

## Bayesian Perspective in the Selection of Bean Genotypes

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### Abstract

Changes in the relative performance of genotypes have made it necessary for more in-depth investigations to be carried out through reliable analyses of adaptability and stability. The present study was conducted to compare the efficiency of different informative priors in the Bayesian method of Eberhart & Russel with frequentist methods. Fifteen black-bean genotypes from the municipalities of Belém do São Francisco and Petrolina (PE, Brazil) were evaluated in 2011 and 2012 in a randomized-block design with three replicates. Eberhart & Russel's methodology was applied using the GENES software and the Bayesian procedure using the R software through the MCMCregress function of the MCMCpack package. The quality of Bayesian analysis differed according to the *a priori* information entered in the model. The Bayesian approach using frequentist analysis had greater accuracy in the estimate of adaptability and stability, where model 1 which uses the *a priori* information, was the most suitable to obtain reliable estimates according to the BayesFactor function. The inference, using information from previous studies, showed to be imprecise and equivalent to the linear-model methodology. In addition, it was realized that the input of *a priori* information is important because it increases the quality of the adjustment of the model.

**Keywords:** Bayes factor, genotypes × environments interaction, *Phaseolus vulgaris* L.

### 1. Introduction

The common bean (*Phaseolus vulgaris* L.), a staple food in Brazil, is one of the most important sources of protein in human nutrition, especially for the low-income population (Rocha, Moda-Cirino, Destro, Fonseca Junior, & Prete, 2010). In recent years, Brazil has stood out in the international agricultural scenario as one of the largest producers and consumers of this Fabaceae member.

One of the main problems found in the attempt to augment production of this crop is the influence of soil-climatic conditions. In this scenario, producing cultivars adaptable to environmental variations is an important strategy.

The genotype  $\times$  environment interaction is one of the major challenges in the selection and recommendation of superior genotypes, as it changes their relative performance due to environmental variations. Thus, the study of this interaction allows to identify the ideal genotypes for planting in each environment, as a result, maximizes the productive potential of grains and reducing production costs.

The literature describes different methodologies to evaluate the adaptability and stability of genotypes, e.g. methods based on Bayesian inference (Nascimento et al., 2011), mixed models (REML/BLUP) (Resende, 2016), simple linear regression (Eberhart & Russell, 1966), segmented linear regression (Verma, Chahal, & Murty, 1978), and non-parametric methods (Lin & Binns, 1988).

Of all methodologies available, only those based on Bayesian inference allow the use of *a priori* information about the parameters of interest in the process of their estimation. In this method, the parameter is considered a random variable and all uncertainty about it can be represented by a probability distribution. Therefore, under the Bayesian approach, all information is useful and should be taken into account, unlike the classical statistical analysis that uses only information of real data, discarding subjective information (Gamerman & Migon, 1993).

Many researchers have shown that the use of Bayesian inference in adaptability is a robust and efficient statistical procedure that allows for greater accuracy in the selection and recommendation of genotypes (Couto, Nascimento, Amaral Junior, Viana, & Vivas, 2015; Nascimento et al., 2011; Teodoro, Nascimento, Torres, Barroso, & Sagrilo, 2015), allowing to identify genotype that presents high productivity, good adaptability and low sensitivity to adverse conditions. However, Resende, Silva, and Azevedo (2014) asserted that, depending on the *a priori* information entered in the model, Bayesian inference can be equal to or even present inferior results when compared with those originating from the 'classical' (frequentist) approach.

The present study was thus conducted to evaluate the influence of *a priori* distribution on the estimate of adaptability and phenotypic stability parameters obtained under the Bayesian approach of Eberhart & Russell's method. For this purpose, we considered informative priors, whose information originated from different sources, and little informative priors.

