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RESEARCH ARTICLE

Genetic parameters, yield adaptability and stability of common bean obtained through mixed models analyses

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ABSTRACT

The common bean provides a diet rich in vitamins, fiber, minerals and especially in proteins, which can provide food security for poor people in many countries. With the increase in demand for food production, cultivars with high grain yield potential that can be planted in different environments have been the focus of common bean breeding programs. Therefore, this study aimed to evaluate genetic parameters, grain yield, adaptability and stability simultaneously of common bean lines that compose the Value for Cultivation and Use trials of the South region of Brazil. The experiments were conducted in 13 environments in the states of Paraná, Santa Catarina and Rio Grande do Sul. The analysis of adaptability and stability were performed using mixed linear models by the Residual Maximum Likelihood and the Best Linear Unbiased Predictor for predicting the genotypic values through Selegen statistical program. The selective accuracy of genotypes for their genotypic values was 87% and the broad-sense heritability for grain yield was 13%. The genotypes CHC 98-42, BRS Esteio, CNFP-10794, CHP 01-238, FT 08-75, IPR Campos Gerais, LP 09-40, CNFC 10762, C 4-7-8-1-2 and LEC 01-11 were superior based on the method of Harmonic Mean of Relative Performance of Genotypic Values. These genotypes presented a higher mean grain yield in comparison to the other evaluated genotypes, and could be recommended for cultivation in these regions. In addition, it was possible to obtain genetic gains of up to 9.5% for the CHC 98-42 line, showing its high genetic potential.

Keywords: Genotypic value, complex interaction, genotype-environment interaction, HMRPGV, *Phaseolus vulgaris* L., REML/BLUP.

INTRODUCTION

Phaseolus vulgaris L. is one of the most important staple foods to humans. It is one of the main sources of iron, zinc, folic acid and corresponds to 65% of the protein consumed by a great part of the population of East Africa and Latin America (Broughton et al., 2003; Petry, Boy, Wirth, & Hurrell, 2015; Coêlho, Gonçalves-Vidigal, Vidigal Filho, Franzon, & Martins, 2020; Ferreira et al., 2022; Paulino et al., 2022). Brazil is one the world's largest producer of common bean surpassing 2.6 million tons in the crop year of 2016 (Food and Agriculture Organization [FAO], 2018). This was possible due to the efforts of researchers to develop genotypes with high commercial value. Several public and private plant breeding institutions worldwide have invested heavily to obtain new and superior genotypes (Friesen, Brûlé-Babel, Crow, & Rothenburger, 2016), which are evaluated in field trials and different locations over the years for many agronomic traits. It aims to predict the performance of the genotypes when planning future series of trials (Laidig, Drobek, & Meyer, 2008).

Several sophisticated statistical methods are used for assessment of genotypes, since they are exposed to environmental effects and their interactions, so called genotype by environment interaction (GEI). The GEI is expressed as an inconsistent response of genotypes in relation to others through environments due to changes in the genotype classification, known as a complex interaction, or an inconsistent response without changing the genotype classification, known as a simple interaction (Crossa, 2012). Currently in Brazil, the trials for registration and recommendation of cultivars are determined by the National Register of Cultivars (RNC) of the Brazilian Ministry of Agriculture, Livestock and Supply (Ministério da Agricultura, Pecuária e do Abastecimento [MAPA], 2013). It is done based on Value for Cultivation and Use (VCU) trials in multiple locations for at least two years, data analyses using the classical statistics by joint Analysis of Variance (ANOVA), F value significant at 5% of probability and coefficient of variation less than 25% (MAPA, 2013).

Based on this, estimation of stability and adaptability enables the identification of genotypes predictable and responsive to environmental variations (Corte, Moda-Cirino, & Destro, 2002). Several methods of stability and adaptability analysis were developed in order to identify superior cultivars in the presence of GEI. They attempted to establish models that could better interpret the phenotypic stability and adaptability. Among these methods, those based on Analysis of Variance (Plaisted & Peterson, 1959; Wricke, 1965; Annicchiarico, 1992), linear regression (Finlay & Wilkinson, 1963; Eberhart & Russell, 1966), bilinear regression (Verma, Chahal, & Murty, 1978), bissegmented linear regression (Cruz, Torres, & Vencovsky, 1989), non-parametric (Lin & Binns, 1988; Huehn, 1990) and AMMI analysis (Additive Main Effects and Multiplicative Interaction analysis) (Zobel, Wright, & Gauch, 1988) stand out. However, the linear mixed models are being widely used in GEI analysis in several plant breeding programs (Burgueño, Crossa, Cornelius, & Yang, 2008). In agriculture, repeated measures are often found and the linear model with mixed effects is suitable for the analysis of these types of data (Wang, 2016).

The prediction of genotypic value of genotypes by the Best Linear Unbiased Predictor (BLUP) and the estimation of variance components by the Restricted Maximum Likelihood (REML) allow the prediction of the random effects of the model in the presence of fixed effects or vice versa (Piepho, Möhring, Melchinger, & Büchse, 2008). Furthermore, REML/BLUP method ensures greater flexibility for analysis of genotypes allocated in different trials, especially in the presence of unbalanced data and heterogeneous variances (Robinson, 1991). For the simultaneously selection of genotypes for grain yield, adaptability and stability, the methodology indicated is the

Harmonic Mean of Relative Performance of Genotypic Value (HMRPGV) proposed by Resende (2007), that is very useful for many crops. Several authors reported the superiority of this method in different types of crops, such as: sugarcane (Oliveira et al., 2005), common bean (Carbonell et al., 2007; Chiorato, Carbonell, Dias, & Resende, 2008; Franzon et al., 2016); cashew (Maia, Resende, Paiva, Cavalcanti, & Barros, 2009), rice (Borges et al., 2010; Colombari-Filho et al., 2013), cotton (Moiana, Vidigal Filho, Gonçalves-Vidigal, Maleia, & Mindo, 2014; Farias, Carvalho, Silva Filho, & Teodoro, 2016) and corn (Rodovalho, Coan, Scapim, Barth Pinto, & Contreras-Soto, 2015), which demonstrates the applicability of this methodology.

