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### Mixed Models to Characterize Adaptability, Stability and Yield of Hybrid Corn

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**ABSTRACT**

Models that estimate genetic parameters and predictions are important as an auxiliary tool to increase hybrids stability, adaptability and yield assessment efficiency. The aim of this study was to estimate genetic parameters via REML, to predict hybrid genotypic values via BLUP and to simultaneously identify the best pre-commercial hybrids regarding stability, adaptability and yield. VCU tests were conducted in eight environments during the 2011/2012 season. 25 simple pre-commercial hybrids and three simple hybrids were assessed as commercial controls for grain yield. Genetic parameter estimates were carried out based on Reml/Blup procedure. Identification, based on adaptability, stability and yield criteria of the best hybrids, was obtained through harmonic mean of the relative performance of genotypic values (HMRPGE) method. HMRPGE was efficient in the selection of hybrids for stability, adaptability and yield. Commercial (P30F53, DKB240) and pre-commercial (KSP25, KSP05, KSP20 and KSP10) hybrids showed the highest magnitudes of predicted values, with high adaptability, stability and yield among the 28 hybrids assessed in eight environments. Hybrids that were superior to the predicted estimates (KSP25, KSP05, KSP20 and KSP10) showed competitive potential against commercial hybrids.

**INTRODUCTION**

Each year, new pre-commercial corn hybrids are obtained in breeding companies, undergoing preliminary assessments in various environments (locations). Before being available on the market, several hybrids are discarded. Thus, the total number of genotypes decreases while the number of environments increases year by year, until a select hybrid group with favorable agronomic characteristics is formed. Finally, these hybrids are subjected to tests of value for cultivation and use (VCU), being subsequently released on the market as commercial cultivars. Among difficulties often faced by breeders during superior genotype selection and subsequent recommendation, there is genotype x environment (GxE) interaction magnitude quantification, as the adoption of strategies that reduce or take advantage of such effects is a decision of the breeder (Cruz and Regazzi, 2001).

During preliminary assessments, there are many candidate genotypes to be included in the select group, hindering selection and requiring the use of appropriate tools to ensure the selection of the most promising hybrids. The adoption of biometric analyzes with consistent statistical models may result in more accurate

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estimates of genetic and residual variance components. Therefore, genotypic value prediction and promising genotype identification are improved (Resende *et al.*, 2001).

Currently, there are more than ten methodologies for adaptability and stability parameters analysis (Schmidt *et al.*, 2011). However, these inferences can be more reliable with the adoption of mixed models by eliminating interaction deviations, allowing the comparison between genotypes assessed in different environments (KalilFilho *et al.*, 2000). In this context, methods based on mixed models are an alternative to assist breeders in simultaneously selecting (identifying) genotypes by yield, adaptability and stability. Moreover, these methods can be applied to both balanced and unbalanced data sets (Henderson, 1984; Resende, 2004).

Mixed model use introduced variance component and genetic parameter estimation changes (Resende *et al.*, 1996). In fixed models, covariances are estimated and interpreted through their mathematical expectations, thus generating variance components. In the "restricted maximum likelihood" (REML) and "best linear unbiased prediction" (REML/BLUP) mixed models, variance components and random effect variances are directly estimated in the data set, not requiring independence of errors. These procedures allow higher modeling flexibility, becoming the standard procedure for some statistical analyzes (Duarte and Vencovsky, 2001; Resende, 2004).

REML, proposed by Patterson and Thompson (1971), became the standard method for estimating variance components and genetic parameters, especially in tests with unbalanced data or where the data set requires more complex models (KalilFilho *et al.*, 2000; Resende, 2004). As REML statistical properties exceed least square estimator methods, that method is preferred (Searle *et al.*, 1992).

Mixed models have been used by many researchers of the plant breeding area for species such as eucalyptus (Resende *et al.*, 1996; Rosado *et al.*, 2012.), coffee (Resende *et al.*, 2001), potato (Souza *et al.*, 2005), sugarcane (Zeni-Neto *et al.*, 2008), corn (Arnhold *et al.*, 2012; Dovale, 2012), beans (Baldissera *et al.*, 2012) and rice (Borges *et al.*, 2009). Thus, the standard analytical procedure recommended for studies involving quantitative genetics is the REML/BLUP, in order to estimate variance components and predict unbiased genotypic values (Resende *et al.*, 2001).

The adoption of models that estimate and make predictions based on genetic parameters and genotype means is important to identify superior hybrids in a select group.

Thus, the objective of this research was to estimate genetic parameters through restricted maximum likelihood (REML), to predict hybrid genotypic values through best linear unbiased prediction (BLUP), and to identify pre-commercial hybrids that simultaneously have the best stability, adaptability and yield estimates.