## 2. Method

### 2.1 Genetic Material and Experiment Conduction

The data used in this study originated from experiments undertaken in the 2011 and 2012 crop years at the Experimental Stations of the Agronomic Institute of Pernambuco, in the municipalities of Belém do São Francisco and Petrolina (Table 1). This study involved 12 lines developed by EMBRAPA (Brazilian Agricultural Research Corporation) and three black-bean cultivars (BRS Esplendor, IPR Uirapuru, and BRS Campeiro).

Table 1. Soil and climatic conditions of the environments evaluated with black bean genotypes

Environment	Region	Topography	Mean temperature (°C)	Pluviometric index (mm)	Type os soil
1	Petrolina	Soft-wavy	26.3°	435.8	Planossolos
2	Belém de são Francisco	Plane	28.5°	272.4	Alluvial

Trials were implemented in a randomized-block design with three replicates. Each experimental unit consisted of four 4-m rows with 50  $\times$  20 cm spacing. Seeds were sown manually at the rate of three seeds per furrow. In the harvest period, the two center rows were harvested to determine grain yield per hectare.

Fertilization was performed based on the result of the soil analysis of each experimental area. The crop was irrigated by conventional spraying, and the control of weeds and pests was performed according to the need of the crop in each region.

### 2.2 Statistical Analyses

Grain-yield data were subjected to analysis of variance, and after the homogeneity of residual variances was checked, a combined analysis of variance was performed using Hartley (1950)'s maximum F test in the GENES software (Cruz, 2006), adopting the following model:  $Y_{ijk} = \mu + R/E_{k(j)} + G_i + E_j + GE_{ij} + \varepsilon_{ijk}$ , where,  $Y_{ijk}$  is the mean phenotypic value of the plot,  $\mu$  is the overall constant;  $R/E_{k(j)}$  is the effect of replicate  $k$  in environment  $j$ ;  $G_i$  is the fixed effect of genotype  $i$ ;  $E_j$  is the effect of environment  $j$  NID  $(0, \sigma_E^2)$ ;  $GE_{ij}$  is the effect of the interaction between genotype  $i$  and environment  $j$  NID  $(0, \sigma_{GE}^2)$ ; and  $\varepsilon_{ijk}$  is the experimental error NID  $(0, \sigma^2)$ .

When a G×E interaction was detected, the grain-yield data were subjected to analyses of adaptability and stability by the methodology of Eberhart and Russell (1966) and by Bayesian approach (Couto et al., 2015; Nascimento et al., 2011).

By Bayesian approach, considering the statistical model  $Y_{ij} = \beta_{0i} + \beta_{1i}I_j + \delta_{ij} + \bar{\epsilon}_{ij}$ , and assuming that each observation  $Y_{ij}$  has a  $Y_{ij} \sim N(\beta_{0i} + \beta_{1i}I_j; \sigma_i^2)$  distribution, the probability function for each genotype  $i$  is given through (Nascimento et al., 2011):

$$L_i(\beta_{0i}, \beta_{1i}, \sigma_i^2, Y_{ij}) = \prod_{j=1}^a \frac{1}{\sqrt{2\pi\sigma_i^2}} \exp\left\{-\frac{1}{2\sigma_i^2} [Y_{ij} - (\beta_{0i} + \beta_{1i}I_j)]^2\right\}$$

$$= \frac{1}{(\sqrt{2\pi\sigma_i^2})^a} \exp\left\{-\frac{1}{2\sigma_i^2} \sum_{j=1}^a [Y_{ij} - (\beta_{0i} + \beta_{1i}I_j)]^2\right\} \tag{1}$$

To estimate the parameters of adaptability and stability, it is necessary to attribute *a priori* distributions for the parameters. The following distributions were considered for  $\beta_{0i}$ ,  $\beta_{1i}$ , and  $\sigma_i^2$ :  $\beta_{0i} \sim N(\mu_{0i}, \sigma_{0i}^2)$ ,  $\beta_{1i} \sim N(\mu_{1i}, \sigma_{1i}^2)$ , and  $\sigma_i^2 \sim \text{GamaInv}(\alpha_i, \beta_i)$ , the latter being an inverse gamma with mean and variance equal to  $\beta_i/\alpha_i$  and  $\beta_i^2/(\alpha_i - 1)^2(\alpha_i - 2)$ , respectively.