The MHPRVG is based on the analysis of the genetic values through mixed models. It allows the selection of genotypes, simultaneously considering their yield, stability, and adaptability (Resende, 2007). In common bean, studies conducted by Carbonell et al. (2007) in 15 different environments in São Paulo state, ranked pretty much the same lines when HMRPGV statistics were compared to traditional methods such as Lin and Binns and Annicchiarico. However, in other crops the HMRPGV is widely used to select genotypes for commercial purposes, as for in sugar cane, the HMRPGV showed the same order of Lin and Binns (*Pi*) and Arnnicchiarico (*Ii*) statistics (Oliveira et al., 2005), and in corn, the HMRPGV had a very strong correlation with Pi and Ii statistics (Rodovalho et al., 2015).

In the context of mixed models with HMRPGV selection, the are several advantages, such as: a) consider genotypic effects as random, therefore, provides genotypic adaptability and stability, not phenotypic; b) allows analysis of experiments with non-orthogonal and unbalanced data, as well as, experiments with different number of replicates; c) allows to handle heterogeneity of variances; d) provides genetic data on the same magnitude of the evaluated characteristic, previously penalized by the instability; and e) allows to compute the genetic gain and selection simultaneously, considering the adaptability, stability and grain yield (Resende, 2007).

From this point of view, with the ease of use of this methodology, in its different approaches, the objective of this study was to evaluate genetic parameters, grain yield adaptability and stability simultaneously of common bean lines that compose the Value for Cultivation and Use trials of the South region of Brazil.

MATERIAL AND METHODS

Genetic material

Table 1 shows the elite lines and cultivars used in this study, as well as their origin, commercial specifications and seed color. We evaluated 14 lines from the main common bean breeding programs in the country, members of the South Brazilian Technical Committee of Common Bean (CTSBF), and four commercial checks (Pérola, IPR Campos Gerais, IPR Uirapuru and BRS Esteio). These 18 genotypes composed the VCU trial of the CTSBF network for common bean cultivars registration and recommendation.

Experimental Design

The experiments were conducted in 13 environments in the states of Paraná, Santa Catarina and Rio Grande do Sul, during the agricultural years of 2012/2013 and 2013/2014. At the rainy season, the experiments were conducted in the municipalities of Maringá (23°23'S - 51°57'O), Ponta Grossa (25°10'S - 50°8'O), Canoinhas (26°11'S - 50°21'O), Lages (27°49'S - 50°17'O), Ponte Serrada (26°52'S - 52°0'O), Chapecó (27°5'S - 52°38'O) in the agricultural year of 2012/2013. In 2013/2014 they were performed in Júlio de Castilho (29°10'S - 53°41'O), Maquiné (29°40'S - 50°12'O) and Maringá. Lastly, the experiments from the dry-season were carried out in the municipalities of Chapecó, Ituporanga (27°25'S - 49°34'O), Águas de Chapecó (27°3'S - 52°56'O) and Urussanga (28°31'S - 49°19'O) only in the agricultural year of 2013/2014. The experiments were conducted using a randomized complete block design with three replicates in the states of Paraná and Rio Grande do Sul, while for Santa Catarina state four replicates were performed instead. The number of genotypes and replicates varied for each region and experiment, characterizing an unbalanced data set. The seeding rate was 15 seeds per meter, resulting in a total of 300,000 plants per hectare. The plots consisted of four rows of 5.0 m in length, spaced at 0.5 m apart. The experimental unit comprised 4.0 m^2, corresponding to the two center rows, as determined by the National Register of Cultivars (RNC) (Figure 1).

Table 1. Characteristics of cultivars and lines evaluated in these experiments.

Nº	Cultivar/Line	Breeder companies	Market class	Seed color
1	Pérola	EMBRAPA[a]	Carioca	Beige with brown stripe
2	IPR Campos Gerais	IAPAR[b]	Carioca	Beige with brown stripe
3	IPR Uirapuru	IAPAR	Black	Black
4	BRS Esteio	CNPAF[c]	Black	Black
5	C 4-7-7-2-2	IAC[d]	Carioca	Beige with brown stripe
6	C 4-7-8-1-2	IAC	Carioca	Beige with brown stripe
7	CHC 98-42	EPAGRI[e]	Carioca	Beige with brown stripe
8	CHP 01-238	EPAGRI	Black	Black
9	CNFC 10762	CNPAF	Carioca	Beige with brown stripe
10	CNFP 10794	CNPAF	Black	Black
11	FT 08-47	FT SEMENTES	Carioca	Beige with brown stripe
12	FT 08-75	FT SEMENTES	Carioca	Beige with brown stripe
13	LEC 01-11	UEM[f]	Carioca	Beige with brown stripe
14	LEP 02-11	UEM	Black	Black
15	LP 09-192	IAPAR	Black	Black
16	LP 09-40	IAPAR	Carioca	Beige with brown stripe
17	TB 02-23	CPACT[g]	Black	Black
18	TB 03-13	CPACT	Colors	Dark yellow

