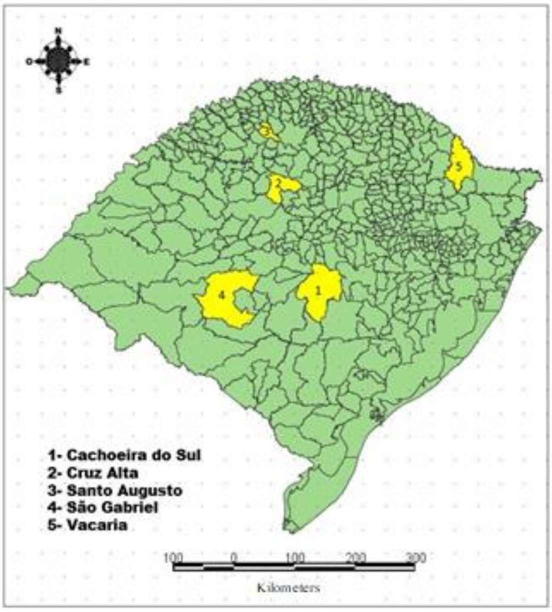

Figure 1. Location of sites where the experiment was carried out.

Through meteorological data and altitude characteristics of regions where the experiment was carried out (Figure 2), the tendency of environments with higher altitudes, such as Vacaria, to exhibit lower average temperatures than environments with lower altitudes, is evident. In addition, São Gabriel and Cachoeira do Sul, characterized by low-altitude environments, showed high rainfall during wheat cultivation. Rainfall in Cruz Alta, Vacaria and Santo Augusto showed the lowest rainfall, respectively. Average temperatures between environments varied from 16.9 ºC to 14.1 ºC. There is a difference of 858 meters in altitude between the highest altitude environment and the lowest altitude. In this way, these discrepancies in the values of meteorological variables and altitude make it possible to distinguish environments from each other, as well as to group those with greater similarity.

The data obtained were submitted to the assumptions of the model, such as additivity, normality of residues and homogeneity of variances (Ramalho *et al.*, 2000). Analysis of variance was performed at 5% probability, later, identification of interaction between genotypes x environments at 5% probability was carried out, with significant interaction, AMMI method was used, which combines effects on the genotype and the cultivation environments and the simple effects attributed to them (Zobel *et al*., 1988). The model was performed based on the inferences of protein, lipid, fiber, mineral material and carbohydrate.

$$Y_{ij} = \mu + g_i + e_j + \Sigma^{n}{}_{k=1}\lambda_k y_{ik}\alpha_{jk} + P_{ij} + \varepsilon_{ij}$$

Where: Yij: represents the average response of experimental units of the *i-th* genotype (i) in the *j-th* cultivation environment (j); μ: corresponds to the general average of genotypes in cultivation environments; g*i:* presents itself as the main effect attributed to genotype i; aj: represents the main effect of cultivation environment j; λk, yik and αjk: correspond to terms referring to decomposition of the matrix G x E that captures the pattern associated with interaction of genotype i with cultivation environment j, weights additive deviations of the character of interest (Yij) in relation to the main effects of gi and aj; ρij: represents the noise that will be eliminated from analysis related to G x E interaction; εij: corresponds to experimental error (Duarte and Vencovsky, 1999).

GGE method combines effects attributed to the genotypes tested and G x E interaction (YAN *et al*., 2000). It enables the identification of the genotype with high performance, which is efficient in a certain tested cultivation environment, in the same way, it allows the formation of macroenvironments (Woyann *et al*., 2016). GGE model was performed based on inferences of protein, lipid, fiber, mineral material and carbohydrate.

$$Y_{ij} - \mu - \beta_j = \lambda_1\xi_{1j}n_{1j} + \lambda_2\xi_{2j}n_{2j+}\ \varepsilon_{ij}$$

Where: Yij: represents the expected magnitude referring to genotype i cultivated in environment j; μ: corresponds to general average of observations Yij; βj: appears as the main effect attributed to cultivation environment j; $\lambda 1$ *and* $\lambda 2$: correspond to the main (PC I) and secondary (PC II) scores which determine the graphic expression through biplot main components; $\xi 1j$ *and* $\xi 2j$: they appear as the eigenvectors that represent genotype i on the axes of abscissa of PC I and PC II; εij: expresses unadjusted residual of effects of statistical model.

The method based on Restricted Maximum Likelihood (REML) was carried out in order to estimate the variance components and genetic parameters, where the significance was obtained through Deviance analysis at 5% probability by the chi-square test (Resende, 2007). For this, the statistical model $Y=Xr+Zg+Wi+e$ was used, where: y: is data vector, r: are effects of repetitions (fixed), g: are genotypic effects (random), i: are effects of the interaction genotypes x environments (random), and: are residues (random). Thus, the variance of interaction between genotypes x environments ($\sigma^2 INT$), phenotypic variance ($\sigma^2 F$), broad-sense heritability of the genotype mean ($\hat{h}^2 mg$), accuracy for selection of genotypes ($Acgen$), coefficient of determination of the effects of genotypes x environments interaction ($C^2 INT$), genotypic correlation among performance of environments ($rgloc$), genotypic coefficient of variation (CVg), residual coefficient of variation (CVe). The REML/BLUP estimates and predictions were used by multivariate GGE method to obtain inferences

