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# Strategic positioning of soybean based on the agronomic ideotype and on fixed and mixed multivariate models

**Abstract** – The objective of this work was to decompose the variations of the genotype × environment interaction through fixed multivariate models, as well as to understand the genetic variations through mixed models, for the estimation and prediction of the genetic value of soybean (*Glycine max*) genotypes in the state of Rio Grande do Sul, Brazil. Tests were carried out during the 2016/2017, 2017/2018, and 2018/2019 crop seasons in different municipalities in six regions of the state, using the additive main effects and multiplicative interaction (AMMI) and genotype main effects + genotype-by-environment interaction (GGE) models. The genotypes were also evaluated using an index that allows weighting between mean performance and stability (WAASBY) and by the restricted maximum likelihood (REML) and the best linear unbiased prediction (BLUP) models. The used experimental design was randomized complete blocks (18 environments x 12 genotypes), with three replicates. The best performing genotypes in favorable environments are: 'BMX Valente RR', 'BMX Alvo RR', 'NS 5959 IPRO', 'DM 5958RSF IPRO', and 'BMX Ativa RR'. The favorable environments are the 2017/2018 season in the municipality of Bagé and the 2016/2017 season in the municipalities of São Luiz Gonzaga and Cachoeira do Sul, where higher grain yields were obtained. The genotypes that show excellent performance in unfavorable environments are cultivars BMX Ativa RR, DM 5958RSF IPRO, NS 5959 IPRO, and TMG 7262 RR. The 2016/2017 season is considered unfavorable in the municipalities of São Luiz Gonzaga and Cachoeira do Sul. The AMMI, GGE, and WAASBY or BLUP models for genotype selection must be used simultaneously.

**Index terms:** *Glycine max*, breeding, genotype x environment interaction, selection.

## Posicionamento estratégico da soja com base no ideótipo agrônômico e nos modelos multivariados fixos e mistos

**Resumo** – O objetivo deste trabalho foi decompor as variações da interação genótipo × ambiente por meio de modelos multivariados fixos, bem como entender as variações genéticas por meio de modelos mistos, para estimativa e predição do valor genético de genótipos de soja (*Glycine max*), no estado do Rio Grande do Sul, Brasil. Foram realizados testes durante as safras de 2016/2017, 2017/2018 e 2018/2019, em diferentes municípios, em seis regiões do estado, com uso dos modelos de efeitos principais aditivos e interação multiplicativa (AMMI) e de efeitos principais dos genótipos + interação genótipo-ambiente (GGE). Os genótipos também foram avaliados pelo índice

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## Introduction

The soybean [*Glycine max* (L.) Merr.] crop is one of the main commodities traded in the world due to its importance as a food source because of the high nutritional value of its grains (Loro et al., 2021). As a result, genetic improvement programs for this crop are constantly developing and registering new cultivars with a high productive and nutritional potential. Before being introduced onto the market, these cultivars must meet the minimum requirements of Ministério da Agricultura, Pecuária e Abastecimento (MAPA), which include at least two years of evaluation in trials to test the value for cultivation and use (VCU) in sites that represent the edaphoclimatic region of interest (Brasil, 2020).

Multi-environment trials are needed to assess the effects of the genotype x environment (GxE) interaction, which will help to select genotypes that are stable and show high performance in the most varied edaphoclimatic conditions (Dalló et al., 2019). The effects on grain yield are derived from the genotypic potential of the new genetic constitution, the intrinsic characteristics of the growing environments, and the differential responses of the GxE interaction (Singh et al., 2019; Carvalho et al., 2020).

In Brazil, the regions for soybean cultivation were defined to represent homogeneous growing environments in terms of altitude, air temperature, and outstanding soil characteristics (Kaster & Farias, 2012). Different biometric approaches are

used to define the productive potential and strategic positioning for the parameters stability and phenotypic adaptability. Several inferences have been made using methods based on deviations from linear (Carvalho et al., 2019) and bissegmented regression (Carvalho et al., 2016), decomposition of sums of squares, factor analysis, nonparametric models, and multivariate models such as those of additive main effects and multiplicative interaction (AMMI) and genotype main effects + genotype-by-environment interaction (GGE) (Szarecki et al., 2018; Schneider et al., 2021). These models fragment the sums of squares of the GxE interaction and allow expressing them through principal component biplots, bringing together all the variation expressed by the nature of the experiment in the form of a graph, enabling a better understanding of tests with a high number of genotypes and environments (Jeberson et al., 2017; Santos et al., 2019). However, due to doubts regarding the strategic positioning of cultivars and the causes of the observed variations, other models, besides those of adaptability and phenotypic stability, are also used. Among these, stand out the restricted maximum likelihood (REML) and the best linear unbiased prediction (BLUP) models, which are used to extract the genetic contributions to genotype performance and increase the accuracy of estimates and predictions.

**Termos para indexação:** *Glycine max*, melhoramento, interação genótipo x ambiente, seleção.

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The objective of this work was to decompose the variations of the G×E interaction through fixed multivariate models, as well as to understand the genetic variations through mixed models, for the estimation and

prediction of the genetic value of soybean genotypes in the state of Rio Grande do Sul, Brazil.