Statistical analysis

Grain yield, expressed in Kg ha^{-1}, had its experimental errors assessed for normality using Shapiro-Wilk test (Shapiro & Wilk, 1965) and homogeneity of variance by Levene's test (Levene, 1960). Deviance analysis was obtained through the Likelihood Ratio Test (LRT) to test the significance of statistical models with and without the effects of genotype and GEI. The LRT is a statistical test of the goodness-of-fit between two models. A relatively more complex model (complete) is compared to a simpler model (reduced) to see if it fits a particular dataset significantly better. If so, the additional parameters of the more complex model are often used in subsequent analyses. The LRT is only valid if used to compare hierarchically nested models. That is, the more complex model must differ from the simple model only by the addition of one or more parameters. The LRT provides one objective criterion for selecting among possible models. Each effect was subtracted from the deviance of the complete model and compared to the value of Chi Square (χ^2) with one degree of freedom and 1% probability, in order to determine if the genotype effect, as well the GEI effect, could be analyzed as a random effect or a fixed effect. The LRT equation is defined as follow (Equation 1), where *ln* is the natural logarithm, and $ML_{reduced}$ and $ML_{complete}$ are the maximum likelihood of reduced and complete model, respectively. The analysis of normality, homogeneity of variance and LRT were performed using the PROC UNIVARIATE, PROC GLM and PROC MIXED respectively, through statistical package SAS 9.1 (Statistical Analysis System [SAS], 2009).

Figure 1. Value for Cultivation and Use trial conducted in Maringa, PR, Brazil.

Best linear unbiased prediction approach was adopted to predict genotypic values, and the estimates of variance components of random effects were obtained by REML. According to the Equation 2, BLUP consists of solving the mixed-model for the parameter vector, where Y, b, g, c, and e correspond to the data vector, the effect of blocks within different environments (fixed), genotype effects (random), effects of GE (random), and random errors, respectively. X, Z, and W are the incidence matrices for b, g, and c, respectively. The genetic parameters were estimated using the REML/BLUP method.

The predicted genotypic values for the genotype *i* for each location *j* use simultaneously data of all locations (Equation 3), where U_j is the mean of the local *j*; g_i is the BLUP value of the genotype *i*; and gl_{ij} is the BLUP value of the interaction between the genotype *i* and/or environment *j*. In this case, both *g* and *gl* are predicted, because the whole data set is used, and the noises (residual effects) of the interaction are eliminated when producing the BLUP's *gl* (Resende, 2007).

For the analysis of genotypic stability, it was applied the Harmonic Mean of

Genotypic Value (HMGV) (Equation 4). This method admits two premises that a cultivar must exhibit to be recommend to farmers according to Eberhart and Russell (1966), which are high grain yield and high stability. A great advantage of this method relies on the fact that breeding values are penalized by instability, which provides an adjusted mean value.

For adaptability, the Relative Performance of Genotypic Value (RPGV) (Equation 5) was used. The predicted genotypic values (or original data) are expressed as a proportion of the overall mean for each environment and then the mean value of this ratio is obtained across environments. Usually, the relative performance has been extensive used for phenotypic data and is the basis of the method of Annicchiarico. The appropriate method to study adaptability is the RPGV which capitalizes on the responsiveness of each genotype to environmental improvement. Ultimately, it computes the effect of each genotype response to stimulation of the environment of evaluation, being it favorable or unfavorable (Resende, Furlani Júnior, Moraes, & Fazuoli, 2001).

For a greater simultaneous analysis of adaptability and stability and grain yield, the Harmonic Mean of Relative Performance of Genotypic Values (HMRPGV) (Equation 6) was applied. Since *l* is the number of locations where the genotype *i* was evaluated; M_j is the overall mean of each local *j*; and *GVij* is the genotypic value of the genotype *i* at the local *j*, expressed as a proportion of the mean for this local. The prediction values based on HMRPGV allow reliable inferences about the prediction of genetic values, emphasizing the advantage of applying a method to assemble productivity, adaptability and stability as a single selection criterion. These values for HMRPGV are penalized for their instability and capitalized by adaptability (Resende, 2007).

To assess the performance of these analyses procedures, the model 54 of the SELEGEN REML/BLUP software was used (Resende, 2007).

$$LRT = -2ln\left(\frac{ML_{reduced}}{ML_{complete}}\right) \qquad (Equation\ 1)$$

$$Y = Xb + Zg + Wc + e \qquad (Equation\ 2)$$

$$GV_{ij} = U_j + g_i + gl_{ij} \qquad (Equation\ 3)$$

$$HMGV = \left(\frac{l}{\sum_{j=1}^{l} \frac{1}{GV_{ij}}}\right) \qquad (Equation\ 4)$$

$$RPGV = \frac{1}{l}\left(\frac{\sum GV_{ij}}{M_j}\right) \qquad (Equation\ 5)$$

$$HMRPGV = \left(\frac{l}{\sum_{j=1}^{l} \frac{1}{RPGV_{ij}}}\right) \qquad (Equation\ 6)$$

RESULTS AND DISCUSSION

Analysis of deviance

The presence of GEI is one of the biggest challenges in plant breeding of major crops, including common bean, both in the selection processes and the recommendation of cultivars. Genotype by environment interaction studies collaborate to understand the premise that the best genotype for a particular environment may not be in another one (Crossa, 2012). Thus, efforts from plant breeders have been focused to identify stable and adaptable genotypes through the years and locals. In the present study, the experimental errors associated with grain yield of 18 common bean genotypes evaluated in 13 environments, showed normal distribution, but not all environments showed homogeneous variances, allowing all subsequent analyzes to consider heterogeneous variances, justifying the use of mixed modeling REML/BLUP.