## MATERIAL AND METHODS

VCU tests were conducted in three states of Brazil, totaling eight environments (six in the state of Paraná, one in Santa Catarina and one in Rio Grande do Sul) during the 2011/2012 season. Pre-commercial hybrids used in the tests were obtained from KSP Sementes Ltda. company breeding program, located in the municipality of Pato Branco-PR.

During tests, 28 hybrids were used, of which three were commercial single cross hybrids (P30F53, DKB240 and SG6303) and 25 were pre-commercial single cross hybrids (KSP Sementes Ltda.). Hybrids were planted according to the agroclimatic zoning of each location. Cultivation was carried out in accordance with corn technical recommendations for each location where tests were conducted. Rows were opened with mechanized seeder and base chemical fertilization was also conducted in the same operation. Hybrids were sown manually.

Tests in Parana were conducted in the municipalities of Clevelândia (26°21'17"S, 52°28'56"O and 860m), Cascavel (24°57'28"S, 53°27'34"O, 738m), Pato Branco (26°13'44"S, 52°40'15"O, 760m), Ampére (25°54'20"S, 53°25'54"O, 718m), Quedas do Iguaçu (25°27'7"S, 52°54'35"O, 578m) and Londrina (23°18'17"S, 51°10'8"O, 539m). In Santa Catarina, tests were conducted in the municipality of Itapiranga (27°10'10"S, 53°42'44"O, 206m). In Rio Grande do Sul, cultivation was conducted in Coxilha (28°7'33"S, 52°17'58"O, 678m). The experimental design was of randomized blocks, with three repetitions in each environment. There were 84 experimental units in each location, totaling 672 experimental units in the total set of environments where tests were conducted.

The experimental unit (plot) consisted of two rows with 5 meters long and 0.70 meters of spacing between rows, totaling 42 plants, equivalent to 60,000 plants per hectare. Grain yield assessment was conducted by manual harvest, humidity was corrected to 13% and mass was measured in kg per plot.

Deviance analysis was conducted with and without heritability estimates, obtaining the deviances. The likelihood ratio (LRT) was obtained subtracting the reduced model from the complete model, which was compared to the chi-square test tabulated value with one degree of freedom. Genetic parameter estimates were obtained through restricted maximum likelihood and best linear unbiased predictor (REML/BLUP) models, using the Selegen software (Resende, 2007b). In order to obtain estimates, the 54 model was used, as follows:  $y = Xr + Zg + Wi + e$ , where  $y$ : is the data vector;  $r$ : is the vector of repetition effect (assumed to be fixed) added to the overall mean;  $g$ : is the phenotypic effect (random) vector;  $i$ : is the genotype x environment interaction

(random) vector;  $e$  is the error or residue (random) vector and  $X$ ,  $Z$  and  $W$ : incidence matrices for  $r$ ,  $g$  and  $i$  effects, respectively.

Predicted genotypic values that were free of any interaction with environments were obtained by  $u + g$ , where:  $u$  = mean of all locations and  $g$  = predicted genotypic value.

Predicted genotypic values considering interaction were obtained by  $u+g+gem$ , which refers to the mean genotypic value in the various environments, and mean interaction was capitalized with all assessed environments (Resende, 2007b).

In order to determine confidence intervals, the equation described by Resende (2007a) was used, as follows:  $CI = V_G \pm t[(1 - r_{aa}^2) \sigma^2]^{1/2}$ , where:  $CI$ : confidence interval;  $V_G$ : genotypic value;  $t$ : Student's  $t$  distribution associated with a certain confidence level ( $t = 1.96$  for 95% confidence);  $r_{aa}^2$ : accuracy, and  $\sigma_G^2$ : genetic variance.

Identification of hybrids with the highest yield and stability was conducted by the harmonic mean of genotypic values (HMGV), and hybrids with the highest adaptability were found through the relative performance of predicted genotypic values (RPPGV). Mean genotypic values capitalized by the interaction were obtained through RPPGV\*GM (harmonic mean of genotypic values multiplied by the general mean (GM) of all locations). Yield, stability and adaptability parameters were obtained jointly, based on the harmonic mean of the relative performance of genotypic values (HMRPGV).

Mean genotypic values penalized by instability and capitalized by adaptability were obtained by HMRPGV\*GM parameter (HMRPGV multiplied by the general mean (GM) of all locations).

## RESULTS AND DISCUSSION

Deviance analysis showed significant differences by likelihood-ratio test (LRT) at 5% error probability, according to the chi-square test with one degree of freedom, and significant differences were also found for the genetic variance component and the determination coefficient (Table 1).

Genotypic variance estimates revealed that the character has genetic variance of 0.376, which is equivalent to 23.8% of phenotypic variance, indicating genetic variation occurrence among hybrids and good chances of success regarding superior hybrids identification for the character (Table 1). According to Maia *et al.* (2009), genetic parameter estimates are important in decision-making and breeding program targeting, since they help in the selection process and serve as theoretical framework to support the recommendation of genotypes to be placed on the market.