### Materials and Methods

The tests were conducted during the 2016/2017, 2017/2018, and 2018/2019 crop seasons in six regions of the state of Rio Grande do Sul, Brazil (Table 1), covering the 101, 102, and 103 soybean macroregions described for VCU trials per region (Kaster & Farias, 2012). The experimental design used was a randomized complete block organized in a 18x12 factorial arrangement, with 18 growing environments (crop seasons x sites) x 12 soybean genotypes, arranged in three replicates. The sites were the following municipalities of the state of Rio Grande do Sul: Bagé, Cachoeira do Sul, Passo Fundo, Santo Augusto, São Luiz Gonzaga, and Vacaria. The genotypes (identification between parentheses) used were cultivars BMX Alvo RR (G1), BMX Ativa RR (G2), BMX Garra IPRO (G3), BMX Ícone IPRO (G4), BMX Tornado RR (G5), BMX Valente RR (G6), DM 5958RSF IPRO (G7), NA 5909 RG (G8), NS 5959 IPRO (G9), NS 6209 RR (G10), TMG 7062 IPRO (G11), and TMG 7262 RR (G12).

The experimental units were composed of 9.0 m<sup>2</sup>, comprising five rows spaced at 0.45 m, with a sowing

density of 280 thousand seed per hectare. The control of weeds, pests, and diseases was preventive, in order to minimize the biotic effects in the experiment (Carvalho et al., 2016). Yield per hectare was obtained by harvesting the three central lines of the experimental unit (5.4 m<sup>2</sup>), where grain mass at 13% moisture was adjusted for the final density of plants per hectare, with results expressed in kg ha<sup>-1</sup>.

The data obtained were subjected to the analysis of normality of residual variances, homogeneity of residual variances, and additivity of the statistical model. Subsequently, the analysis of variance was performed using the F-test, at 5% probability. The presence of GxE interaction was broken down to simple effects and expressed by the heatmap analysis after using the AMMI and GGE methods, based on the following AMMI model:

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

where  $Y_{ij}$  is the mean response of population  $i$  ( $i = 1, 2, \dots, G$ ) in environment  $j$  ( $j = 1, 2, \dots, E$ );  $\mu$  is the general average of the tests;  $g_i$  is the fixed effect of population  $i$ ;  $e_j$  is the fixed effect of environment  $j$ ;  $\lambda_k$  is the  $k$ -th singular (scalar) value of the original interaction matrix (denoted by GE);  $\gamma_{ik}$  is the element

**Table 1.** Characterization of the studied environments in the state of Rio Grande do Sul, Brazil – including crop season, site (municipality), code, macroregion, sowing date, altitude, latitude and longitude, and rainfall –, of the evaluated soybean (*Glycine max*) genotypes.

Environment	Crop season	Municipality	Code	Macro-region <sup>(2)</sup>	Sowing date	Altitude (m)	Latitude	Longitude	Rainfall (mm)
E1	2016/2017	Bagé	1617B	101	30/11/2016	189	31°21'36"S	53°56'38"W	562.8
E2	2016/2017	Cachoeira do Sul	1617C	101	24/11/2016	123	30°17'11"S	52°58'33"W	979.0
E3	2016/2017	Passo Fundo	1617P	102	11/11/2016	714	28°13'18"S	52°19'36"W	1,230.9
E4	2016/2017	Santo Augusto	1617S	102	21/11/2016	520	27°54'33"S	53°47'34"W	699.6
E5	2016/2017	São Luiz Gonzaga	1617G	102	22/11/2016	171	28°18'35"S	55°06'32"W	1018.4
E6	2016/2017	Vacaria	1617V	103	17/11/2016	945	28°32'31"S	50°55'33"W	609.4
E7	2017/2018	Bagé	1718B	101	15/11/2017	205	31°21'16"S	53°57'29"W	391.6
E8	2017/2018	Cachoeira do Sul	1718C	101	15/11/2017	145	30°20'23"S	52°59'05"W	607.0
E9	2017/2018	Passo Fundo	1718P	102	2/11/2017	707	28°13'17"S	52°19'33"W	802.9
E10	2017/2018	Santo Augusto	1718S	102	7/11/2017	518	27°53'33"S	53°47'15"W	807.5
E11	2017/2018	São Luiz Gonzaga	1718G	102	21/11/2017	223	28°24'02"S	55°55'50"W	690.6
E12	2017/2018	Vacaria	1718V	103	7/11/2017	879	28°27'04"S	51°0'18"W	771.2
E13	2018/2019	Bagé	1819B	101	5/11/2018	190	31°21'34"S	53°56'29"W	812.5
E14	2018/2019	Cachoeira do Sul	1819C	101	7/11/2018	143	30°19'19"S	52°58'23"W	765.0
E15	2018/2019	Passo Fundo	1819P	102	30/11/2018	703	28°6'57"S	52°20'09"W	721.0
E16	2018/2019	Santo Augusto	1819S	102	12/11/2018	544	27°54'37"S	53°46'24"W	539.8
E17	2018/2019	São Luiz Gonzaga	1819G	102	20/11/2018	223	28°24'05"S	54°55'50"W	959.8
E18	2018/2019	Vacaria	1819V	103	12/11/2018	913	28°25'29"S	51°01'04"W	758.8

corresponding to the  $i$ -th population, in the  $k$ -th column of the singular vector of the GE matrix;  $e_{jk}$  is the element corresponding to the  $j$ -th environment, in the  $k$ -th singular row vector of the GE matrix;  $\rho_{ij}$  is the residual associated with the term  $(ge)_{ij}$  of the classical interaction of population  $i$  with environment  $j$ ; and  $\varepsilon_{ij}$  is the mean experimental error (Carvalho et al., 2016).