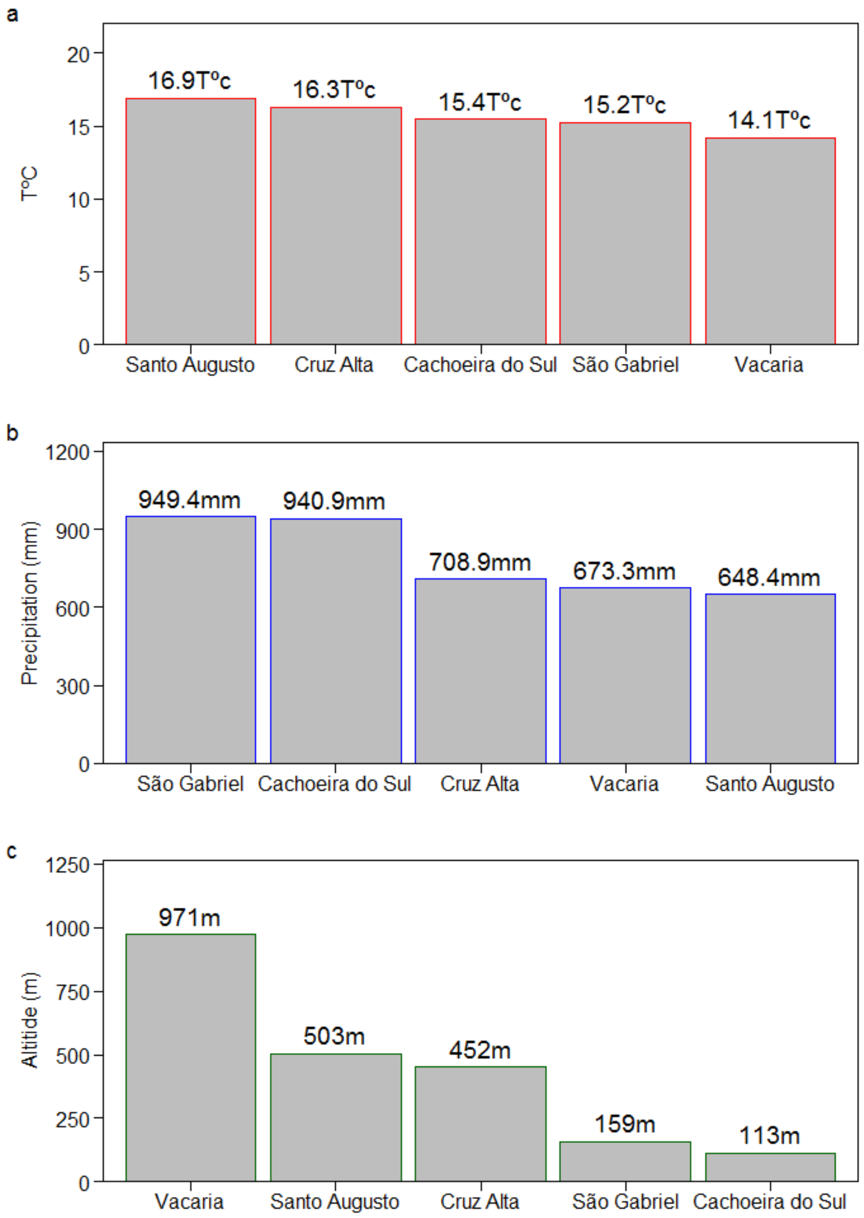

Figure 2. Average temperature and precipitation information during the wheat development period in the 2019 crop and altitude of the five environments where the plants were growing.

based on genetic effects and it was called predicted genetic GGE approach. To perform statistical analysis, the R software was used through metan, tidyverse, ExpDes.pt, rio, agricolae and cowplot packages (R Core Team, 2015®).

RESULTS AND DISCUSION

The variance analysis (Table 2) for the characters: proteins (PTN), lipids (LIP), fibers (FIB), mineral material (MM) and carbohydrates (CHO) were significant for environments, genotypes and the interaction between genotypes x environments (G x E), as well as for the principal components.

The performance of wheat genotypes in each production environment was estimated from the establishment of the main components. The accumulated variation of PC I + PC II in proteins was 53.5%, lipids 60.0%, fiber 55.8%, mineral material 55.9% and for carbohydrate contents 51.7% (Figure 3). For protein, there was the formation of four mega-environments composed of Vacaria - Seeding 1st fortnight (E5) and São Gabriel - Seeding 1st fortnight (E4) environments; Cruz Alta – Seeding 1st fortnight (E2) and Cachoeira do Sul – Seeding 1st fortnight (E1); Santo Augusto – Seeding 1st fortnight (E3) and Cruz Alta – Seeding 2nd fortnight (E7); Cachoeira do Sul – Seeding 2nd fortnight (E6), São Gabriel – Seeding 2nd fortnight (E9) and Vacaria –

Seeding 2nd fortnight (E10) with the most adaptable genotypes and the highest average corresponding to Ametista (G1), CD 1550 (G8) , CD 1440 (G7) and Tbio Toruk (G30), respectively (Figure 3 PTN). Nine genotypes were needed to form polygon that presupposes indication of which cultivars show high productive performance, these being Tbio Toruk (G30), CD 1303 (G6), Celebra (G10), Tbio Tibagi (G29), CD 1104 (G5), Quartzo (G23), Jadeíte 11 (G14), Tbio Sinuelo (G27) and CD 1550 (G8).

In this study, an environment is formed by the association of place and sowing time. A mega-environment is characterized by the grouping of environments that are similar to each other, so that there is dissimilarity between the mega-environments. Thus, Vacaria – Seeding 2nd fortnight (E10) and São Gabriel – Seeding 1st fortnight (E4); Santo Augusto - Seeding 1st fortnight (E3), Vacaria - Seeding 1st fortnight (E5), Cruz Alta - Seeding 2nd fortnight (E7) and São Gabriel - Seeding 2nd fortnight (E9); Cachoeira do Sul – Seeding 1st fortnight (E1) and Santo Augusto – Seeding 2nd fortnight (E8) formed three mega-environments. This indicates that within each mega-environment formed the performance of the evaluated genotypes

Table 2. Analysis of variance for the main components of protein (PTN), lipid (LIP), fiber (FIB), mineral material (MM) and carbohydrate (CHO) characters of 30 wheat genotypes in 10 environments.

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)
PTN					
ENV	9	736.809.785	8.186.775.394	701.906.769	0.000000e+00*
REP(ENV)	20	2.332.724	0.11663622	2.054.664	4.56E+03
GEN	29	581.435.350	2.004.949.482	353.191.956	0.000000e+00*
GEN:ENV	261	355.170.685	136.080.722	23.971.984	3.53E-199
PC1	37	120.212.820	324.900.000	57.230.000	0.000000e+00*
LIP					
ENV	9	26.22	2.914	395.0	0.
REP(ENV)	20	0.1475	0.007376	1.172	2.73E+02
GEN	29	14.62	0.5042	80.13	7.22E-179
GEN:ENV	261	16.70	0.06399	10.17	5.20E-114
PC1	37	5.115	0.1382	21.97	0.00001*
FIB					
ENV	9	349.466.278	0.388295864	93.029.756	2.42E-08
REP(ENV)	20	0.08347778	0.004173889	1.633.665	4.04E+04
GEN	29	631.377.389	0.217716341	85.214.431	4.88E-182
GEN:ENV	261	1.243.699.389	0.047651318	18.650.782	6.42E-172
PC1	37	410.917.000	0.111060000	43.470.000	0.000000e+00*
MM					
ENV	9	861.005.556	0.956672840	647.859.711	0.000000e+00*
REP(ENV)	20	0.02953333	0.001476667	1.322.933	1.57E+05
GEN	29	802.843.556	0.276842605	248.020.870	0.000000e+00*
GEN:ENV	261	438.576.444	0.016803695	15.054.284	1.65E-149
PC1	37	161.375.000	0.043610000	39.070.000	0.000000e+00*
CHO					
ENV	9	1.207.222.709	13.413.585.659	118.442.490	0.000000e+00*
REP(ENV)	20	2.264.996	0.11324978	137.554	1.27E+05
GEN	29	971.059.732	3.348.481.833	40.670.895	0.000000e+00*
GEN:ENV	261	566.885.231	217.197.406	2.638.095	7.99E-210
PC1	37	223.894.150	605.119.000	7.350.000	0.000000e+00*

* Significant at 5% probability.