**Table 1:** Deviance analysis and genetic parameter estimates by restricted maximum likelihood (REML) for grain yield in 28 corn hybrids related to eight sowing locations.

Effects	Deviance	LRT	Comp. var.	Determ. coeff
Complete model	869.342	65.895**	0.376**	0.856**
Reduced model	935.237			
Genetic parameter				GY
Genotypic variance - $V_G$				0.376
Variance of interaction - $G \times E$				0.167
Residual variance - $V_r$				1.037
Individual phenotypic variance - $V_{fi}$				1.581
Heritability individual - $h_{MI}^2$				0.237 $\pm$ 0.054
Heritability average $h_M^2$				0.854
Accuracy selective - $A_c$				0.924
$R^2$ of $G \times E$ interaction - $R_{G \times E}^2$				0.105
Genotypic correlation				0.691
$CV_{gi}^a$ (%)				7.849
$CV_e^b$ (%)				13.033
Overall average				7.813

\*\* Significant at 1% error probability by chi-square test.

<sup>a</sup> $CV_{gi}$ : Genotypic coefficient of variation.

<sup>b</sup> $CV_e$ : Residual variation coefficient.

Mean broad-sense heritability ( $h_M^2$ ) showed a high value, 0.85 (Table 1). The estimate is important when the goal is to "select" and/or identify genotypes, as genetic values are predicted based on phenotypic values obtained from several repetitions. Furthermore, the magnitude of this parameter also indicated that the experimental arrangement was adequate to control environment effects, properly estimating genotypic values for grain yield in this experiment.

Individual broad-sense heritability ( $h_{MI}^2$ ), which is free of interaction effects and was obtained through dividing genotypic variance by phenotypic variance ( $V_G/V_F$ ), showed low magnitude estimates (0.238). This indicates that interaction variance affected phenotypic variance estimates, as  $h_M^2$  (0.854), which does not include environment interaction, was four times higher than individual estimates, free of interaction effects ( $h_{MI}^2$ ) (Table 1). Among parameters analyzed, heritability is one of the most important ones. However, it is not a constant

parameter, as its estimates undergo variations depending on character, estimation method, sample size, number of environments and accuracy during experiment conduction. In this study, broad-sense heritability served as a way to measure the environment effect on grain yield expression.

$V_{G \times E}$  interaction variance represents 10.59% of the total phenotypic variation, showing that intrinsic characteristics of the environments where hybrids were evaluated influenced character phenotypic expression with this change rate (Table 1). GxE interaction variance allows estimating genotype response constancy related to environmental variations, that is, the yield maintenance of a specific hybrid at different locations (Rosado *et al.*, 2012).

Simple GxE interaction is characterized by hybrid classification maintenance in different environments, and complex interaction is caused by lack of correlation between genotypes from one environment to another, causing hybrid classification inversion (Resende, 2007a). Simple interaction does not cause major problems for genotype "selection" or indication. Complex or cross interaction hinders the identification of genotypes with broader adaptability, compromising cultivar recommendation by the breeder.

Comparatively,  $V_{G \times E}$  (0.16) estimates with  $V_G$  (0.37) and  $h_M^2$  (0.85) were high (Table 1), which resulted from performance genotypic correlation in different environments of 0.69 for grain yield, indicating that there was maintenance trend in the superiority order of hybrids assessed in environments with correlation higher than 0.50.

The genetic variation coefficient ( $CV_{GI}$ ) was of 7.84% and the residual coefficient ( $CV_E$ ) was of 13%, indicating genetic differences between hybrids. Proximity between  $CV_{GI}$  and  $CV_E$  percentages indicates good experimental quality. In this experiment,  $CV_{GI}$  and  $CV_E$  values reflected in selective accuracy of 92% (Table 1). The estimation of a character that has high accuracy is an indication of good relation between predicted genotypic values and actual genotypic values (Resende and Duarte, 2007). Accuracy values above 0.90 are considered of excellent experimental precision (Resende, 2002). The good quality of these tests in different environments resulted in securing agronomically superior hybrids, and indicated that estimates predicted by the model were close to true values.

Genotypic values are unobservable variables and should be predicted by breeders from phenotypic values observed in the experiment. Predicted genotypic values are not equal to the actual genotypic values. However, Van Vlecket *al.* (1987) stated that predicted value proximity with the actual value can be measured by accuracy, which refers to the correlation between predicted genetic values and actual genetic values. The higher the assessment accuracy, the higher the predicted genetic value accuracy. This parameter can be highlighted in this study, as accuracy was higher than 0.90, indicating that predicted genetic values were close to the actual genetic values.