The GGE method was used to form macroenvironments, since it combines the effects attributed to genotypes and the GxE interaction, allowing the identification of genotypes with high yields and a greater efficiency in certain environments. The model used for the method was:

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

where  $Y_{ij}$  represents the expected magnitude of genotype  $i$  cultivated in environment  $j$ ;  $\mu$  corresponds to the general mean of observation  $Y_{ij}$ ;  $\beta_j$  is the main effect attributed to the growing environment;  $\lambda_1$  and  $\lambda_2$  correspond to the determinants of the main (PC I) and secondary (PC II) score for the graphic expression of the main components of the biplot;  $\xi_{1j}$  and  $\xi_{2j}$  are the eigenvectors that represent the  $i$  genotype on the axis of abscissa PC I and PC II; and  $\varepsilon_{ij}$  expresses the unadjusted residual of the statistical model (Dalló et al., 2019). The adaptability and stratification analyzes of environments were carried out using the methodology of Murukami & Cruz (2004).

Subsequently, the variance components and genetic parameters were estimated using REML, by the model:

$$y = Xr + Zg + Wi + e$$

where  $y$  is the data vector,  $r$  are the fixed effects of replicates,  $g$  is the random genotypic effect,  $i$  are the random effects of the GxE interaction, and  $e$  are the random residues.

Genotypic stability was measured with the qualitative index that allows weighting between mean performance and stability (WAASBY), with values ranging from 0–100; the higher the value, the more stable and better performing is the genotype (Olivoto et al., 2019).

Significance was evaluated by deviance (log-likelihood and likelihood ratio tests), at 5% probability, using the chi-square test and Akaike's Bayesian informative criterion. Individual phenotypic variance, broad-sense heritability for total genotypic effects, genotype mean heritability, coefficient of genotypic variation, coefficient of residual variation, and overall

mean were also estimated. BLUP estimates were used to obtain the components of the predicted means. All analyzes were performed using the R statistical software, version 3.5.6 (R Core Team, 2019), with the functions contained in ExpDes.pt, agricolae, GGEBiplot, and metan.

## Results and Discussion

The analysis of variance showed a significant interaction ( $p \leq 0.05$ ) between soybean genotypes and environments (Table 2), i.e., the effect of environments on the performance of different soybean genotypes, which made it possible to obtain adaptability and phenotypic stability estimates. The heatmap showed the effects of interactions between GxE for the variable grain yield (Figure 1), and the highest yield was obtained for cultivar NS 5959 IPRO in 2018/2019 in the municipality of Santo Augusto.

The AMMI probability had a significant effect. At least five main components would be needed to explain more than 80% of the variation, but since only two were used for the graphs, 61.7% of the variation was explained.

Variance components and genetic parameters are important as they present information related to the heritable genetic proportion attributed to the gene effect as a function of character variation, showing the similarity between progenies (Carvalho et al., 2017). With the used models, a significant interaction was observed between genotypes and environments (Table 2). For the variance components and genetic parameters, the coefficient used to determine the effects of the GxE interaction showed 28% of the model's applicability, and there was a genotypic correlation of 29% between the genotypes in the environments. Heritability shows the genetic variation within phenotypic variance, besides indicating the experimental precision for the phenotype, which was 0.02, classified as low (Carvalho et al., 2020).

In the graph considering the first principal component and yield (Figure 2 A), the genotypes that are in the first quadrant show high performance in favorable environments, with the highest average and stability due to the vertical line. In this case, the BMX Alvo RR and BMX Ícone IPRO cultivars stood out for the following environments: 1617B, 2016/2017 season in Bagé; 1617S, 2016/2017 season in Santo Augusto;

1819G, 2018/2019 season in São Luiz Gonzaga; 1617C, 2016/2017 season in Cachoeira do Sul; and 1617G, 2016/2017 season in São Luiz Gonzaga.

The genotypes in the second quadrant have low-medium averages, but under unfavorable environments. The cultivars that stood out were NS 6209 RR, BMX Tornado RR, BMX Valente RR, and BMX Garra IPRO, mainly for the following environments: 1718P, 1718B, 1718G, and 1718C, 2017/2018 season in Passo Fundo, Bagé, São Luiz Gonzaga, and Cachoeira do Sul, respectively; and 1819C, 2018/2019 season in Cachoeira do Sul.

The third quadrant is formed by genotypes with lower averages and that are not very stable in unfavorable environments. The NA 5909 RG and TMG 7062 IPRO cultivars stood out in the following environments: 1819B, 2018/2019 season in Bagé; and 1617P, 2016/2017 season in Passo Fundo.

The fourth quadrant has the most productive genotypes under unfavorable environmental conditions. In this case, cultivars BMX Ativa RR, DM 5958RSF IPRO, NS 5959 IPRO, and TMG 7262 RR stood out for environments: 1718V, 2017/2018 season in Vacaria; 1617V, 2016/2017 season in Vacaria; 1718S, 2017/2018 season in Santo Augusto; 1819P, 2018/2019

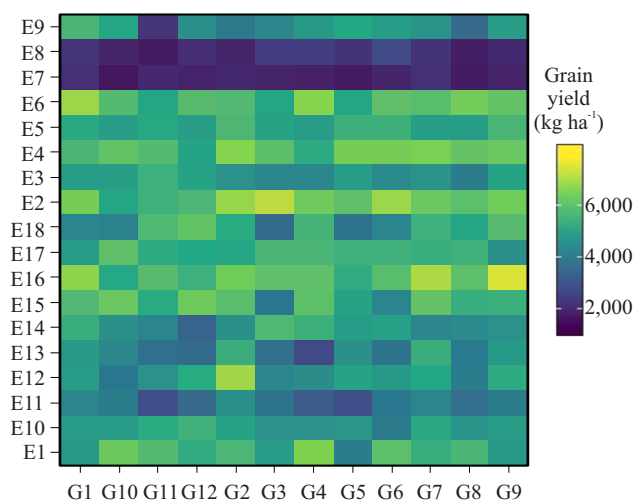
**Table 2.** Analysis of variance, analysis of variance for the additive main effects and multiplicative interaction (AMMI) method, analysis of variance for the deviance (log-likelihood and likelihood ratio tests) method, variance components, and genetic parameters<sup>(1)</sup>.