The analysis of deviance for random effects showed that the effects of genotype, and genotype by environment interaction (GEI) were significant at 1% by Chi-square test (χ^2) (Table 2). It was feasible to further evaluate the data using a complete statistical model, which could take into consideration random effects of GEI. In this case, where the GEI was significant, variability and different performances of the genotypes through environments was observed. Thus, adaptability and stability studies are interesting to provide effective selection of genotypes for all environments under study (Coimbra, Guidolin, Carvalho, Coimbra, & Hemp, 1999; Corte et al., 2002), since it is possible to predict and infer genotypic values for genetic treatments for different environments.

Table 2. Values of the deviance analysis for grain yield of 18 common bean genotypes in 13 environments in the states of Paraná, Santa Catarina and Rio Grande do Sul in the harvest seasons of 2012/13 and 2013/14.

Effect	*Deviance*[a]	LRT[b] (χ^2)
Genotype	10577.8	95.8*
Genotype × Environment	10504.9	22.9*
Complete Model	10482.0	-

[a] Deviance of the fitted model without the corresponding effects;
[b] LRT= Likelihood Ratio Test;
* and ** significant by the Chi-square test at 1% (6.63) and 10% (2.71) respectively;
[ns] not significant.

Genetic parameters

In Table 3 presents the estimates of variance components (individual REML). The value of 16.26% obtained in this study for the residual coefficient of variation (*CVe*) indicates a good experimental precision for VCU trials, as required by the National Register of Cultivars (RNC) (MAPA, 2013). The *CVe* is strictly analyzed in VCU trials, aiming the registration of cultivars at the RNC. Thus, in this work, the residual coefficient of variation was satisfactory, and its estimate was below the limit observed for common bean trials (< 25%). Pereira et al. (2014) found a medium experimental precision (*CVe=21%*) in their study on the stability of Andean common bean lines and they emphasize that residual coefficient of variation is an important parameter for genotype selection accuracy.

In general, high values for the genetic variation coefficient (*CVg%*) indicates that a substantial fraction of the genotypic variance was extracted from the phenotypic variance, since this value is obtained by dividing the square root of the genotypic variance for the overall mean. In this study, the value of 7.98% for *CVg* was low because the evaluated genotypes were at the final stage of evaluation, therefore low rate of loci in heterozygosis are expected for these lines, leading to a reduced genetic variability. This low value is partly because of the low genetic variance observed (40675.84) and the high overall yield mean (2525.48 kg ha^{-1}). The most part of the economic and agronomic characteristics of importance in common bean are quantitative, since the grain yield is controlled by several genes of low effect on the phenotype and highly influenced by the environment (Table 3). Similar results were also obtained by Chiorato et al. (2008), with a CVg value of 8.55%. The same authors suggested that this CVg value combined with low broad sense heritability resulted in low genetic variance among genotypes.

Table 3. Estimates of genotypic variance (Vg), variance of genotype × environment interaction (Vint), residual variance (Ve), individual phenotypic variance (Vf), broad sense heritability of individual plot level, ie, the total genotypic effects (h^2g), mean heritability of genotype (h^2mg), accuracy in the selection of genotypes (Acgen), coefficient of determination of the G×E interaction effects (c^2int), genotypic correlation through the environments (rgloc), genotypic variation coefficient (CVg%) and residual variation coefficient (CVe%), for grain yield of 18 common bean genotypes in 13 environments in the states of Paraná, Santa Catarina and Rio Grande do Sul in the harvest seasons of 2012/13 and 2013/14.

Parameters	**Estimates**
Vg	40675.84
Vint	100226.79
Ve	168726.06
Vf	309628.69
h^2g	0.13
h^2mg	0.76
Acgen	0.87
c^2int	0.32
rgloc	0.29
CVg%	7.98
CVe%	16.26
Overall Mean (μ)	2525.48 Kg ha^{-1}

Regarding the broad sense heritability estimation of individual plot level (h^2g) (Table 3), the genetic effect for grain yield, considering the total genetic dispersion, demonstrated a low magnitude (13%). Studies performed by Coimbra et al. (2008), using the REML/BLUP method to select common bean accessions based on adaptive characters, showed broad sense heritability estimates of low magnitude (5.5 to 23.2%). Thus, the same authors concluded that the selection should cautiously be applied to these traits, since the environment has a strong influence on phenotypic expression.

The grain yield in field trials is related to the phenotypic value of a character, which is composed by genetic, environmental and GEI effects. The obtained results in this study, the largest contribution on the phenotypic value for grain yield is associated with the environment (*Ve*), which corresponds to 54.5% of the total variance. Likewise, Coimbra et al. (2008) showed that the highest variation among the means of 24 lines evaluated was attributed to the environment, consequently the contribution of the genetic variation exhibited lower magnitude.

This residual variance between experimental plots may be responsible for numerous errors, promoting the random nature of the residues that occur in agricultural experimentation to recommend cultivars. Besides that, study conducted by Bertoldo et al. (2009) showed that environmental effects were superior to the genetic effects, and there is the opportunity of better understands new allelic associations to explore the GEI in breeding programs.