Table 2 shows phenotypic effects (g), predicted genotypic values (u+g) and mean genotypic values in environments (u+g+gem), considering the interaction of 28 hybrids in the joint analysis of eight locations. Genotypic estimates indicated high performance of P30F53 DKB240, KSP25, KSP20, KSP05, KSP10 and KSP15 hybrids, with superior predicted estimates than those of other genotypes.

**Table 2:** Genetic gain estimates predicted by best linear unbiased prediction (BLUP) for the grain yield character in corn hybrids, considering mean performance in the eight environments.

Order	Hybrid	$g^a$	$u+g^b$	Gain	Average new(Yield)	$u+g+gem$
1	P30F53	1.33	9.14	1.33	9.14	9.22
2	DKB240	1.32	9.13	1.32	9.14	9.21
3	KSP25	0.77	8.59	1.14	8.95	8.63
4	KSP20	0.50	8.31	0.98	8.79	8.34
5	KSP05	0.47	8.29	0.88	8.69	8.31
6	KSP10	0.39	8.20	0.80	8.61	8.22
7	KSP15	0.35	8.16	0.73	8.55	8.18
8	KSP23	0.24	8.06	0.67	8.49	8.07
9	SG6302	0.15	7.96	0.61	8.43	7.97
10	KSP07	0.12	7.93	0.56	8.38	7.94
11	KSP16	0.05	7.86	0.52	8.33	7.86
12	KSP02	0.04	7.85	0.48	8.29	7.85
13	KSP06	0.03	7.84	0.44	8.26	7.85
14	KSP04	0.02	7.84	0.41	8.23	7.84
15	KSP17	-0.00	7.81	0.38	8.20	7.81
16	KSP21	-0.04	7.76	0.36	8.17	7.76
17	KSP24	-0.11	7.69	0.33	8.14	7.68
18	KSP14	-0.13	7.68	0.30	8.12	7.67
19	KSP09	-0.27	7.54	0.27	8.09	7.52
20	KSP03	-0.27	7.53	0.24	8.06	7.51
21	KSP22	-0.37	7.43	0.21	8.03	7.41
22	KSP01	-0.38	7.42	0.19	8.00	7.40
23	KSP08	-0.43	7.37	0.16	7.97	7.34
24	KSP19	-0.54	7.26	0.13	7.94	7.23
25	KSP18	-0.67	7.14	0.10	7.91	7.10
26	KSP11	-0.74	7.06	0.07	7.88	7.02

27	KSP13	-0.91	6.90	0.03	7.84	6.85
28	KSP12	-0.91	6.89	0.00	7.81	6.84

<sup>a</sup>g, genotypic effect.

<sup>b</sup>u+g, genotypic value.

Similarity between commercial and pre-commercial hybrid predictions is important for the breeder to identify hybrids with higher competitive potential. According to Resende *et al.* (1996), best linear unbiased prediction (BLUP) of genotypic values is equal or superior to other methods for genotype ordering, genetic value prediction and genetic gain estimation. The application of this method results in secure data regarding genetic parameter estimates. It was found that predicted values for u+g genotypic means, which are free of GxE interaction, were lower than genotypic magnitudes that considered the (u+g+gem) interaction for P30F53, DKB240, KSP25, KSP20, KSP05, KSP10, KSP15, KSP23, SG6302, KSP07, KSP16, KSP02, KSP06 e KSP04 hybrids.

Predicted phenotypic magnitudes (u+g) were higher than predicted genotypic estimates for u+g+gem interaction in KSP17, KSP21, KSP24, KSP14, KSP09, KSP03, KSP22, KSP01, KSP08, KSP19, KSP18, KSP11, KSP13 e KSP12 hybrids. Thus, GxE interaction effects caused grain yield reduction because effect capitalization was not favorable to hybrid performance (Rosado *et al.*, 2012).

In Table 3, adaptability (RPGV) and stability (HMGV) estimates are shown. Joint mean genotypic values for interaction (u+g+gem) had similar results to the method in which adaptability and stability estimates are capitalized simultaneously. With this comparison, it is shown that the classification of the first seven hybrids is quite similar in the estimates of the two methods. Similar results were obtained by Bastos *et al.* (2007), who obtained the same ranking in both methods for sugarcane.

**Table 3:** Stability and adaptability analysis results of 28 corn hybrids grown in eight different environments regarding grain yield.