Source	DF	Sum of squares	Mean square	F-value	Pr (>F)	Percentage	Accumulated
Environment (E)	17	915,156,117.5	53,832,712.8	185.7	0.0	-	-
Block/ Environment (B)	36	10,438,590.3	289,960.8	1.2	0.2	-	-
Genotype (G)	11	10,290,415.1	935,492.3	3.8	0.0	-	-
GxE interaction	187	103,297,792.8	552,394.6	2.2	0.0	-	-
PC1	27	39,292,023.0	1,455,260.1	5.9	0.0	38.0	38.0
PC2	25	24,451,945.9	978,077.8	3.9	0.0	23.7	61.7
PC3	23	10,613,669.1	461,463.9	1.9	0.0	10.3	72.0
PC4	21	8,080,869.8	384,803.3	1.6	0.1	7.8	79.8
PC5	19	6,816,257.6	358,750.4	1.4	0.1	6.6	86.4
PC6	17	4,944,678.8	290,863.5	1.2	0.3	4.8	91.2
PC7	15	3,371,780.6	224,785.4	0.9	0.6	3.3	94.5
PC8	13	2,644,320.9	203,409.3	0.8	0.6	2.6	97.0
PC9	11	1,393,464.8	126,678.6	0.5	0.9	1.3	98.4
PC10	9	934,827.5	103,869.7	0.4	0.9	0.9	99.3
PC11	7	753,954.8	107,707.8	0.4	0.9	0.7	100.0
Residual	396	98,397,379.0	248,478.2	-	-	-	-
Total	647	1,137,580,294.8	1,758,238.5	-	-	-	-
Model	NP	logLik	AIC	LRT	DF	Pr (>chi-square)	
Complete	57	-4,681.60	9,477.19	-	-	-	-
G	56	-4,682.44	9,476.88	1.69	1.00	0.19	-
GxE interaction	56	-4,703.38	9,518.75	43.56	1.00	0.00	-
Parameter	Value	Parameter	Value	Parameter	Value	Parameter	Value
Phenotypic variance	356,878.09	GEI <sub>r2</sub>	0.28	Accuracy	0.64	CV <sub>g</sub>	1.71
Heritability	0.02	Heritability of means	0.41	r <sub>ge</sub>	0.29	CV <sub>r</sub>	10.13
						CV ratio	0.17

<sup>(1)</sup>DF, degrees of freedom; NP, number of parameters; logLik, log-likelihood ratio test; AIC, Akaike's information criterion; LRT, likelihood ratio test; GEI<sub>r2</sub>, coefficient for determining the effects of the genotype x environment interaction; r<sub>ge</sub>, genotypic correlation of genotype performance between environments; CV<sub>g</sub>, coefficient of genotypic variation; CV<sub>r</sub>, coefficient of residual variation; and CV ratio, ratio between the genetic and residual coefficients.

season in Passo Fundo; 1819S, 2018/19 season in Santo Augusto; and 1819V, 2018/2019 season in Vacaria.

For the graph between the first and second principal components (Figure 2 B), the first quadrant shows the most productive genotypes, close to the favorable environment, with cultivar BMX Icon IPRO standing out in 1819G and NS 6209 RR in 1617B. The second quadrant has the cultivars with lower yields in favorable environments, specifically TMG 7062 IPRO and TMG 7262 RR in 1718S and 1819V. The third quadrant presents the environments that were unfavorable and



**Figure 1.** Heatmap of the effects of the genotype x environment interaction for the soybean (*Glycine max*) grain yield variable. Evaluated genotypes (cultivars): G1, BMX Alvo RR; G2, BMX Ativa RR; G3, BMX Garra IPRO; G4, BMX Ícone IPRO; G5, BMX Tornado RR; G6, BMX Valente RR; G7, DM 5958RSF IPRO; G8, NA 5909 RG; G9, NS 5959 IPRO; G10, NS 6209 RR; G11, TMG 7062 IPRO; and G12, TMG 7262 RR. Environments (crop season + municipality in the state of Rio Grande do Sul, Brazil): E1, 2016/2017 season in Bagé; E2, 2016/2017 season in Cachoeira do Sul; E3, 2016/2017 season in Passo Fundo; E4, 2016/2017 season in Santo Augusto; E5, 2016/2017 season in São Luiz Gonzaga; E6, 2016/2017 season in Vacaria; E7, 2017/2018 season in Bagé; E8, 2017/2018 season in Cachoeira do Sul; E9, 2017/2018 season in Passo Fundo; E10, 2017/2018 season in Santo Augusto; E11, 2017/2018 season in São Luiz Gonzaga; E12, 2017/2018 season in Vacaria; E13, 2018/2019 season in Bagé; E14, 2018/2019 season in Cachoeira do Sul; E15, 2018/2019 season in Passo Fundo; E16, 2018/2019 season in Santo Augusto; E17, 2018/2019 season in São Luiz Gonzaga; and E18, 2018/2019 season in Vacaria.