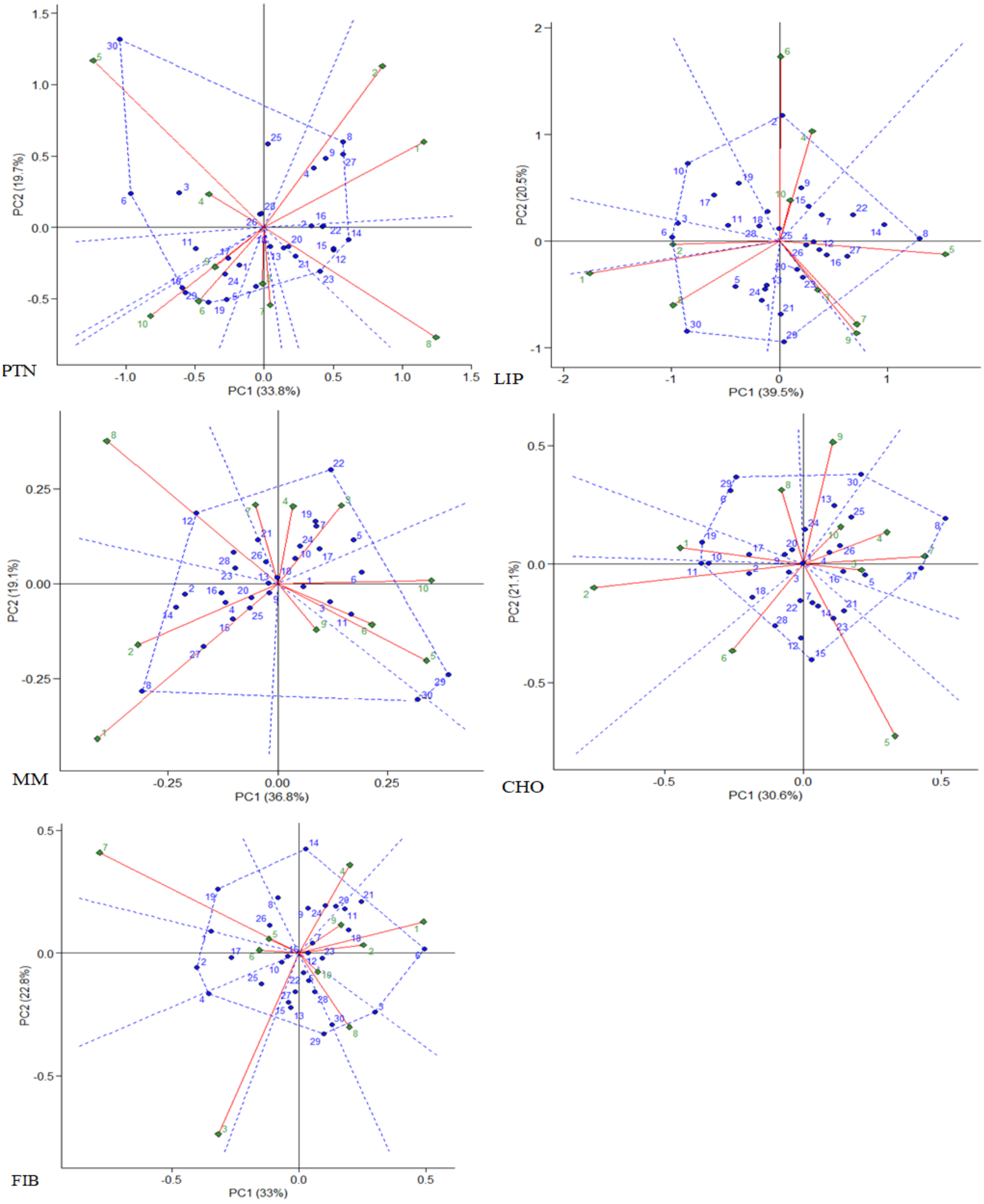

Figure 3. AMMI and biplot, referring to the best performance of wheat genotypes in each production environment tested for protein (PTN), lipid (LIP), fiber (FIB), mineral material (MM) and carbohydrate (CHO) content. Environments: Cachoeira do Sul - 1st fortnight (E1), Cruz Alta - 1st fortnight (E2), Santo Augusto - 1st fortnight (E3), São Gabriel - 1st fortnight (E4), Vacaria - 1st fortnight (E5), Cachoeira do Sul - 2nd fortnight (E6), Cruz Alta - 2nd fortnight (E7), Santo Augusto - 2nd fortnight (E8), São Gabriel - 2nd fortnight (E9), Vacaria - 2nd fortnight (E10). Genotypes: Ametista (G1), BRS 327 (G2), BRS 331 (G3), BRS Parrudo (G4), CD 1104 (G5), CD 1303 (G6), CD 1440 (G7), CD 1550 (G8), CD 1705 (G9), Celebra (G10), Esporão (G11), Estrela Átria (G12), FPS Certero (G13), Jadeíte 11 (G14), LG Cromo (G15), LG ORO (G16), LG Prisma (G17) , LG Supra (G18), Marfim (G19), Mirante (G20), ORS 1405 (G21), ORS 25 (G22), Quartzo (G23), Tbio Iguaçu (G24), Tbio Mestre (G25), Tbio Sintonia (G26), Tbio Sinuelo (G27), Tbio Sossego (G28), Tbio Tibagi (G29), Tbio Toruk (G30).

are similar, which makes it possible to indicate a single genotype for the entire mega-environment. For these, the genotypes with greater adaptability and higher lipid content were BRS 327 (G2), CD 1550 (G8) and Ametista (G1), respectively (Figure 3 LIP). The genotypes necessary to form polygon that presupposes indication of which cultivars show high productive performance, was composed of six, being: Tbio Toruk (G30), CD 1303 (G6), Celebra (G10), Tbio Tibagi (G29), BRS 327 (G2) and CD 1550 (G8).

For fiber values found, the environments Vacaria – Seeding 1st fortnight (E5) and Cruz Alta - Seeding 2nd fortnight (E7) formed a mega-environment with Ametista genotype (G1) of greater adaptability. The environments Cruz Alta – Seeding 1st fortnight (E2), Cachoeira do Sul – Seeding 1st fortnight (E1) and São Gabriel – Seeding 2nd fortnight (E9) formed the second mega-environment, with emphasis on the genotype CD 1303 (G6). The third mega-environment was composed by the environments Santo Augusto – Seeding 2nd fortnight (E8) and Vacaria – Seeding 2nd fortnight (E10) with the genotype BRS 331 (G3) (Figure 2 FIB). The genotypes necessary to form polygon that presupposes indication of which cultivars with high productive performance were BRS 331 (G3), CD 1303 (G6), Marfim (G19), Tbio Tibagi (G29), BRS 327 (G2), BRS Parrudo (G4) and Jadeíte 11 (G14).

For mineral material character, the formation of two mega-environments was observed, composed by the environments Santo Augusto – Seeding 1st fortnight (E3), São Gabriel – Seeding 1st fortnight (E4) and Cruz Alta – Seeding 2nd fortnight (E7) contemplating the Quartzo genotype (G23) as the most prominent. Tbio Toruk genotype (G30) was adaptable and had the highest average in the mega-environment formed by the environments Vacaria – Seeding 1st fortnight (E5), Cachoeira do Sul – Seeding 2nd fortnight (E6) and Vacaria – Seeding 2nd fortnight (E10) (Figure 3 MM), nine genotypes were needed to form the polygon that presupposes the indication of which cultivars show high productive performance, these being Tbio Toruk (G30), CD 1306 (G6), Estrela Átria (G12), Tbio Tibagi (G29) , CD 1104 (G5), ORS 25 (G22), Jadeíte 11 (G14), Tbio Sinuelo (G27) and CD 1550 (G8).