Order	Hybrid <sup>a</sup>	HMGV	Hybrid <sup>b</sup>	RPGV	RPGV*GM	HMRPGV	HMRPGV*GM
1	P30F53	8.95	P30F53	1.19	9.31	1.19	9.28
2	DKB240	8.91	DKB240	1.19	9.28	1.19	9.26
3	KSP25	8.30	KSP25	1.11	8.67	1.11	8.66
4	KSP05	7.96	KSP05	1.07	8.33	1.07	8.33
5	KSP20	7.92	KSP20	1.07	8.33	1.07	8.32
6	KSP15	7.82	KSP10	1.05	8.22	1.05	8.21
7	KSP10	7.81	KSP15	1.05	8.19	1.05	8.18
8	KSP23	7.66	KSP23	1.03	8.06	1.03	8.05
9	SG6302	7.63	SG6302	1.02	7.98	1.02	7.98
10	KSP16	7.55	KSP07	1.01	7.92	1.01	7.91
11	KSP07	7.53	KSP16	1.01	7.89	1.01	7.88
12	KSP02	7.52	KSP02	1.01	7.87	1.01	7.86
13	KSP17	7.50	KSP17	1.00	7.84	1.00	7.83
14	KSP04	7.47	KSP04	1.00	7.84	1.00	7.83
15	KSP24	7.41	KSP06	1.00	7.82	1.00	7.81
16	KSP06	7.41	KSP21	0.99	7.75	0.99	7.74
17	KSP21	7.38	KSP24	0.99	7.73	0.99	7.72
18	KSP14	7.37	KSP14	0.99	7.70	0.98	7.69
19	KSP03	7.22	KSP03	0.97	7.54	0.96	7.53
20	KSP09	7.09	KSP09	0.96	7.50	0.96	7.48
21	KSP22	7.09	KSP22	0.95	7.42	0.95	7.42
22	KSP01	7.00	KSP01	0.94	7.37	0.94	7.37
23	KSP08	6.92	KSP08	0.94	7.31	0.93	7.30
24	KSP19	6.87	KSP19	0.92	7.22	0.92	7.22
25	KSP18	6.77	KSP18	0.91	7.10	0.91	7.09
26	KSP11	6.62	KSP11	0.89	6.99	0.89	6.98
27	KSP13	6.44	KSP13	0.87	6.81	0.87	6.80
28	KSP12	6.44	KSP12	0.87	6.80	0.87	6.79

<sup>a</sup>HMGV: harmonic mean of genotypic values; RPGV: relative performance of genotypic values; RPGV\*GM: mean genotypic values capitalizing adaptability; HMRPGV: harmonic mean of relative performance of genotypic values; HMRPGV\*GM: harmonic mean of relative performance of genotypic values penalized by instability and capitalized by adaptability.

<sup>a</sup>Sorted by HMGV values.

<sup>b</sup>Sorted by RPGV values.

P30F53 and DKB240 hybrids, used as controls, stood out in genotypic value ordering (u + g) for grain yield. However, it was observed that some pre-commercial hybrids, such as KSP25, KSP20, KSP05, KSP10 and KSP15 showed similar behavior for the character, showing that such hybrids have the potential to be released on the market, according to predicted estimates.

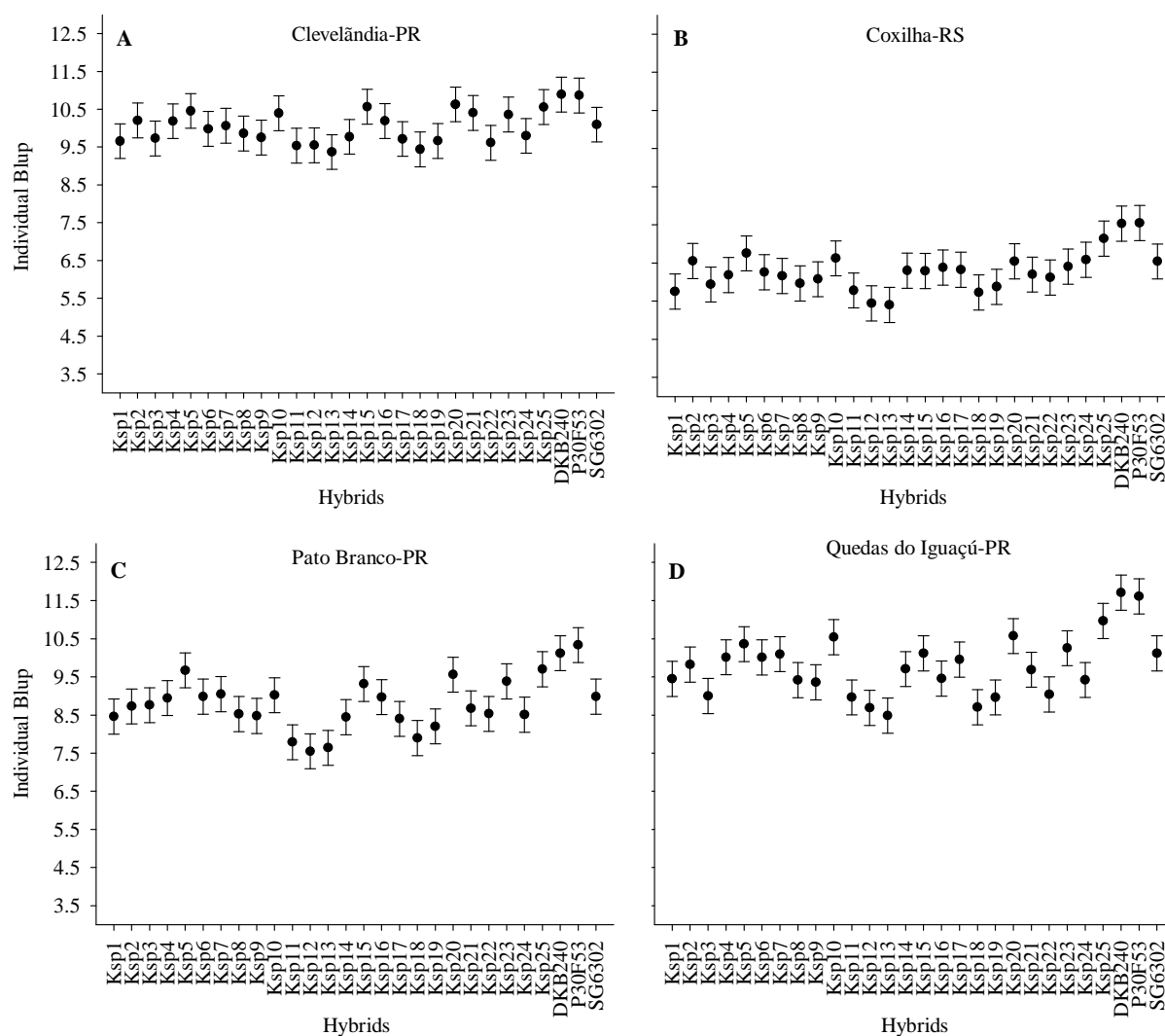
It is also noteworthy that estimates for these hybrids were superior to those of the SG6302 commercial hybrid, indicating that new pre-commercial hybrids may outperform hybrids used as control, with good agronomic performance.