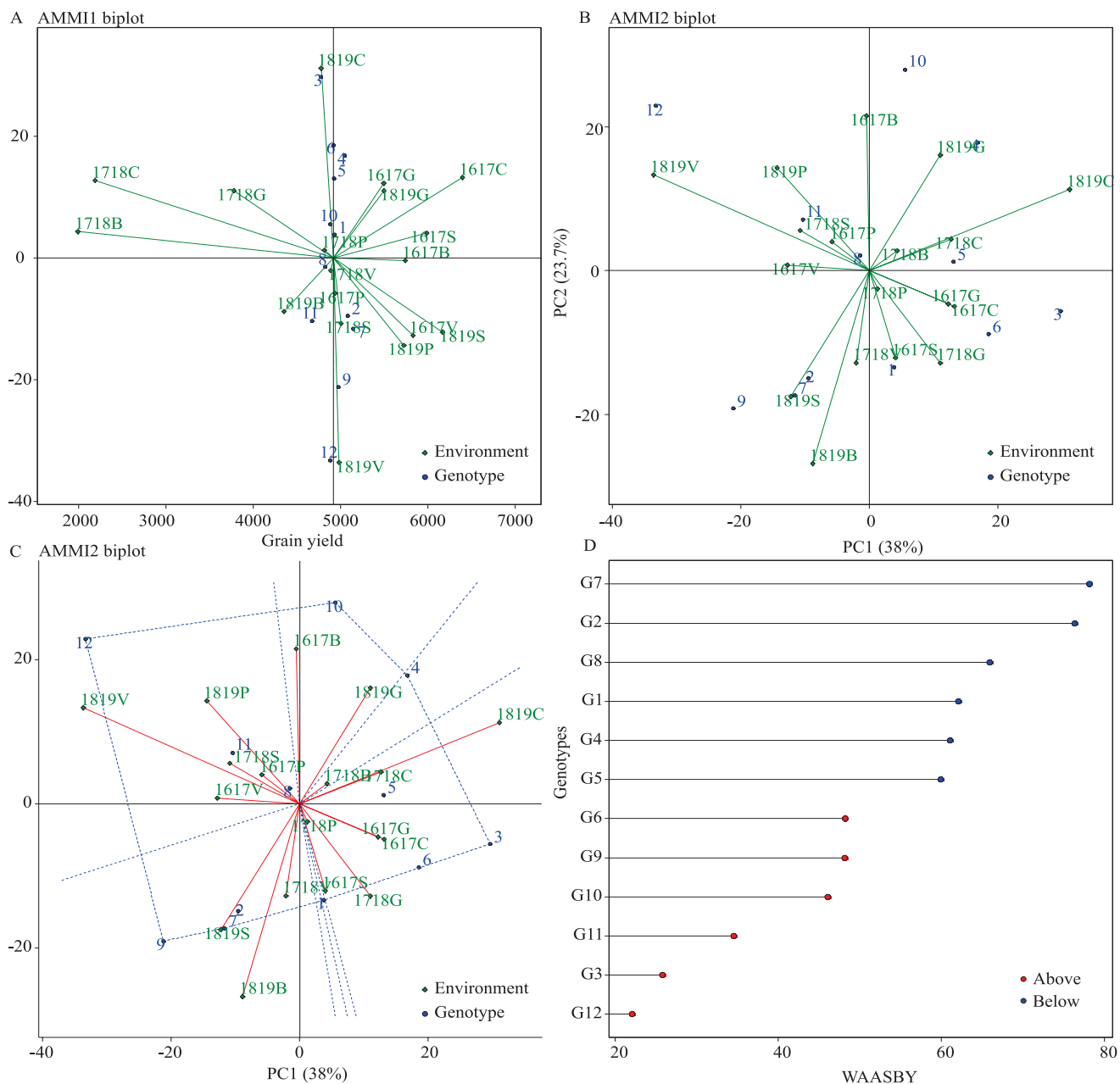
the least yielding cultivars, particularly BMX Ativa RR, DM 5958RSF IPRO, and NS 5959 IPRO in 1819S. The fourth quadrant shows the most productive cultivars in unfavorable environments, namely BMX Alvo RR, BMX Valente RR, and BMX Garra IPRO in 1617S and 1617C. The NA 5909 RG cultivar is characterized as the most stable among the genotypes evaluated in the different environments, since it contributed the least to the sum of squares of the interaction. Because of this result and its average grain yield, this genotype can be indicated for cultivation in the studied environments.

The AMMI graph, considering the first and second components (Figure 2 C), shows the formation of the following five macroenvironments with similar crop seasons: 1819G and 1617B; 1819P, 1617P, 1718S, and 1617V; 1718V and 1819S; 1718P, 1617S, 1617C, 1617G, and 1718C; and 1718B as an isolated environment. The high-performance environments – that exceed the delimited area of the high-performance polygon – were 1819C, 1819V, 1819S, 1819B, and 1718G, which shows that these seasons had an important role in soybean yield in these sites.