For carbohydrate component, there was formation of only one mega-environment, formed by the municipalities of Santo Augusto – Seeding 1st fortnight (E3), São Gabriel – Seeding 1st fortnight (E4), Cruz Alta – Seeding 2nd fortnight (E7) and Vacaria – Sowing 2nd fortnight (E10) with the CD 1550 (G8) genotype responsible for the highest level of this character and for greater stability for the described mega-environment (Figure 2 CHO). Genotypes Tbio Tibagi (G29), CD 1705 (G19), ORS 1405 (G11), LG Supra (G28), LG Cromo (G15), Tbio Sinuelo (G27), CD 1550 (G8) and Tbio Toruk (G30) formed polygon of cultivars that present the most productive genotypes. In a study carried out by Cotrim *et al.* (2019), mega-environments are formed according to the proximity of environments, such as characteristics of latitude, altitude, climatic condition, with this, it becomes important to study environmental stratification that help in definition of considerable environments for evaluation, in addition to reduction of places for evaluation of the genotypes by breeding programs.

In order to demonstrate the representativeness and discrimination of genotypes and environments, the GGE methodology was applied, in which most of the data variation was explained by the first two main components, in orders of: 46.94%, 64.31%, 59, 43%, 80.76% and 80.91% for characteristics of proteins (PTN), lipids (LIP), fibers (FIB), mineral material (MM) and carbohydrates (CHO), respectively (Figure 4). Genotypes Tbio Sintonia (G26) for proteins (PTN), Estrela Átria (G12), Jadeíte 11 (G14) and LG Cromo (G15) for lipids (LIP), CD 1104 (G5), CD 1440 (G7), Jadeíte 11 (G14) and LG Cromo (G15) in fibers (FIB), LG Supra (G18) for mineral material (MM) and Ametista (G1), CD 1705 (G9), LG Supra (G18) and Tbio Tibagi (G29) for carbohydrate (CHO), as they are closer to the origin of the data, it is evident that these genotypes contribute to differential effects of the interaction of genotypes x environments (Figure 4).

Multivariate definitions indicate that Tbio Mestre (G25) and LG Prisma (G17) genotypes can be defined as ideal genotypes, since they exhibited excellent stability and predictability for variable protein content, and are related to Cachoeira do Sul – Seeding environment - 2nd fortnight (E6) (Figure 4 PTN). For the lipid content, it was observed for the genotype Tbio Iguaçú (G24), correlated with the environments Santo Augusto – Seeding 1st fortnight (E3), São Gabriel – Seeding 2nd fortnight (E9) and Vacaria – Seeding 2nd fortnight (E10) (Figure 3 LIP). In terms of fiber (Figure 4 FIB) and mineral material (Figure 4 MM), no genotype approached the ideotype region, demonstrating that none of the genotypes in studies have affinities for these characters in proposed crop environments. For carbohydrate levels, it was represented by genotypes ORS 1405 (G21) and Tbio Iguaçú (G24), positively correlated with the environment Vacaria - Sowing 2nd fortnight (E10) (Figure 4 CHO).

Pearson's linear correlations between the characters analyzed (Figure 5) account for the formation of nine significant pairs ($p \leq 0.01$), most of them with negative effects. With the increase in levels of proteins (PTN), there is a reduction in levels of lipids (LIP), fiber (FIB), carbohydrates (CHO) and an increase in mineral material (MM). For lipid, with the increase of this molecule, there is a reduction in

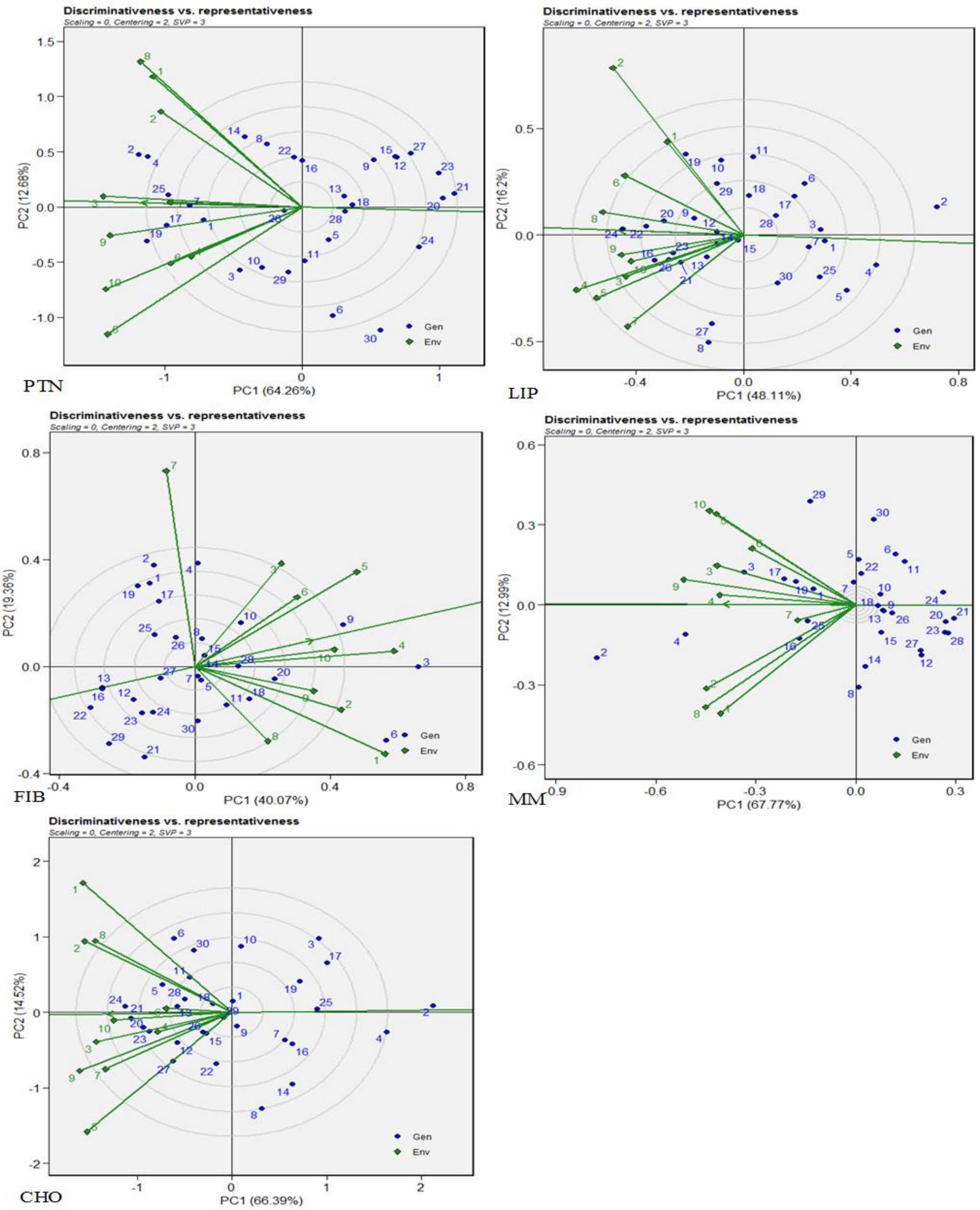

Figure 4. GGE biplot for the discrimination and representativeness of wheat genotypes in each tested production environment for protein (PTN), lipid (LIP), fiber (FIB), mineral material (MM) and carbohydrate (CHO) content. Environments: Cachoeira do Sul - 1st fortnight (E1), Cruz Alta - 1st fortnight (E2), Santo Augusto - 1st fortnight (E3), São Gabriel - 1st fortnight (E4), Vacaria - 1st fortnight (E5), Cachoeira do Sul - 2nd fortnight (E6), Cruz Alta - 2nd fortnight (E7), Santo Augusto - 2nd fortnight (E8), São Gabriel - 2nd fortnight (E9), Vacaria - 2nd fortnight (E10). Genotypes: Ametista (G1), BRS 327 (G2), BRS 331 (G3), BRS Parrudo (G4), CD 1104 (G5), CD 1303 (G6), CD 1440 (G7), CD 1550 (G8), CD 1705 (G9), Celebra (G10), Esporão (G11), Estrela Átria (G12), FPS Certero (G13), Jadeíte 11 (G14), LG Crome (G15), LG ORO (G16), LG Prisma (G17) , LG Supra (G18), Marfim (G19), Mirante (G20), ORS 1405 (G21), ORS 25 (G22), Quartzo (G23), Tbio Iguaçu (G24), Tbio Mestre (G25), Tbio Sintonia (G26)), Tbio Sinuelo (G27), Tbio Sossego (G28), Tbio Tibagi (G29), Tbio Toruk (G30).