In the genotype analysis within each environment (Figure 1 and 2), in order to identify specific hybrids for assessment locations, it is possible to highlight the superior performance of P30F53 and DKB240 commercial

hybrids for all environments, and P30F53 performed better in Coxilha-RS, PatoBranco-PR, Londrina-PR and Itapiranga-SC. The DKB240 hybrid was superior in Clevelândia-PR, Quedas do Iguaçu-PR, Cascavel-PR and Ampère-PR

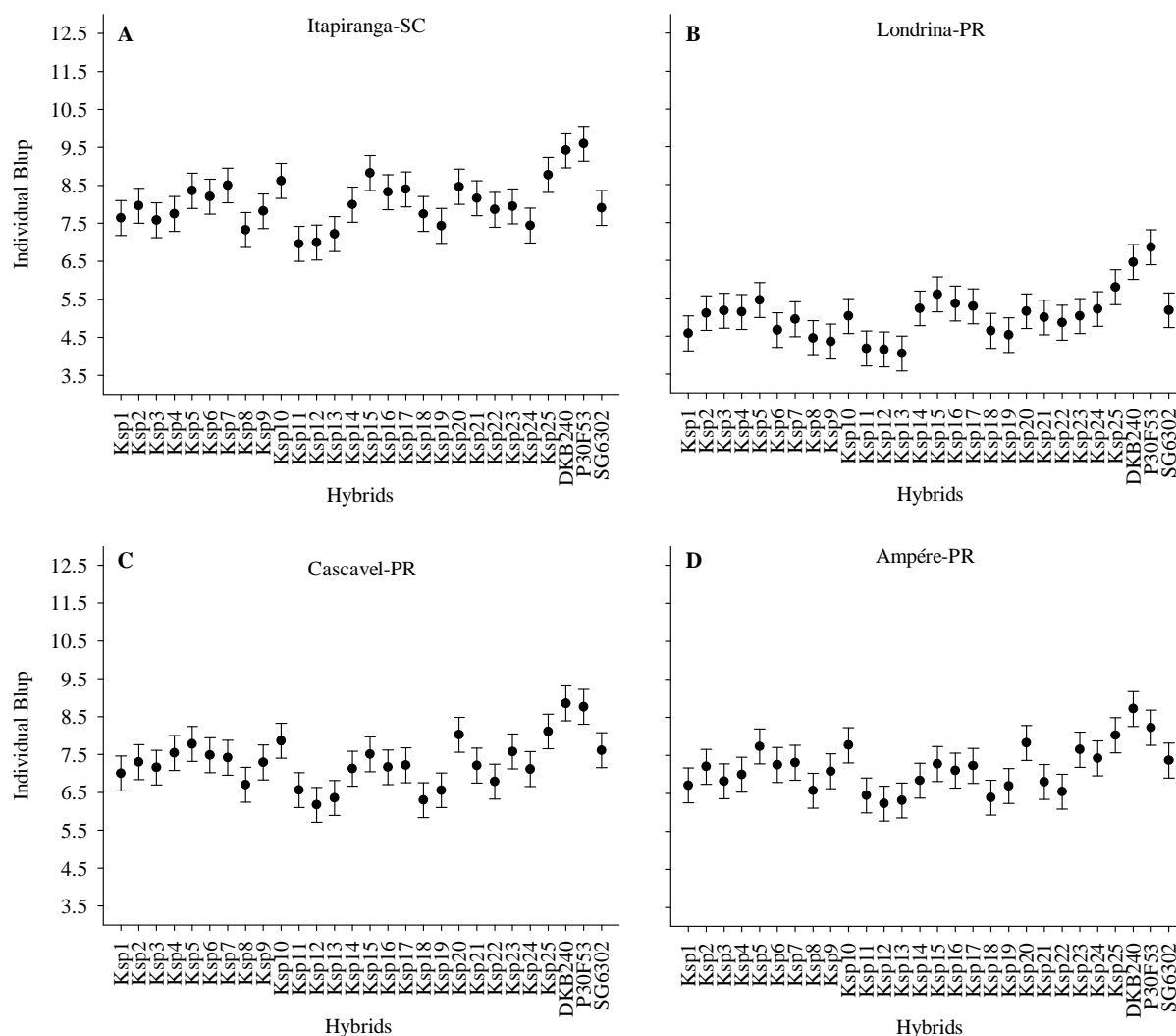
The breakup of the best individual Blup predictor by environment is important to infer more carefully on superior hybrid performance in each environment. The effects of the best predictor through Blup (Table 2) and measured genotypic values for stability and adaptability (Table 3) showed that P30F53 exceeded in the two genotypic prediction methodologies. However, with the break-up by environment, as shown in Figures 1 and 2, it can be inferred that the DKB240 hybrid also has good performance in four of eight locations assessed.