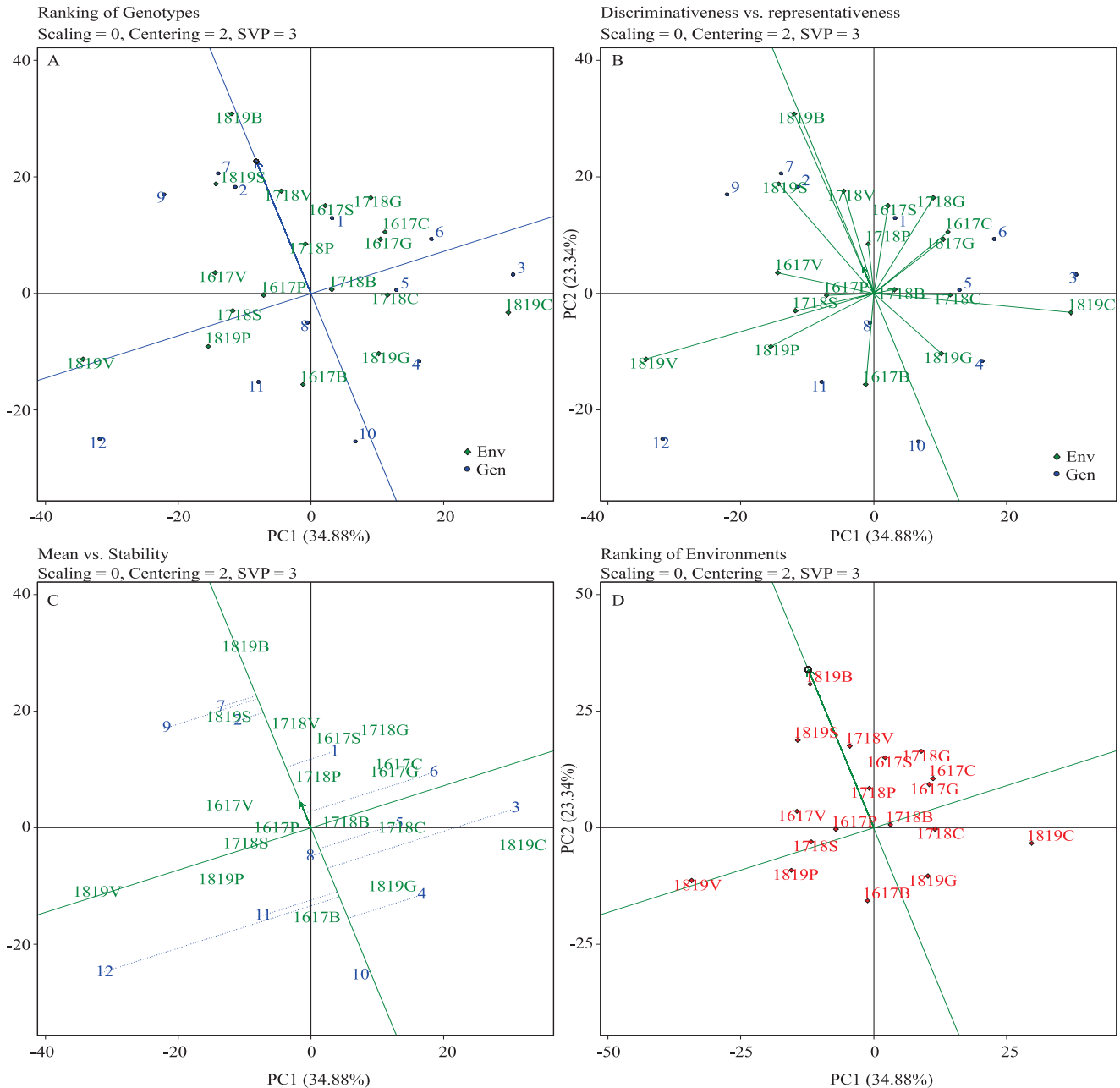
According to the WAASBY index (Figure 2 D), the genotypes that stood out were cultivars: DM 5958RSF IPRO and BMX Ativa RR, with the best performance; and TMG 7262 RR and BMX Garra IPRO, with the worst performance.

Genotype ranking (Figure 3 A) using the GGE methodology explained 58.22% of the obtained results, and the ideal genotypes with the best performance were cultivars BMX Tornado RR and BMX Ativa RR. The discrimination and representativeness graph (Figure 3 B), which relates the environments with the genotypes, showed that, for 1819S, the genotypes that showed the best performance were cultivars NS 5959 IPRO, DM 5958RSF IPRO, and BMX Ativa RR. For 1617S and 1617C, the genotypes that stood out were cultivars BMX Alvo RR and BMX Valente RR, respectively. The unfavorable environments were 1819V, 1819P, 1819G, and 1617B for cultivars TMG 7262 RR, TMG 7062 IPRO, BMX Ícone IPRO, and NS 6209 RR, respectively.

The mean and stability of the genotypes (Figure 3 C) showed that the cultivars with the highest mean for the favorable environment were BMX Valente RR, BMX Alvo RR, NS 5959 IPRO, DM 5958RSF IPRO, and BMX Ativa RR; the latter is the most stable for this type of environment. By analyzing the ranking



**Figure 2.** Graphs used to identify stability between genotypes using the additive main effects and multiplicative interaction (AMMI) method: type I, for soybean (*Glycine max*) grain yield (A) and the first and second principal components (PC1 and PC2, respectively) (B); and type II, for PC1 and PC2 (C) and the index that allows weighting between mean performance and stability (WAASBY) (D). Evaluated genotypes (cultivars): G1, BMX Alvo RR; G2, BMX Ativa RR; G3, BMX Garra IPRO; G4, BMX Ícone IPRO; G5, BMX Tornado RR; G6, BMX Valente RR; G7, DM 5958RSF IPRO; G8, NA 5909 RG; G9, NS 5959 IPRO; G10, NS 6209 RR; G11, TMG 7062 IPRO; and G12, TMG 7262 RR. Environments (crop season + municipality in the state of Rio Grande do Sul, Brazil): 1617B, 2016/2017 season in Bagé; 1617C, 2016/2017 season in Cachoeira do Sul; 1617P, 2016/2017 season in Passo Fundo; 1617S, 2016/2017 season in Santo Augusto; 1617G, 2016/2017 season in São Luiz Gonzaga; 1617V, 2016/2017 season in Vacaria; 1718B, 2017/2018 season in Bagé; 1718C, 2017/2018 season in Cachoeira do Sul; 1718P, 2017/2018 season in Passo Fundo; 1718S, 2017/2018 season in Santo Augusto; 1718G, 2017/2018 season in São Luiz Gonzaga; 1718V, 2017/2018 season in Vacaria; 1819B, 2018/2019 season in Bagé; 1819C, 2018/2019 season in Cachoeira do Sul; 1819P, 2018/2019 season in Passo Fundo; 1819S, 2018/2019 season in Santo Augusto; 1819G, 2018/2019 season in São Luiz Gonzaga; and 1819V, 2018/2019 season in Vacaria.