The lower is *Vint* value, the lower is the influence of interaction in the total phenotypic variance value. Consequently, a genotype with a good performance in an environment tends to remain good in other environments, as pointed out by Maia et al. (2009). The results obtained of *Vint* in this study represented 32.5% (Table 3), of the total phenotypic variance, indicating that a high partition of the interaction variance inflated the genotypic correlation through environments (*rgloc*), detecting difference in the ranking of genotypes across environments and indicating low similarity among the evaluated environments. Due to the low value of *rgloc* (0.29) found in this study, the inconstancy of the ranking of genotypes across the environments was evidenced, because of the complex type of interaction, where is very important studies of adaptability and stability of genotypes. In contrast, Rodovalho et al. (2015) found a high value for *rgloc* (0.86), showing similarity among the evaluated environments. Based on this finding, the authors can conclude that selection of genotypes must be based on the mean of the environments, rather than on estimation of genetic values for each environment, which makes the selection of genotypes with broad adaptation easier.

Clearly, the main goal for all breeding programs is the successful selection for cultivar recommendation, as the genotypes are chosen based on their genotypic values across different trials and locations replicates. For that reason, the number of replicates is a key factor to reduce the variation between the phenotypic and genotypic mean. Consequently, the accuracy becomes higher as the absolute deviations between the genetic parametric value and the estimated or predicted genetic value becomes lower Resende and Duarte (2007). The selective accuracy order of 0.87 and according to Resende and Duarte (2007), the selective accuracy is classified as very high (≥ 0.90), high (≥ 0.70 and <0.90), moderate (≥ 0.50 and <0.70) and low (<0.50). Thus, in our study high selective accuracy was achieved showing high experimental quality. High values for selective accuracy were also obtained by Pereira et al. (2014) in their study.

Individual BLUP´s

The values obtained for individual BLUP (μ + g) comes from an improved technique that estimates the genetic merit of the genotype, which are free of the mean interaction of the environments (Robinson, 1991). The genotypes selected by this method can be planted elsewhere with an environmental effect different from the current assessed environment (Resende, 2007). Table 4 exhibits the selection of genotypes with the best genotypic values for an environment mean, represented to 13 environments. We have obtained high average grain yields ranging from 2157 to 2765 kg ha^{-1}. The genotypes that stand out with individual BLUP superior to the overall mean were: CHC 98-42, CNFP 10794, CHP 01-238, BRS Esteio, C 4-7-8-1-2, LP

09-40, IPR Campos Gerais, FT 08-75, CNFC 10762, LEC 01-11 and LP 09-192, and presented BLUP higher than the check Pérola, with estimates of genetic gains of approximately 9.50%, equivalent to 240 Kg ha^{-1} and 8.03% (202 Kg ha^{-1}), in the case of the CHC 98-42 and CNFP 10794 lines, respectively. Studies conducted by Chiorato et al. (2008) in the state of São Paulo, Brazil, showed genetic gains in the order of 16.25%, which was higher than gain obtained in our study. As previously observed by Resende (2007), our results demonstrated that the above-mentioned selection do not compromise the genetic potential of genotypes, even under different environmental conditions.

Table 4. Predicted genotypic values μ + g (individual BLUP) for grain yield of 18 common bean genotypes in 13 environments in Paraná, Santa Catarina and Rio Grande do Sul in the harvest seasons of 2012/13 and 2013/14.

Genotype	g	μ + g	g%	New mean
CHC 98-42	239.9477	2765.4323	9.50	2765.4323
CNFP 10794	202.8304	2728.3150	8.03	2746.8737
CHP 01-238	138.1238	2663.6084	5.46	2719.1186
BRS Esteio	135.4383	2660.9229	5.36	2704.5697
C 4-7-8-1-2	108.7535	2634.2382	4.30	2690.5034
LP 09-40	105.3641	2630.8487	4.17	2680.5609
IPR Campos Gerais	100.4333	2625.9179	3.97	2672.7548
FT 08-75	99.3065	2624.7912	3.93	2666.7593
CNFC 10762	78.5361	2604.0208	3.10	2659.7884
LEC 01-11	14.2165	2539.7011	0.56	2647.7797
LP 09-192	10.7843	2536.2689	0.42	2637.6423
Pérola	-19.1348	2506.3498	-0.75	2626.7013
FT 08-47	-48.9714	2476.5133	-1.93	2615.1483
LEP 02-11	-107.0739	2418.4107	-4.23	2601.0957
C 4-7-7-2-2	-189.5249	2335.9597	-7.50	2583.4199
IPR Uirapuru	-196.2373	2329.2473	-7.77	2567.5341
TB 02-23	-305.1431	2220.3415	-12.08	2547.1110
TB 03-13	-367.6491	2157.8356	-14.55	2525.4846

μ= 2525.48 Kg ha^{-1}; **g**= gain Kg ha^{-1}; **g%**= gain in percent.

Grain yield stability and adaptability

The results of the HMGV analysis for 18 common bean genotypes are presented in Table 5. The most stable genotypes, in comparison to control Pérola, across the environments in descending order were: BRS Esteio, IPR Campos Gerais, CHC 98-42, IPR Uirapuru, CHP 01-238, 08-75 FT, LP 09-40, CNFC 10762, CNFP 10794, C 4-7-8-1-2 and LEC 01-11. This method showed the grain yield values penalized by instability, which facilitates the selection of the most productive genotypes, as well as the most stable ones.

The appropriate method to study adaptability is the relative performance of genotypic values (RPGV) which capitalizes on the responsiveness of each genotype to environmental improvement. In this work, the genotype that stand out as more adaptable are described in descending order: CHC 98-42, CNFP 10794, BRS Esteio, CHP 01-238, IPR Campos Gerais, FT 08-75, C 4-7-8-1-2, LP 09-40, CNFC 10762 and LEC

01-11. Among them, the index of relative performance of genotypic value of the CHC 98-42 genotype had a magnitude of 1.13 times higher than the overall mean, showing the superiority of these genotypes across the environments.