Assuming independence between the parameters of these distributions, the combined *a priori* approach for each genotype is given by:

$$P_i(\beta_{0i}, \beta_{1i}, \sigma_i^2) = \frac{1}{\sqrt{2\pi\sigma_{0i}^2}} \exp\left\{-\frac{1}{2\sigma_{0i}^2} (\beta_{0i} - \mu_{0i})^2\right\} \times \frac{1}{\sqrt{2\pi\sigma_{1i}^2}} \tag{2}$$

$$\exp\left\{-\frac{1}{2\sigma_{1i}^2} (\beta_{1i} - \mu_{1i})^2\right\} \times \frac{1}{(\beta_i^{\alpha_i} \Gamma(\alpha_i))} \left(\frac{1}{\sigma_i^2}\right)^{\alpha_i+1} \exp\left\{-\frac{1}{\beta_i \sigma_i^2}\right\} \tag{3}$$

$$\propto \exp\left\{-\frac{1}{2\sigma_i^2} (\beta_{0i} - \mu_{0i})^2\right\} \times \frac{1}{\sqrt{2\pi\sigma_{1i}^2}} \exp\left\{-\frac{1}{2\sigma_{1i}^2} (\beta_{1i} - \mu_{1i})^2\right\} \tag{4}$$

$$\times \left(\frac{1}{\sigma_i^2}\right)^{\alpha_i+1} \exp\left\{-\frac{1}{\beta_i \sigma_i^2}\right\} \tag{5}$$

To draw inferences about the parameters of interest, one must obtain their marginal *a posteriori* distributions. Denoting the vector of parameters for each genotype  $i$  by  $\theta_{pi} = (\beta_{1i}, \beta_{2i}, \sigma_i^2)$ , where  $p = 1, 2, 3$ , the marginal *a posteriori* distribution for parameter  $\theta_{pi}$  was obtained by the following integer model:  $P(\theta_{pi}|x) = \int P(\theta_{pi}|x) d\theta_{pi}$ , which corresponds to the integer pertaining to all parameters of the vector, except the  $p$ -th component.

In the first analysis under Bayesian approach—Model 1 (M1)—the following estimates of the adaptability and stability parameters obtained in previous literature studies were considered *a priori* information: Bertoldo et al. (2009), Rocha et al. (2010), Oliveira et al. (2011), and Barili et al. (2015) (Table 1). In the second analysis, herein termed Model 2 (M2), informative *a priori* distributions were also considered, but the information originated from the frequentist analysis by the methodology proposed by Eberhart & Russell (1966).

For the adjustment of both models (M1 and M2), the information was entered through the values assumed for the parameters of the *a priori* distributions, termed ‘hyperparameters’. These values were obtained from the average and from the variance of the sample composed of the estimates of the parameters obtained in the frequentist analysis, which resulted in the following distributions:

$$\beta_{0i} \sim N[\mu_{0i} = \bar{\beta}_{0i}, \sigma_{0i}^2 = \text{Var}(\bar{\beta}_{0i})], \tag{6}$$

$$\beta_{1i} \sim N[\mu_{1i} = \bar{\beta}_{1i}, \sigma_{1i}^2 = \text{Var}(\bar{\beta}_{1i})], \text{ and} \tag{7}$$

$$\sigma_i^2 \sim \text{GamaInv}(\alpha_i, \beta_i) \tag{8}$$

where,  $\bar{\beta}_{0i}$  = estimates of  $\beta_{0i}$ ;  $\bar{\beta}_{1i}$  = estimates of  $\beta_{1i}$ ;  $\text{Var}(\bar{\beta}_{0i})$  = variance of  $\beta_{0i}$  values;  $\text{Var}(\bar{\beta}_{1i})$  = variance of  $\beta_{1i}$  values;  $\alpha_i$  and  $\beta_i$  = values obtained from the following ratios:

$$E(\bar{\sigma}_i^2) = \frac{\beta_i}{\alpha_i - 1} \tag{9}$$

$$\text{Var}(\bar{\sigma}_i^2) = \frac{\beta_i^2}{(\alpha_i - 1)^2 + (\alpha_i - 2)}, \text{ namely:} \tag{10}$$

$$\alpha_i = 2 \times \frac{E(\hat{\sigma}_i^2)^2}{V(\hat{\sigma}_i^2)} + 2, \beta_i = 2 \times \frac{E(\hat{\sigma}_i^2)^3}{V(\hat{\sigma}_i^2)} + 1 \quad (11)$$

The third model—M3—is characterized by the use of little informative *a priori* distributions; *i.e.*, distributions that represent great variance. The following distributions were adopted:

$\beta_{0i} \sim N(\mu_{0i} = 0, \sigma_{0i}^2 = 1000000)$ ,  $\beta_{1i} \sim N(\mu_{1i} = 0, \sigma_{1i}^2 = 1000000)$ , and  $\sigma_i^2 \sim \text{GamaInv}(\alpha_i = 0.0001; \beta_i = 5,000)$ .

The comparison between M1, M2, and M3 was based on the Bayes Factor (BF) (Kass & Raftery, 1995). According to Jeffreys (1961), BF can be interpreted as follows:  $BF_{ij} < 1$  shows strong evidence in favor of model *j*;  $1 \leq BF_{ij} < 3$  shows moderate evidence in favor of model *i*;  $3 \leq BF_{ij} < 10$  shows substantial evidence in favor of model *i*;  $10 \leq BF_{ij} < 30$  shows strong evidence in favor of model *i*;  $30 \leq BF_{ij} < 100$  shows very strong evidence in favor of model *i*; and  $BF_{ij} \geq 100$  shows decisive evidence in favor of model *i*.

In the present study, the methodology was implemented in the R software (R Foundation, 2017) and the sample of the combined distribution was obtained by the MCMCregress function of the MCMC pack (Martin et al., 2011), which uses Gibbs sampler to obtain a sample of the marginal distribution of interest. The Bayes Factor, in turn, was calculated by the Bayes Factor function of the MCMCpack package.

With respect to the stability parameter ( $\sigma_{di}^2$ ), the samples of its marginal distribution were obtained indirectly, since this parameter represents a function of  $\sigma_i^2$ . When obtaining values for  $\sigma_i^2$  indirectly in each iteration,  $\hat{\sigma}_{di}^2$  values are obtained by the following expression:  $\hat{\sigma}_{di}^2 = \hat{\sigma}_i^2 - (\text{RMS}/r)$ , where, RMS = residual mean square provided by the analysis of variance; and *n* = number of replicates in the experiment.

The hypotheses of interest were tested by creating credibility intervals for the parameters. The intervals were obtained directly from the *a posteriori* marginal distribution of the parameters.

Because the *Gibbs sampler* is an iterative algorithm, its convergence must be verified. In this study, this step was performed by applying the criteria of Heidelberger and Welch (1983), Geweke (1991), and Raftery and Lewis (1992), implemented into the Bayesian Output Analysis (BOA) package of the R software (R Foundation, 2017).

In the Bayesian analysis of adaptability and stability, 250,000 iterations were considered in the Gibbs sampler algorithm for each parameter of the adopted regression model, with a burn-in period of 10,000 iterations. To obtain a non-correlated sample, we considered a spacing of five iterations between sampled points ('thinning'), which resulted in samples of the marginal *a posteriori* distributions of each parameter, under which the inference of each parameter was drawn.

### 3. Results

The analysis of variance for grain yield showed significance for the sources of variation *genotype* and *environment*, revealing variation between the genotypes, environments evaluated and genotype  $\times$  environment interaction (Table 2). These variations in behavior suggest the need of an in-depth study of the behavior of these lines in the different environments by an analysis of adaptability and stability, making it possible to predict the behavior of each genotype in the different environments with greater detail.