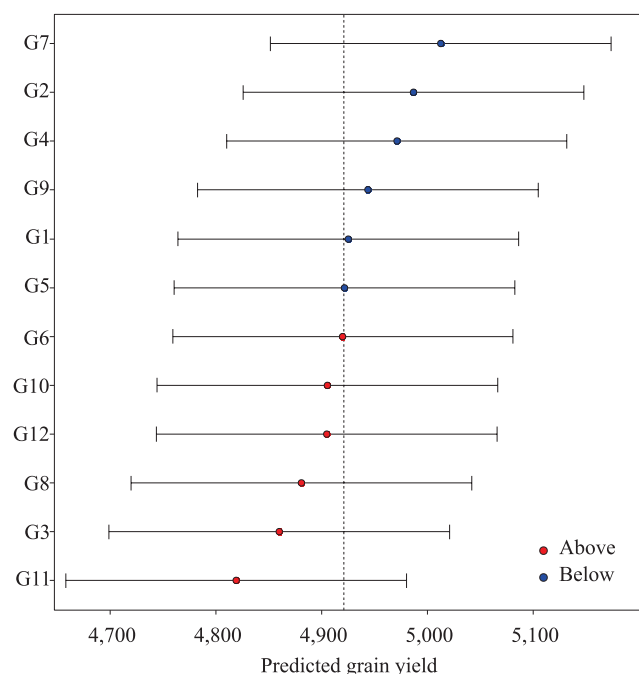


**Figure 3.** Graph with the genotype-by-environment interaction methodology for ranking of soybean (*Glycine max*) genotypes (A), genotype discrimination x representation (B), genotype mean x stability (C), and ranking of environments (D). Evaluated genotypes (cultivars): G1, BMX Alvo RR; G2, BMX Ativa RR; G3, BMX Garra IPRO; G4, BMX Ícone IPRO; G5, BMX Tornado RR; G6, BMX Valente RR; G7, DM 5958RSF IPRO; G8, NA 5909 RG; G9, NS 5959 IPRO; G10, NS 6209 RR; G11, TMG 7062 IPRO; and G12, TMG 7262 RR. Environments (crop season + municipality in the state of Rio Grande do Sul, Brazil): 1617B, 2016/2017 season in Bagé; 1617C, 2016/2017 season in Cachoeira do Sul; 1617P, 2016/2017 season in Passo Fundo; 1617S, 2016/2017 season in Santo Augusto; 1617G, 2016/2017 season in São Luiz Gonzaga; 1617V, 2016/2017 season in Vacaria; 1718B, 2017/2018 season in Bagé; 1718C, 2017/2018 season in Cachoeira do Sul; 1718P, 2017/2018 season in Passo Fundo; 1718S, 2017/2018 season in Santo Augusto; 1718G, 2017/2018 season in São Luiz Gonzaga; 1718V, 2017/2018 season in Vacaria; 1819B, 2018/2019 season in Bagé; 1819C, 2018/2019 season in Cachoeira do Sul; 1819P, 2018/2019 season in Passo Fundo; 1819S, 2018/2019 season in Santo Augusto; 1819G, 2018/2019 season in São Luiz Gonzaga; and 1819V, 2018/2019 season in Vacaria.



of environments (Figure 3 D), four groups were considered favorable: 1718B, 1617G, and 1617C, with average yields of 1,991, 5,495, and 6,397 kg ha<sup>-1</sup>, respectively; 1617V, 1718P, 1617S, and 1718G, with yields of 5,830, 4,816, 5,959, and 3,779 kg ha<sup>-1</sup>; 1819S and 1718V, with yields of 6,171 and 4,888 kg ha<sup>-1</sup>; and 1819B, with a yield of 4,353 kg ha<sup>-1</sup> and considered the most stable environment.

The use of REML models together with BLUP considers the known variance components and random genetic effects. This methodology increments the prediction of genetic value with true value, reducing prediction error (Carvalho et al., 2017). When this methodology was applied to the grain yield character (Figure 4), cultivars DM 5958RSF IPRO, BMX Ativa RR, BMX Ícone IPRO, and NS 5959 IPRO stood out with the highest grain yield independently of the evaluated environment, showing a greater adaptability to the different environments.



**Figure 4.** Best unbiased linear prediction for the grain yield character of soybean (*Glycine max*) genotypes. Evaluated genotypes (cultivars): G1, BMX Alvo RR; G2, BMX Ativa RR; G3, BMX Garra IPRO; G4, BMX Ícone IPRO; G5, BMX Tornado RR; G6, BMX Valente RR; G7, DM 5958RSF IPRO; G8, NA 5909 RG; G9, NS 5959 IPRO; G10, NS 6209 RR; G11, TMG 7062 IPRO; and G12, TMG 7262 RR.

The stratification of environments by the factor analysis showed the formation of macroenvironments (Table 3). The 18 assessed environments were stratified into six extracts or factors. In the first, the environments were 1819C, 1819G, 1819V, and 1617C; in the second, 1819B, 1819S, 1617S, and 1617G; in the third, 1617P and 1718P; in the fourth, 1718V and 1617V; in the fifth, 1718S, 1718G, 1718B, and 1718C; and, in the sixth, 1617B and 1819P (Table 4). The stratification of these environments occurred due to the proximity

**Table 3.** Analysis of factors for environment stratification of the studied environments in the state of Rio Grande do Sul, Brazil, for the evaluated soybean (*Glycine max*) genotypes<sup>(1)</sup>.