Regarding VCU pre-commercial hybrid predicted estimates by environment, taking into account the respective confidence intervals in the figures, KSP20, KSP15 and KSP25 hybrids (Figure 1A) stood out in Clevelândia, PR. In Coxilha, RS, KSP05, KSP10 and KSP25 (Figure 1B) hybrids performed better. For PatoBranco-PR, KSP05, KSP15, KSP20, KSP23 and KSP25 hybrids enabled predicted estimates close to controls (P30F53 and DKB240) (Figure 1C). In Quedas do Iguaçu-PR (Figure 1D), KSP10, KSP20 and KSP25 hybrids stood out.



**Fig. 1:** Individual Blup genetic value estimates ( $u+g+ge$ ) representing 28 hybrids assessed in Clevelândia-PR, Coxilha-RS, PatoBranco-PR and Quedas do Iguaçu-PR regarding the grain yield character.

For Itapiranga-SC (Figure 2A) KSP10, KSP15 and KSP25 hybrids proved to be the most promising. For Londrina, PR, constitutions with high predicted estimates were KSP05, KSP15 and KSP25 (Figure 2B). For Cascavel-PR, promising hybrids were KSP05, KSP10, KSP20 and KSP25 (Figure 2C). In Ampère-PR, KSP05, KSP10, KSP20 and KSP25 hybrids stood out (Figure 2D).



**Fig. 2:** Individual Blup genetic value estimates ( $u+g+ge$ ) representing 28 hybrids assessed in Itapiranga-SC, Londrina, Cascavel-PR and Ampère-PR regarding the grain yield character.

Through Blup break-up in each environment, it was also found that the KSP25 hybrid showed no complex interaction with the environment, showing constancy in all environments analyzed. This suggests that among all hybrids tested, KSP25 showed the highest competition potential against commercial hybrids, although its performance was lower than that of two of the three controls used.

The study of GxE interaction predicted genotypic effects should be analyzed simultaneously with phenotypic adaptability and stability estimates. Therefore, it is possible to infer on the response level of hybrids to environmental stimuli. In addition, it is also possible to infer on their yield maintenance performance related to environmental variation (Maia *et al.*, 2009). The use of different stability and adaptability study methods, as well as the amount of locations, may alter the classification of genotypes under study (Vencovsky and Barriga, 1992).

With regard to Table 3, stability results based on the method of harmonic mean of genotypic values (HMGV), simultaneous genotype ordering by their genetic values (yield), and stability by BLUP (Best Linear Unbiased Prediction) under harmonic means indicate that the lower the genotype behavior standard deviation among locations, the higher the harmonic mean of genotypic values (HMGV). Thus, the BLUP procedure considers hybrid performance and stability simultaneously (Resende, 2004, 2007a).