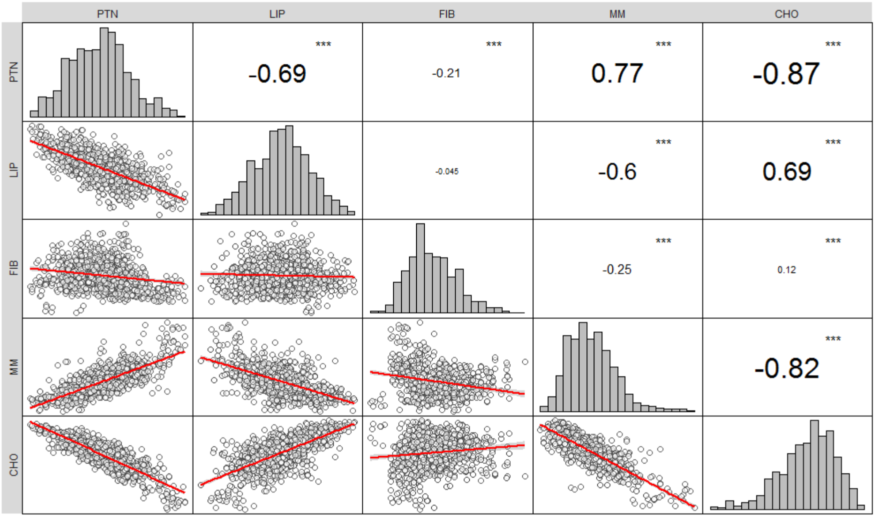

Figure 5. Pearson's linear correlation estimates for characters evaluated in 30 wheat genotypes in five different environments, significant at 1,00% error probability for proteins (PTN), lipids (LIP), fibers (FIB), mineral material (MM) and carbohydrates (CHO).

mineral material and an increase in carbohydrate content, the same case occurs for fiber content. With the increase in content of mineral material in the grain, there is a reduction in levels of carbohydrates present. This negative association was found by Bender *et al*. (2021), that there is a reduction for the characters of lipids and mineral material evaluating dual-purpose wheat.

Deviance analysis was performed on the interaction genotypes x environments for protein (PTN), lipid (LIP), fiber (FIB), mineral material (MM) and carbohydrate (CHO) content, characterizing significance (Szareski *et al*., 2019) by chi-square test, for all of these (Table 3). Such significant interactions suggest that the genotypes presented different responses when submitted to different cultivation environments. Therefore, respective additive variance components and heritability coefficients were significantly different from zero, which shows existence of genetic variability for these characters (Pimentel *et al*., 2014). This made it possible to prove the reliability of REML/BLUP estimates and predictions obtained in this study.

Heritabilities without interaction effects were high, which characterizes high genotypic additive variance, that is, 93.2%, 87.3%, 78.1%, 93.9% and 93.5% of averages obtained in characters of proteins (PTN), lipids (LIP), fiber (FIB), mineral material (MM) and carbohydrates (CHO), respectively, are attributed to genetic factor of wheat genotypes. With

Table 3. Deviance analysis, estimation of variance components and genetic parameters (REML) for protein (PTN), lipid (LIP), fiber (FIB), mineral material (MM) and carbohydrate (CHO) characters of 30 wheat genotypes in different environments in Brazil.

Parameters	PTN	LIP	FIB	MM	CHO
Deviance (LRT x2)	933	527	807.65	7.045.274	982.11
E x G[1]	0.0001*	0.0001*	0.0001*	0.0001*	0.0001*
$\hat{h}^2mg.s$	0.932	0.873	0.781	0.939	0.935
$\hat{h}^2mg.c$	0.559	0.365	0.244	0.577	0.573
C^2INT	0.390	0.478	0.646	0.348	0.382
Rgloc	0.884	0.753	0.855	0.824	0.894
σ^2F	1.11	0.0402	0.0233	0.0150	1.82
Acgen	0.965	0.934	0.884	0.969	0.967
CVg	5.47	8.35	2.80	5.45	1.75
CVe	1.65	5.47	1.88	1.96	0.493
CVratio	3.31	1.53	1.49	2.79	3.56

$\hat{h}^2$mg.s: Heritability without interaction effects; $\hat{h}^2$mg.c: Heritability with interaction effects; C^2INT: Coefficient of determining the effects of the genotype x environment interaction; rgloc: Genotypic correlation between the performance of environments (interclass); σ^2F: Phenotypic variance; Acgen: Accuracy for the selection of genotypes; CVg: Genotypic variation coefficients; CVe: Relative variation coefficient; CVratio: ratio between genetic variations and residual effects (CVg/CVe). Content of proteins (PTN), lipids (LIP), fibers (FIB), mineral material (MM) and carbohydrates (CHO).