The HMRPGV study of adaptability and stability revealed that CHC 98-42, BRS Esteio, CNFP 10794, CHP 01-238, FT 08-75, IPR Campos Gerais, LP 09-40, CNFC 10762, C 4-7- 8-1-2 and LEC 01-11 genotypes are the most promising ones due to their high grain yield, extremely predictability and broad adaptability. The performance of those genotypes may increase in response to favorable environments, being able to maintain it in adverse environmental conditions. The mean of CHC 98-42 line is 1.11 times higher than the overall mean of the 13 environments, indicating its superiority for grain yield in terms of adaptability and stability. This result was similar to the ones presented by Franzon et al. (2016), where the most stable and adaptable genotype selected by HMRPGV was 1.14 times higher compared to the overall mean of the all environments in study. Carbonell et al. (2007) found similar results for HMRPGV, since the superior genotype was 1.10 times higher the overall mean.

Table 5. Stability of the genotypic values (HMGV), adaptability of the genotypic values (RPGV), mean genotypic values capitalized by the interaction (RPGV*µ), stability and adaptability of the genotypic values (HMRPGV) and mean genotypic values in the environments (HMRPGV*µ) for grain yield of 18 common bean genotypes in 13 environments in Paraná, Santa Catarina and Rio Grande do Sul in the harvest seasons of 2012/13 and 2013/14.

Genotypes[1]	HMGV	RPGV	RPGV*µ	HMRPGV	HMRPGV*µ
CHC 98-42	2344.78	1.13	2852.62	1.12	2825.59
BRS Esteio	3069.90	1.07	2700.94	1.06	2688.18
CNFP 10794	2115.29	1.08	2723.00	1.06	2674.78
CHP 01-238	2188.16	1.06	2686.01	1.06	2672.24
FT 08-75	2183.22	1.05	2655.69	1.05	2647.57
IPR Campos Gerais	3021.80	1.05	2664.67	1.04	2642.00
LP 09-40	2136.64	1.04	2631.30	1.03	2606.15
CNFC 10762	2118.80	1.03	2608.25	1.02	2589.34
C 4-7-8-1-2	2113.22	1.05	2650.23	1.02	2588.55
LEC 01-11	2098.05	1.00	2542.69	1.00	2530.48
Pérola	2068.97	0.99	2515.32	0.99	2495.76
LP 09-181	2015.09	0.99	2505.87	0.98	2489.39
FT 08-47	2026.59	0.98	2470.10	0.97	2459.47
LEP 02-11	1976.45	0.95	2400.56	0.95	2396.65
IPR Uirapuru	2222.72	0.92	2326.74	0.91	2302.93
C 4-7-7-2-2	1664.36	0.88	2236.43	0.87	2211.57
TB 02-23	1762.96	0.86	2184.55	0.83	2110.78
TB 03-13	1703.08	0.83	2092.42	0.82	2060.63

[1] classification of genotypes by HMRPGV*µ values.

CONCLUSIONS

The genotypes CHC 98-42, BRS Esteio, CNFP 10794 and CHP 01-238 exceeded the overall mean by 12, 6, 6 and 6%, respectively, in all 13 environments, highlighting the promising common bean genotypes that could be recommended for cultivation in the South region of Brazil. Our results demonstrate that it was possible to obtain genetic gains of up to 9.5% for the CHC 98-42 line, showing its high genetic potential.

The HMRPGV statistically ranked the superior genotypes with broad adaptability, high stability, and grain yield performance. Additionally, this method had the advantage to provide results in the same range of magnitudes as the original data for each evaluated trial. Thus, which can be interpreted directly as a genotypic value related to yield production and stability and adaptability indexes simultaneously, even when it faces problems as the heterogeneity of variances among environments, constantly present in Value for Cultivation and Use trials.

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REFERENCES

Annicchiarico, P. (1992) Cultivar adaptation and recommendation from alfalfa trials in Northern Italy. *Journal of Plant Breeding*, 46, 269-278.

Bertoldo, J. G., Coimbra. J. L. M., Guidolin, A. F., Nodari, R. O., Elias, H. T., Barili, L. D. Vale, N, M., & Rozzetto, D. S. (2009) Rendimento de grãos em feijão preto: o componente que mais interfere no valor fenotípico é o ambiente. *Ciência Rural*, 39, 1974-1982. http://dx.doi.org/10.1590/S0103-84782009005000166

Borges, V., Soares, A. A., Reis, M. S., Resende, M. D. V., Cornélio, V. M. O., Leite, N. A., & Vieira, A. R. (2010) Desempenho genotípico de linhagens de arroz de terras altas utilizando metodologia de modelos mistos. *Bragantia*, 69, 833-842. http://dx.doi.org/10.1590/S0006-87052010000400008

Broughton, W. J., Hernandez, G., Blair, M. W., Beebe, S. E., Gepts, P., & Vanderleyden, J. (2003) Bean (*Phaseolus* sp.*)* model food legumes. *Plant and Soil*, 252, 55-128. http://dx.doi.org/10.1023/A:1024146710611

Burgueño, J., Crossa, J., Cornelius, P.L., & Yang, R.-C. (2008) Using factor analytic models for joining environments and genotypes without crossover genotype × environment interaction. *Crop Science*, 48, 1291-1305. http://dx.doi.org/%2010.2135/cropsci2007.11.0632

Carbonell, S. A. M., Chiorato, A. F., Resende, M. D. V., Dias, L. A. S., Beraldo, A. L. A., & Perina, E. F. (2007) Estabilidade de cultivares e linhagens de feijoeiro em diferentes ambientes no Estado de São Paulo. *Bragantia*, 66, 193-201. http://dx.doi.org/10.1590/S0006-87052007000200003