PCA <sup>(1)</sup>	Eigenvalue	Accumulated variance	Percentage
PC I	5.51e+0	3.06e+1	30.6
PC II	3.82e+0	2.12e+1	51.8
PC III	1.93e+0	1.07e+1	62.5
PC IV	1.76e+0	9.76e+0	72.3
PC V	1.40e+0	7.75e+0	80.0
PC VI	1.03e+0	5.72e+0	85.7

Environment <sup>(2)</sup>	Extract	Grain yield (kg ha <sup>-1</sup> )	CV (%)
E2	I	6,397	6.13
E14	I	4,778	12.90
E17	I	5,499	5.87
E18	I	4,985	13.80
E4	II	5,989	4.86
E5	II	5,495	7.15
E13	II	4,353	13.80
E16	II	6,171	8.91
E3	III	4,940	5.24
E9	III	4,816	9.02
E6	IV	5,830	6.11
E12	IV	4,888	9.36
E7	V	1,991	7.31
E8	V	2,188	12.50
E10	V	5,007	6.71
E11	V	3,779	12.20
E1	VI	5,742	7.56
E15	VI	5,727	8.33

<sup>(1)</sup>PCA, principal component analysis; PC, principal component. <sup>(2)</sup>See characterization of the environment in the Table 1. CV, coefficient of variation.

of the means between each environment when related to each other.

The results obtained for the adaptability and stability of genotypes may differ according to the used methods. With AMMI, the NS 5909 RG genotype can be selected as the most stable and indicated cultivar for the studied environments. With GGE, cultivars BMX Tornado RR and BMX Ativa RR stood out. With WAASBY and BLUP, the same genotypes – DM 5958 IPRO and BMX Ativa RR – were identified as showing the best performance; therefore, it can be inferred that the simultaneous use of both of these methods is not necessary. However, AMMI, GGE, and WAASBY or

BLUP should be used concomitantly to enhance the selection of superior genotypes.

## Conclusions

1. The soybean (*Glycine max*) genotypes that perform the best in favorable environments are cultivars BMX Valente RR, BMX Alvo RR, NS 5959 IPRO, DM 5958RSF IPRO, and BMX Ativa RR.

2. Favorable environments in the state of Rio Grande do Sul, Brazil, are defined as the 2017/2018 crop season in the municipality of Bagé and the 2016/2017 season in the municipalities of São Luiz Gonzaga and Cachoeira do Sul due to the higher grain yields obtained.

3. The genotypes that show excellent performance in unfavorable environments are cultivars BMX Ativa RR, DM 5958RSF IPRO, NS 5959 IPRO, and TMG 7262 RR; the 2016/2017 season is considered unfavorable in the municipalities of São Luiz Gonzaga and Cachoeira do Sul.

4. To enhance the selection of superior genotypes, the following models for genotype selection must be used simultaneously: additive main effects and multiplicative interaction (AMMI), genotype main effects + genotype-by-environment interaction (GGE), and weighting between mean performance and stability (WAASBY) or best linear unbiased prediction (BLUP).

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**Table 4.** Stratification of environments by the factor analysis<sup>(1)</sup>.

Environment	Factor	Average (kg ha <sup>-1</sup> )	Minimum (kg ha <sup>-1</sup> )	Maximum (kg ha <sup>-1</sup> )	CV (%)
1819C	1	4,778	3,781	5,854	12.90
1819G	1	5,499	5,000	6,134	5.87
1819V	1	4,985	3,977	6,633	13.80
1617C	1	6,397	5,806	7,071	6.13
1819B	2	4,353	3,681	5,269	13.80
1819S	2	6,171	5,393	7,247	8.91
1617S	2	5,989	5,280	6,306	4.86
1617G	2	5,495	4,791	6,037	7.15
1617P	3	4,940	4,549	5,295	5.24
1718P	3	4,816	3,609	5,284	9.02
1718V	4	4,888	4,324	6,033	9.36
1617V	4	5,830	5,349	6,448	6.11
1718S	5	5,007	4,197	5,484	6.71
1718G	5	3,779	3,250	4,553	12.20
1718B	5	1,991	1,735	2,231	7.31
1718C	5	2,188	1,880	2,656	12.50
1617B	6	5,742	5,033	6,394	7.56
1819P	6	5,727	4,675	6,258	8.33

<sup>(1)</sup>Environments (crop season + municipality in the state of Rio Grande do Sul, Brazil): 1617B, 2016/2017 season in Bagé; 1617C, 2016/2017 season in Cachoeira do Sul; 1617P, 2016/2017 season in Passo Fundo; 1617S, 2016/2017 season in Santo Augusto; 1617G, 2016/2017 season in São Luiz Gonzaga; 1617V, 2016/2017 season in Vacaria; 1718B, 2017/2018 season in Bagé; 1718C, 2017/2018 season in Cachoeira do Sul; 1718P, 2017/2018 season in Passo Fundo; 1718S, 2017/2018 season in Santo Augusto; 1718G, 2017/2018 season in São Luiz Gonzaga; 1718V, 2017/2018 season in Vacaria; 1819B, 2018/2019 season in Bagé; 1819C, 2018/2019 season in Cachoeira do Sul; 1819P, 2018/2019 season in Passo Fundo; 1819S, 2018/2019 season in Santo Augusto; 1819G, 2018/2019 season in São Luiz Gonzaga; and 1819V, 2018/2019 season in Vacaria. CV, coefficient of variation.

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