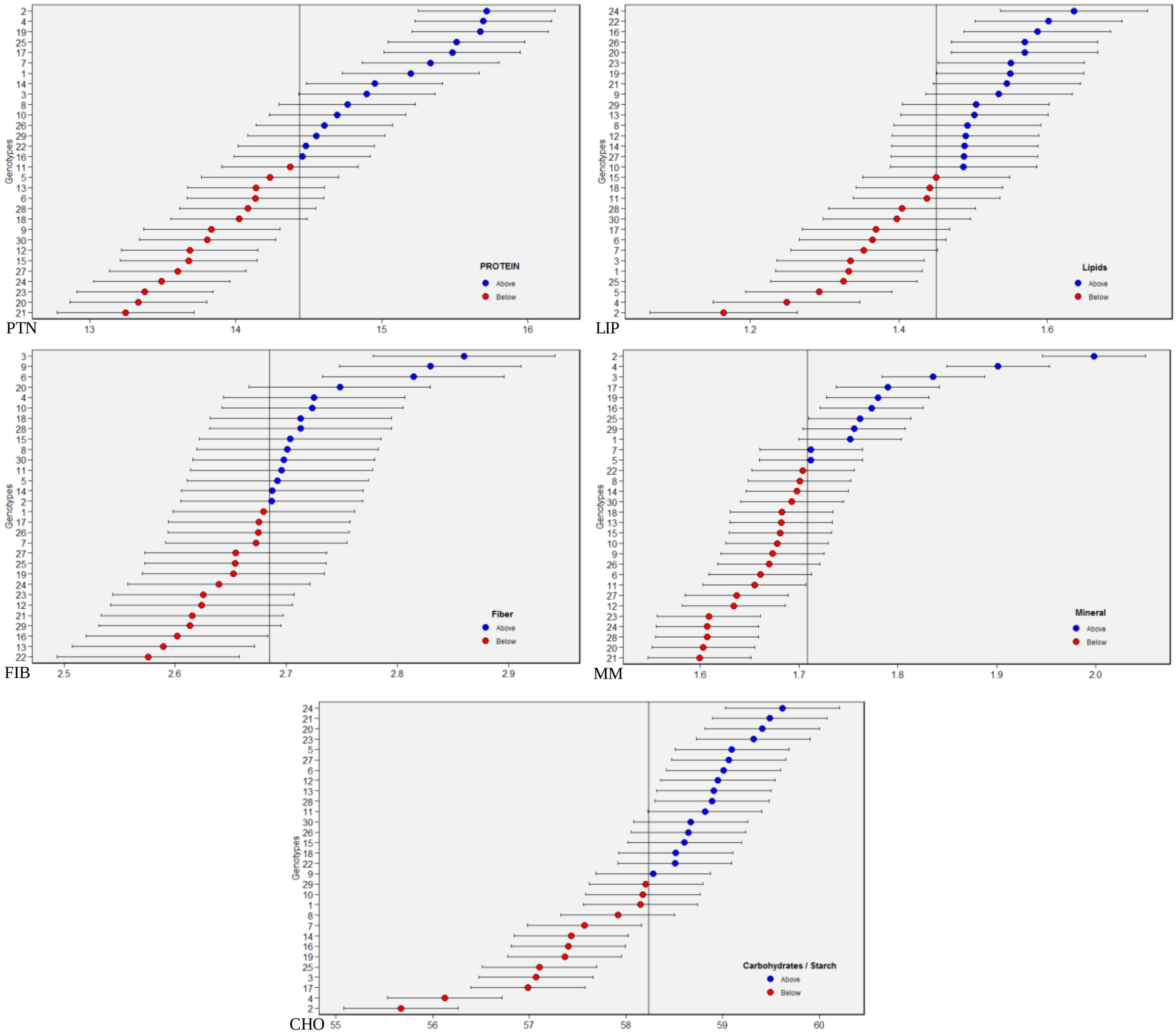

Figure 6. Predictions for the best unbiased linear predictor BLUP for protein (PTN), lipid (LIP), fiber (FIB), mineral material (MM) and carbohydrate (CHO) content for 30 wheat genotypes in different environments in Brazil. Environments: Cachoeira do Sul - 1st fortnight (E1), Cruz Alta - 1st fortnight (E2), Santo Augusto - 1st fortnight (E3), São Gabriel - 1st fortnight (E4), Vacaria - 1st fortnight (E5), Cachoeira do Sul - 2nd fortnight (E6), Cruz Alta - 2nd fortnight (E7), Santo Augusto - 2nd fortnight (E8), São Gabriel - 2nd fortnight (E9), Vacaria - 2nd fortnight (E10). Genotypes: Ametista (G1), BRS 327 (G2), BRS 331 (G3), BRS Parrudo (G4), CD 1104 (G5), CD 1303 (G6), CD 1440 (G7), CD 1550 (G8), CD 1705 (G9), Celebra (G10), Esporão (G11), Estrela Átria (G12), FPS Certero (G13), Jadeíte 11 (G14), LG Crome (G15), LG ORO (G16), LG Prisma (G17) , LG Supra (G18), Marfim (G19), Mirante (G20), ORS 1405 (G21), ORS 25 (G22), Quartzo (G23), Tbio Iguaçu (G24), Tbio Mestre (G25), Tbio Sintonia (G26), Tbio Sinuelo (G27), Tbio Sossego (G28), Tbio Tibagi (G29), Tbio Toruk (G30).

effects of interaction, heritabilities declined with greater expressiveness verified in the fiber content. This information is validated by the high accuracy the estimated values ranged from medium ($0.15<h2<0.50$) to high ($h2 \geq 0.50$). In this way, it is considered that the genotypes have considerable genetic variability, able to be used and worked on throughout the breeding program. value found in characters, all of which are greater than 88% (Table 3). According to Resende (2002), Coefficient of determination of interaction effects (C^2INT) varied from 0.348 for mineral material and 0.646 for the fiber content, demonstrating from low to medium the degree of interaction between genotypes x environments. The genotypic interclass correlation (*rgloc*) was classified as simple (>0.55) for all characters, triggering the great genetic variability existing in analyzed characters. For genotypic coefficient of variation (*CVg*) in descending order by lipids (8.35), proteins (5.47), mineral material (5.45), fiber (2.80) and carbohydrates (1.75). This variability can be used for increments in breeding programs in all analyzed characters (*CV ratio>1*) (Table 3).