Chiorato, A. F., Carbonell, S. A. M., Dias, L. A. S., & Resende, M. D. V. (2008) Prediction of genotypic values and estimation of parameters in common bean. *Brazilian Archives of Biology and Technology*, 51(3), 465-472. http://dx.doi.org/10.1590/S1516-89132008000300005

Coêlho, M., Gonçalves-Vidigal, M. C., Vidigal Filho, P. S., Franzon, R. C., & Martins, V. S. R. (2020). Genetic diversity of Colletotrichum lindemuthianum races based on ITS-rDNA regions. *Agronomy Science and Biotechnology*, *6*, 1–18. https://doi.org/10.33158/asb.r112.v6.2020

Coimbra, J. L. M., Barili, L. D., Vale, N. M., Guidolin, A. F., Bertoldo, J. G., Rocha, F., & Toaldo, D. (2008). Seleção para caracteres adaptativos em acessos de feijão usando REML/BLUP. *Magistra*, 20, 177-185.

Coimbra, J. L. M., Guidolin, A. F., Carvalho, F. I. F., Coimbra, S. M. M., & Hemp, S. (1999) Reflexos da interação genótipo × ambiente e suas implicações nos ganhos de seleção em genótipos de feijão (*Phaseolus vulgaris* L.). *Ciência Rural*, 29, 433-439. http://dx.doi.org/10.1590/S0103-84781999000300009

Colombari-Filho, J. M., Resende, M. D. V., Morais, O. P., Castro, A. P., Guimarães, E. P., Pereira, J. A., Utumi, M. M., & Breseghello, F. (2013) Upland rice breeding in Brazil: a simultaneous genotypic evaluation of stability, adaptability and grain yield. *Euphytica*, 192, 117-129. http://dx.doi.org/10.1007/s10681-013-0922-2

Corte, A. D., Moda-Cirino, V., & Destro, D. (2002) Adaptability and phenotypic stability in early common bean cultivars and lines. *Crop Breeding and applied Biotechnology*, 2(4), 525-534. http://dx.doi.org/%2010.12702/1984-7033.v02n04a05

Crossa, J. (2012) From genotype × environment interaction to gene × environment interaction. *Current Genomics*, 13, 225-244. http://dx.doi.org/%2010.2174/138920212800543066

Cruz, C. D., Torres, R. A. A., & Vencovsky, R. (1989) An alternative approach to the stability analysis proposed by Silva and Barreto. *Genetics and Molecular Biology*, 12, 567-580.

Eberhart, S. A., & Russell, W. A. (1966) Stability parameters for comparing varieties. *Crop Science*, 6, 36-40. http://dx.doi.org/10.2135/cropsci1966.0011183X000600010011x

FAO - Food and Agriculture Organization (2018) http://www.fao.org

Farias, F. J. C., Carvalho, L. P., Silva Filho, J. L., & Teodoro, P. E. (2016) Usefulness of the HMRPGV method for simultaneous selection of upland cotton genotypes with greater fiber length and high yield stability. *Genetics and Molecular Research,* 15, 1-7. DOI http://dx.doi.org/10.4238/gmr.15038439

Ferreira, L. L. F., Carvalho, I. R., Conte, G. G., Amaral, G. C. L., Campos, J. N., Tomazele, A. A. S., … Loro, M. V. (2021). Effect of biostimulant on yield characters of common bean cultivars under Southwestern Goiás conditions. *Agronomy Science and Biotechnology*, *8*, 1–13. https://doi.org/10.33158/asb.r148.v8.2022

Finlay, K. W., & Wilkinson, G. N. (1963) The analysis of adaptation in a plant-breeding programme. *Australian Journal of Agricultural Research*, 14, 742-754.

Franzon, R. C., Gonçalves-Vidigal, M. C., Caixeta, M. P., Vidigal Filho, P.S., Gilio, T. A. S., & Castro, S. A. L. (2016) Genotype x environment interaction analysis by mixed models in Brazilian common bean inbred lines. *Annual report of the Bean Improvement Cooperative*, 59, 51-52.

Friesen, L. F., Brûlé-Babel, A. L., Crow, G. H., & Rothenburger, P. A. (2016) Mixed model and stability analysis of spring wheat genotype yield evaluation data from Manitoba, Canada. *Canadian Journal of Plant Science*, 96, 305-320. http://dx.doi.org/10.1139/cjps-2015-0252

Huehn, M. (1990) Nonparametric measures of phenotypic stability. Part 1. *Euphytica*, 47, 189-194. http://dx.doi.org/10.1007/BF00024241

Laidig, F., Drobek, T., & Meyer, U. (2008) Genotypic and environmental variability of yield for cultivars from 30 different crops in German official variety trials. *Plant Breeding*, 127, 541–547. http://dx.doi.org/10.1111/j.1439-0523.2008.01564.x

Levene, H. (1960) Robust tests for equality of variances. In: Olkin, I., Ghurye, S. G., Hoeffding, W., Madow, W. G., & Mann H. B. (Eds.) *Contributions to Probability and Statistics: Essays in Honor of Harold Hotelling*, Menlo Park, CA: Stanford University Press, p.278–292.

Lin, C. S., & Binns, M. R. (1988) A method of analysing cultivars x location x year experiments: a new stability parameter. *Theoretical and Applied Genetics,* 76(3), 425-430. http://dx.doi.org/10.1007/BF00265344.