Resende (2007a) reports that, in addition to penalization by the highest standard deviation, HMGV penalizes genotypic values of each genotype by instability, which ensures higher precision and accuracy in genotype ordering, within and between locations. For genotypic values, P30F53, DKB240, KSP25, KSP20, KSP05 and KSP10 hybrids stood out in the classification. The first two are commercial hybrids (controls), and along with this group, four pre-commercial hybrids showed competitive potential to be selected within the group and to be subsequently sold.

Regarding predicted estimates for adaptability by the method of relative performance of predicted genotypic values (RPGV) in the environments, P30F53, DKB240, KSP25, KSP05, KSP20, KSP10 and KSP15

hybrids were highlighted, with the highest magnitudes. These estimates express predicted values as the ratio of the overall mean for each location (Resende, 2007). Relative performance has been used in terms of phenotypic data, forming the basis of the method by Annicchiarico (1992). According to the predicted values, the most unstable hybrids for assessment locations were KSP08, KSP19, KSP18, KSP11, KSP13 and KSP12, showing that such hybrids should not be recommended for these environments, as their conditions are not suitable for these genotypes to obtain high agronomic performance.

Simultaneous identification for stability, adaptability and yield with the use of mixed models can be performed following the method of harmonic mean of relative performance of predicted genetic values (HMRPGV). This method considers genotypic effects as random and provides stability and genotypic adaptability, generating results by the own character scale (Resende, 2007a). According to the author, the HMRPGV is suitable for hybrid selection and/or indication aimed at seeding in different environments with GxE interaction variations.

Comparing HMRPGV (Table 3) predicted values of the 28 hybrids assessed in eight environments, P30F53, DKB240, KSP25, KSP05, KSP20 and KSP10 stood out with the highest magnitudes, and their yield means were 9.27, 9, 26, 8.66, 8.32, 8.32 and 8.21 kg per plot, respectively. The yield intervals in these hybrids was of approximately 13 Mg ha<sup>-1</sup> and 11 Mg ha<sup>-1</sup>. The classification of the first two P30F53 and DKB240 hybrids was expected, as they are commercial hybrids with long market time grown widely throughout the Brazilian South region. However, behavior similarity between KSP25 and KSP05 hybrids and commercial hybrids is emphasized, as they showed potential to be indicated with commercial hybrids. Moreover, these hybrids performed better than the SG6302 commercial hybrid.

KSP08, KSP19, KSP18, KSP11, KSP13 and KSP12 hybrids showed similar behavior for all selection criteria, with the lowest predict magnitudes. However, low relative performance for adaptability, stability and yield cannot be a discarding criterion for breeders, as hybrids should only not be recommended for these environments. Higher performances can be obtained by these hybrids in other environments.

The three adaptability, stability and yield estimation methods used were consistent in hybrid ordering. According to Rosado *et al.* (2012), this is due to positive correlation in the genotypic behavior among environments. According to the results, the indication of hybrids with high adaptability and performance can be conducted. In the analysis of hybrids that showed agronomic performances below commercial indication levels, there are KSP12, KSP13, KSP11, KSP18 and KSP19. For Blup estimates and adaptability, stability and yield criteria, these hybrids showed identical ordering in the classification.

Selection of the first seven hybrids through HMRPGV\*MG method resulted in a new grain yield mean of 8.60 kg per plot (12 Mg ha<sup>-1</sup>) (Table 3), which was higher than the mean yield obtained in all u+g+gem environments, 8.59 Mg ha<sup>-1</sup>kg per plot. It can be observed that magnitudes were very close. However, though the harmonic mean of the relative performance of genotypic values method has the advantage of selecting genotypes according to their adaptability and phenotypic stability, which is an extremely important attribute on the recommendation of cultivars for commercial use (Rosado *et al.*, 2012).

HMGV, RPGV and HMRPGV statistics proved useful in the "selection" and indication of agronomically superior hybrids, providing option choices on criteria to be adopted, which corroborates the efficiency and success that was already observed by other researchers, such as SturionandResende (2005); ZeniNeto *et al.* (2008); Bastos *et al.*, (2009); and Maia *et al.* (2009) in the obtainment of predicted estimates and simultaneous selection regarding genotypic parameters.

### Conclusions:

REML/BLUP genetic parameter and genotypic value estimates and predictions are consistent and reliable in this set of hybrids, what was guaranteed by the high accuracy of this study.

The harmonic mean of the relative performance of genotypic values is efficient for use in the selection of hybrids for stability, adaptability and yield.

30F53, DKB240, KSP25 KSP05, KSP20 and KSP10 hybrids had the highest predicted value magnitudes, showing high adaptability, stability and yield among the 28 hybrids assessed in eight environments.

KSP25, KSP05, KSP20 and KSP10 hybrids, tested regarding predicted estimates of adaptability, stability and yield, showed potential for use as commercial hybrids.

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