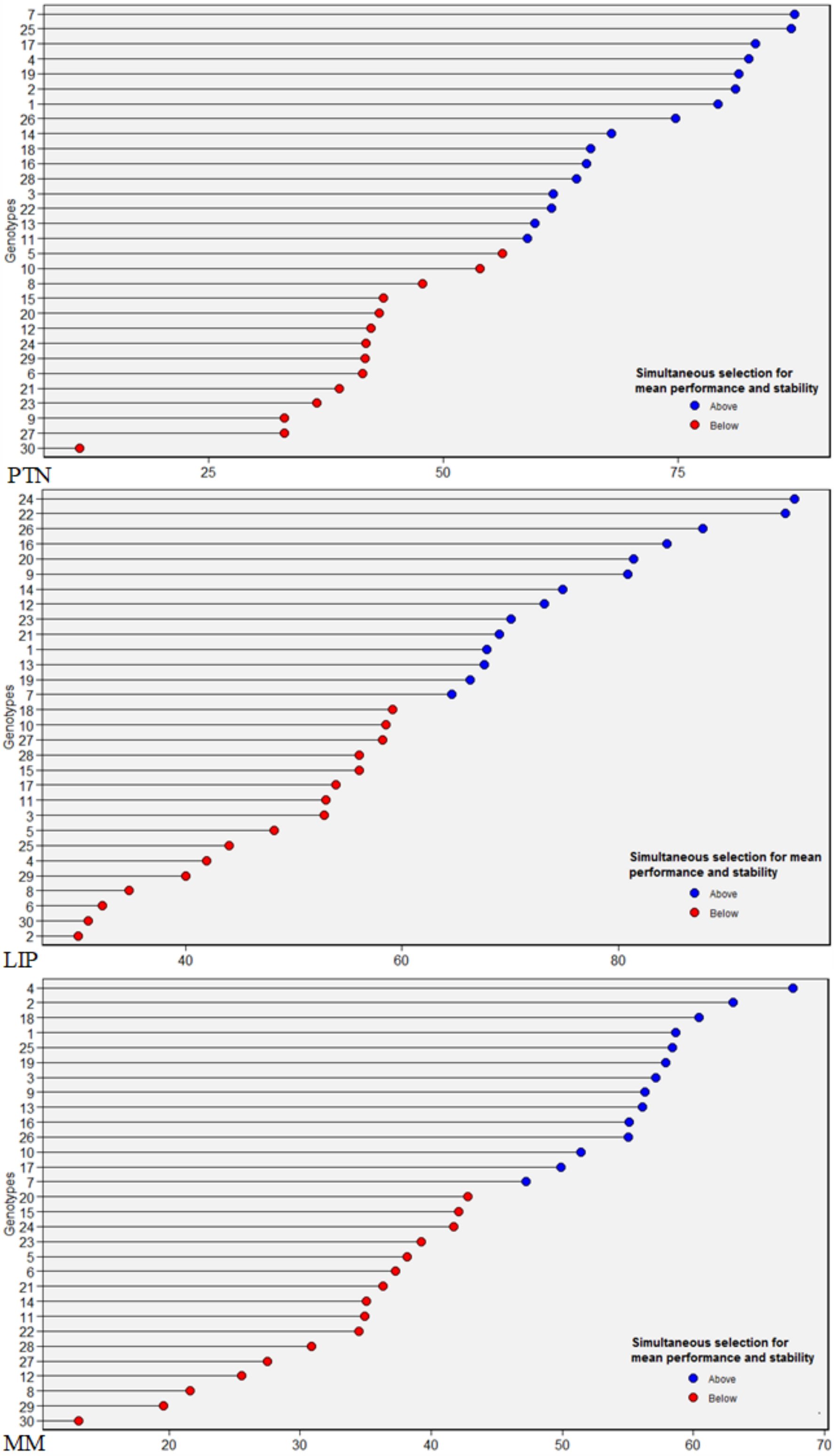

Figure 7. Simultaneous selection by estimated values of weighted average of the stability and mean performance for protein (PTN), lipid (LIP) and mineral material (MM) content for 30 wheat genotypes in different environments in Brazil. Environments: Cachoeira do Sul - 1st fortnight (E1), Cruz Alta - 1st fortnight (E2), Santo Augusto - 1st fortnight (E3), São Gabriel - 1st fortnight (E4), Vacaria - 1st fortnight (E5), Cachoeira do Sul - 2nd fortnight (E6), Cruz Alta - 2nd fortnight (E7), Santo Augusto - 2nd fortnight (E8), São Gabriel - 2nd fortnight (E9), Vacaria - 2nd fortnight (E10). Genotypes: Ametista (G1), BRS 327 (G2), BRS 331 (G3), BRS Parrudo (G4), CD 1104 (G5), CD 1303 (G6), CD 1440 (G7), CD 1550 (G8), CD 1705 (G9), Celebra (G10), Esporão (G11), Estrela Átria (G12), FPS Certero (G13), Jadeíte 11 (G14), LG Crome (G15), LG ORO (G16), LG Prisma (G17) , LG Supra (G18), Marfim (G19), Mirante (G20), ORS 1405 (G21), ORS 25 (G22), Quartzo (G23), Tbio Iguaçu (G24), Tbio Mestre (G25), Tbio Sintonia (G26), Tbio Sinuelo (G27), Tbio Sossego (G28), Tbio Tibagi (G29), Tbio Toruk (G30).

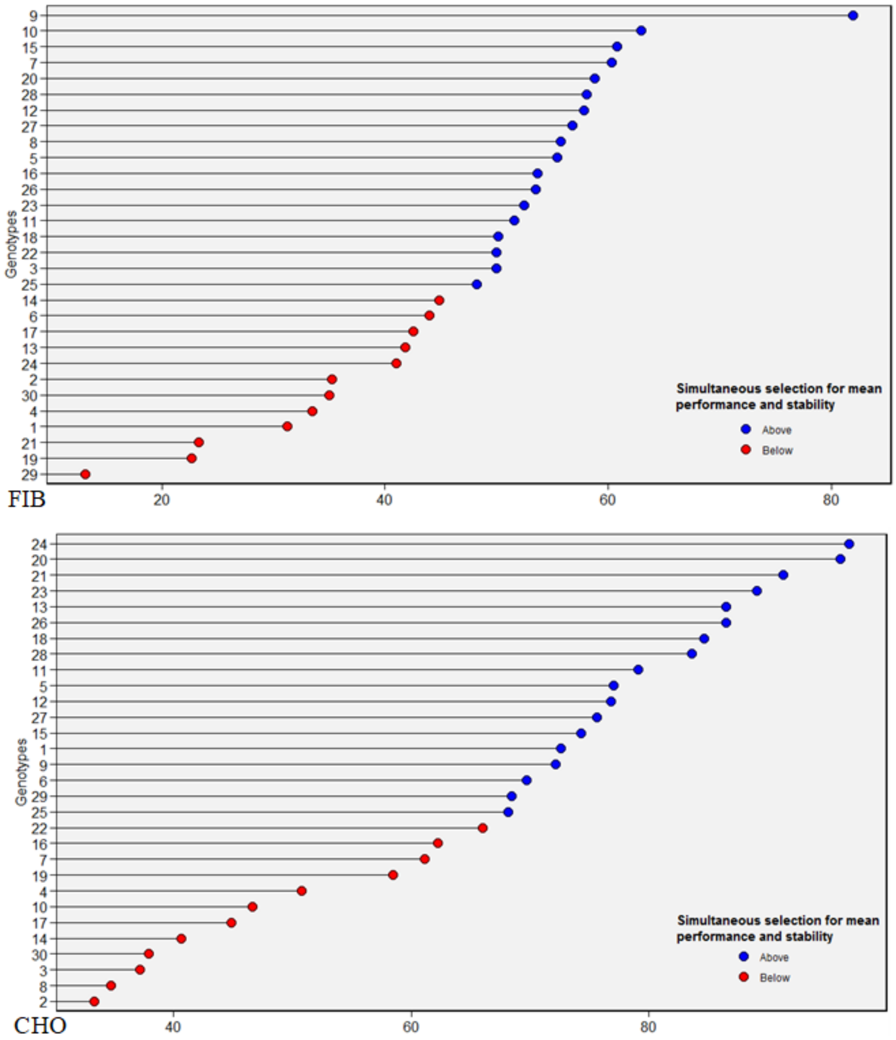

Figure 8. Simultaneous selection by estimated values of weighted average of the stability and mean performance for fiber (FIB) and carbohydrate (CHO) content for 30 wheat genotypes in different environments in Brazil. Environments: Cachoeira do Sul - 1st fortnight (E1), Cruz Alta - 1st fortnight (E2), Santo Augusto - 1st fortnight (E3), São Gabriel - 1st fortnight (E4), Vacaria - 1st fortnight (E5), Cachoeira do Sul - 2nd fortnight (E6), Cruz Alta - 2nd fortnight (E7), Santo Augusto - 2nd fortnight (E8), São Gabriel - 2nd fortnight (E9), Vacaria - 2nd fortnight (E10). Genotypes: Ametista (G1), BRS 327 (G2), BRS 331 (G3), BRS Parrudo (G4), CD 1104 (G5), CD 1303 (G6), CD 1440 (G7), CD 1550 (G8), CD 1705 (G9), Celebra (G10), Esporão (G11), Estrela Átria (G12), FPS Certero (G13), Jadeíte 11 (G14), LG Crome (G15), LG ORO (G16), LG Prisma (G17) , LG Supra (G18), Marfim (G19), Mirante (G20), ORS 1405 (G21), ORS 25 (G22), Quartzo (G23), Tbio Iguaçu (G24), Tbio Mestre (G25), Tbio Sintonia (G26), Tbio Sinuelo (G27), Tbio Sossego (G28), Tbio Tibagi (G29), Tbio Toruk (G30).