Maia, M. C. C., Resende, M. D. V., Paiva, J. R., Cavalcanti, J. J. V., & Barros, L. M. (2009) Seleção simultânea para produção, adaptabilidade e estabilidade genotípicas em clones de cajueiro, via modelos mistos. *Pesquisa Agropecuária Tropical*, 39, 43-50.

MAPA - Ministério da Agricultura, Pecuária e do Abastecimento (2013) *Registro Nacional de Cultivares* (RNC). Brasília, DF: MAPA https://www.gov.br/agricultura/pt-br/assuntos/insumos-agropecuarios/insumos-agricolas/sementes-e-mudas/registro-nacional-de-cultivares-2013-rnc-1

Moiana, L. D., Vidigal Filho, P. S., Gonçalves-Vidigal, M. C., Maleia, M. P., & Mindo, N. (2014) Application of mixed models for the assessment genotype and environment interactions in cotton (*Gossypium hirsutum*) cultivars in Mozambique. *African Journal of Biotechnology*, 13(19), 1985-1991. http://dx.doi.org/10.5897/AJB2013.12926

Oliveira, R. A., Resende, M. D. V., Daros, E. J., Bespalhok, F. J. C., Zambon, J. L. C., Ido, O. T., Weber, H., & Koehle, H. S. (2005) Genotypic evaluation and selection for sugarcane clones in three environments in state of Parana. *Crop Breeding and Applied Biotechnology*, 5, 426-434. http://dx.doi.org/%2010.12702/1984-7033.v05n04a08

Paulino, P. P. S., Gonçalves-Vidigal, M. C., Bisneta, M. V., Vidigal Filho, P. S., Nunes, M. P. B. A., Xavier, L. F. S., … Lacanallo, G. F. (2021). Occurrence of anthracnose pathogen races and resistance genes in common bean across 30 years in Brazil. *Agronomy Science and Biotechnology*, *8*, 1–21. https://doi.org/10.33158/asb.r140.v8.2022

Pereira, H. S., Bueno, L. G., Del Peloso, M. J., Abreu, A. F. B., Moreira, J. A. A., Martins, M., Wendland, A., Faria, L. C., Souza, T. L. P. O., & Melo, L. C. (2014) Agronomic performance and stability of Andean common bean lines with white grains in Brazil. *Bragantia*, 73 (2), 130-137. http://dx.doi.org/10.1590/brag.2014.020

Petry, N., Boy, E., Wirth, J. P., & Hurrell, R. F. (2015). Rewiew: The potential of the common bean (*Phaseolus vulgaris*) as a vehicle for iron biofotification. *Nutrients*, 7(2), 1144-1173. http://dx.doi.org/10.3390/nu7021144

Piepho, H. P., Möhring, J., Melchinger, A. E., & Büchse, A. (2008) BLUP for phenotypic selection in plant breeding and variety testing. *Euphytica*, 161, 209-228. http://dx.doi.org/10.1007/s10681-007-9449-8

Plaisted, R. L., & Peterson, L. C. (1959) A technique for evaluating the ability of selection to yield consistently in different locations or seasons. *American Potato Journal*, 36, 385-395. http://dx.doi.org/%2010.1007/BF02852735

Resende, M. D. V. (2007) *SELEGEN-REML/BLUP: Sistema estatístico e seleção genética computadorizada via modelos lineares mistos*. Colombo, PR: Embrapa Florestas.

Resende, M. D. V., & Duarte, J. B. (2007) Precisão e controle de qualidade em experimentos de avaliação de cultivares. *Pesquisa Agropecuária Tropical*, 37(3), 182-194.

Resende, M. D. V., Furlani Júnior, E., Moraes, M. L. T., & Fazuoli, L. C. (2001) Estimação de parâmetros genéticos e predição de valores genotípicos no melhoramento do cafeeiro pelo procedimento REML/BLUP. *Bragantia*, 60(3), 185-193. http://dx.doi.org/10.1590/S0006-87052001000300005

Robinson, G. K. (1991) That BLUP is a good thing: the estimation of random effects. *Statistical Science*, 6(1), 15-32. http://dx.doi.org/10.1214/ss/1177011926

Rodovalho, M. A., Coan, M. M. D., Scapim, C. A., Barth Pinto, R. J., & Contreras-Soto, R. I. (2015) Comparison of HMRPGV, Lin and Binn's, and Annichiarico's methods for maize hybrid selection for high and stable yield. *Maydica*, 60(1), M 10.

SAS - Statistical Analysis System (2009) *Software SAS 9.1.* Cary, NC: SAS Institute Inc.

Shapiro, S. S., & Wilk, M. B. (1965) An Analysis of Variance Test for Normality (Complete Samples). *Biometrika*, 52(3/4), 591-611. http://dx.doi.org/%2010.1093/biomet/52.3-4.591

Verma, M. M., Chahal, G. S., & Murty, B. R. (1978) Limitations of conventional regression analysis: a proposed modification. *Theoretical and Applied Genetics*, 53, 89-91. http://dx.doi.org/10.1007/BF00817837

Wang, W. (2016) Identifiability of covariance parameters in linear mixed effects models. *Linear Algebra and its Applications*, 506, 603-613. http://dx.doi.org/10.1016/j.laa.2016.06.022

Wricke, G. (1965) Zur berechnung der okovalenz bei sommerweizen und hafer. Zeitschrift fur Pflanzenzuchtung, 52, 127-138.

Zobel, R. W., Wright, M. J., & Gauch, H. G. (1988). Statistical analysis of a yield trial. *Agronomy Journal*, 80, 388-393. http://dx.doi.org/10.2134/agronj1988.00021962008000030002x