BLUPs for proteins, lipids, fiber, mineral material and carbohydrates revealed positive and negative genotypic effects for the genotypes under study. Follmann *et al*. (2019), emphasize that the genotypic effect is the difference between the point and the vertical line (demonstrating the general mean of the trait).

BRS 327 (G2) genotype had the highest predicted mean for protein content. Additions over the average are also foreseen for the genotypes BRS Parrudo (G4), Marfim (G19), Tbio Mestre (G25), LG Prisma (G17), CD 1440 (G7), Ametista (G1), Jadeíte 11 (G14), BRS 331 (G3), CD 1550 (G8), Celebra (G10), Tbio Sintonia (G26), Tbio Tibagi (G29), ORS 25 (G22) and LG ORO (G16) in (Figure 6 PTN). The same genotype and BRS 327 (G2) is also the greatest predictor for mineral material (Figure 5 MM). The prediction for the lipid content is that 53.33% of the genotypes have a higher content than the average of these. Among these, Celebra (G10) is responsible for the lowest increase and Tbio Iguaçú (G24) for the highest predicted value for lipid content (Figure 6 LIP) and for carbohydrates (Figure 6 CHO). For fiber, BLUP described that among the 50% of genotypes with potential for genetic gain on this trait, the BRS 331 (G3) genotype has the highest prediction (Figure 6 FIB). Therefore, it can be inferred that genotypes with a genotypic mean higher than the general mean can be selected in order to increase the levels of the compounds of interest.

Analyzing the simultaneous selection for performance and average stability (Figure 7 and 8) for protein content, it showed stability above average for 16 genotypes, among these, the genotype with the highest percentage for the Tbio Mestre (G25) and CD 1440 (G7) genotypes, for lipid content and mineral material showed a total of 14 genotypes with stability, highlighting as the largest Tbio Iguaçú (G24), ORS 25 (G22) and BRS Parrudo (G4), respectively. For fiber content, it presented a total of 17 more stable genotypes and carbohydrates a total of 18 genotypes, with emphasis on wheat genotypes LG Prisma (G17) and LG Supra (G18) respectively.

Multi-trait Stability Index (WAASB) (weighted average of absolute scores) is used in order to select multi-characters in various environments, thus, genotypes that exhibit the lowest values in the WAASB index are the ones which present greater stability considering all characteristics in evaluated environments (Olivoto *et al*., 2019). The index allowed selection of the best genotypes for evaluated environments by information from the set of nutritional characters (Figure 9). When considering the index for multiple environments, TBio Mestre (G25), CD 1440 (G7), LG Prisma (G17), Marfim (G19) genotypes can be selected as the most stable among the 30 evaluated genotypes.

Multi-environment experiments aim to test and select genotypes within target regions. For this, it is necessary to identify environments with similar characteristics in which genotypes can be efficiently positioned within these environments, that is, to position a genotype that expresses its ideotype within the conditions of a macro environment formed by several similar environments. Thus, in the present research, the formation of mega-environments was evidenced through the existing similarity among environments and made possible the stratification of the genotypes with greater adaptation and expression of characteristics of interest for each mega-environment formed. Thus, it can be inferred that the identification of associations between environments and the identification of the best locations promote positive responses on the genotypes, which present high performance and stability in these environments.

However, in order to select genotypes based on multi-characters for wide environments, the use of selection indices promotes greater efficiency in positioning, since it promotes identification of genotypes that present stable performance in various environments. Thus, TBio Mestre, CD 1440, LG Prisma and Marfim genotypes show high performance and stability in the study environments, expressing stability characteristics that can be used both for better cultivation efficiency of these genotypes and as parents in breeding genetic, since the characters showed high heritability.

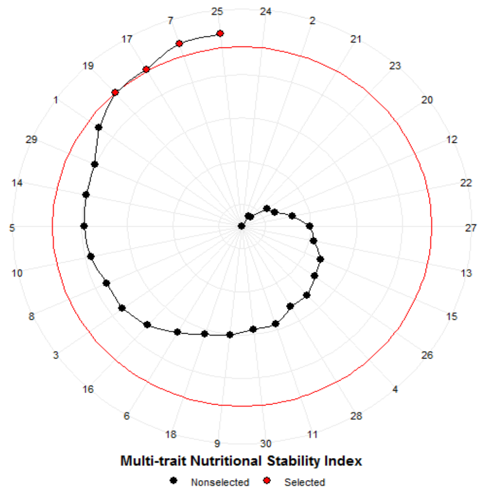

Figure 9. Classification of selected genotypes for Multi-trait Stability Index (WAASB) considering a selection intensity of 15%. Genotypes: Ametista (G1), BRS 327 (G2), BRS 331 (G3), BRS Parrudo (G4), CD 1104 (G5), CD 1303 (G6), CD 1440 (G7), CD 1550 (G8), CD 1705 (G9), Celebra (G10), Esporão (G11), Estrela Átria (G12), FPS Certero (G13), Jadeíte 11 (G14), LG Crome (G15), LG ORO (G16), LG Prisma (G17) , LG Supra (G18), Marfim (G19), Mirante (G20), ORS 1405 (G21), ORS 25 (G22), Quartzo (G23), Tbio Iguaçu (G24), Tbio Mestre (G25), Tbio Sintonia (G26), Tbio Sinuelo (G27), Tbio Sossego (G28), Tbio Tibagi (G29), Tbio Toruk (G30).

CONCLUSIONS

In terms of lipids and fibers, three mega environments were formed, highlighting the genotypes BRS 327, CD 1550, Ametista, CD 1303 and BRS 331, respectively. For mineral material, there was the formation of two mega environments and the genotypes that stood out were Quartz and Tbio Toruk, while for carbohydrate there was the formation of a mega environment and the genotype that stood out was CD 1550.

The Tbio Mestre and LG Prisma genotypes were the ideal genotypes, with high performance in the Cachoeira do Sul environment – Sowing 2nd fortnight. Tbio Iguaçú expressed high levels of lipids in Santo Augusto – Seeding 1st fortnight, São Gabriel – Seeding 2nd fortnight and Vacaria – Seeding 2nd fortnight. ORS 1405 and Tbio Iguaçú expressed high levels of carbohydrates in the Vacaria - Seeding 2nd fortnight environment.

Heritabilities without interaction effects were high, which characterizes high genotypic additive variance. The TBio Mestre, CD 1440, LG Prisma and Marfim genotypes expressed greater performance and stability of the evaluated traits.

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Compliance with ethical standards. Does not apply.

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Author contribution statement (CRediT) - **N. Moura** - Conceptualization, formal analysis and writing original draft., **I. R. Carvalho** - Conceptualization, supervision and formal analysis., **K. Kehl** - Conceptualization and writing-review & editing., **L. C. Pradebon** – Conceptualization and writing-review & editing., **M. V. Loro** - Conceptualization, supervision and formal analysis., **E. D. Port** - Data curation, writing-review & editing., **I. C. Sfalcin** - Conceptualization, formal analysis and writing original draft., **J. A. G. Silva** - Conceptualization, formal analysis and writing original draft., **A. U. Bester** – Conceptualization and supervision.

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