Table 2. Estimates of the mean yield squares of 15 black bean genotypes assessed in four environments

Sources of Variation	DF	Medium Square
Genotypes	14	215859.00**
Environments	3	26641562.59**
Genotypes $\times$ Environments	42	232077.45**
Residue	112	102289.14
MS>/MS<		3.20

Note. \* and \*\* Related to ( $p < 0.01$ ) and ( $p < 0.05$ ), respectively.

The estimates of adaptability and stability parameters considering the Bayesian analysis whose *a priori* information were obtained from previous studies in the literature (Bertoldo et al., 2009; Rocha et al., 2010; Oliveira et al., 2011; Barili et al., 2015) were obtained by the calculation of the *a posteriori* mean, and the credibility intervals were 95% (Table 3).

Table 3. Estimates of *a posteriori* mean ( $\bar{\beta}_{0i}$ ) and of the credible intervals (95%) of the adaptability ( $\bar{\beta}_{1i}$ ) and stability ( $\bar{\sigma}_{di}^2$ ) 365 parameters, considering prior informative M1, from previous studies, prior informative M2 and non-informative priors M3

Genotypes	LI $\bar{\beta}_{0i}$	$\bar{\beta}_{0i}$	LS $\bar{\beta}_{0i}$	LI $\bar{\beta}_{1i}$	$\bar{\beta}_{1i}$	LS $\bar{\beta}_{1i}$	LI $\bar{\sigma}_{di}^2$	$\bar{\sigma}_{di}^2$	LS $\bar{\sigma}_{di}^2$
<i>Informative priors considering M1</i>									
BRS Esplendor	2164.38	2164.47	2164.55	-0.55	0.95	2.53	166417.67	1477092.74	6944075.80
BRS Campeiro	2899.92	2900.00	2900.08	-1.36	0.99	3.55	759022.49	5405284.56	24675006.70
IPR Uirapuru	2737.42	2737.50	2737.58	-1.55	0.91	3.62	920502.26	6407937.29	27623136.60
<i>Informative priors considering M2</i>									
BRS Esplendor	1469.62	1469.79	1469.96	0.74	0.96	1.20	-30768.47	-5079.36	116122.20
BRS Campeiro	1497.54	1497.71	1497.87	0.42	0.92	1.45	-17048.40	111611.05	732746.40
IPR Uirapuru	1196.50	1196.67	1196.83	0.29	0.80	1.34	-16375.79	117213.93	762657.20
CNFP10104	1324.41	1324.59	1324.75	0.71	1.04	1.40	-26638.95	30488.50	302566.90
CNFP10794	1439.21	1439.38	1439.54	0.44	1.30	2.20	19236.09	403660.22	2161793.60
CNFP15171	1667.75	1667.92	1668.08	0.50	1.19	1.92	-837.41	244405.37	1446577.30
CNFP15174	1284.62	1284.79	1284.96	0.76	1.04	1.34	-28838.52	11598.73	203252.90
CNFP15177	1296.71	1296.88	1297.04	0.81	1.14	1.49	-26811.97	29007.03	294755.30
CNFP15178	1412.75	1412.92	1413.08	0.79	1.26	1.76	-19354.65	92278.17	629722.40
CNFP15188	1426.71	1426.88	1427.04	0.73	1.12	1.54	-23690.10	55635.17	435331.90
CNFP15193	1271.08	1271.25	1271.41	0.36	0.87	1.42	-16223.70	118479.45	769415.40
CNFP15194	1412.96	1413.13	1413.29	0.10	0.65	1.24	-13248.34	143149.39	901396.20
CNFP15198	1168.79	1168.96	1169.12	0.54	0.98	1.44	-21385.24	75161.28	538763.50
CNFP15207	1276.71	1276.88	1277.04	0.40	0.65	0.92	-29865.90	2733.10	156869.00
CNFP15208	1215.46	1215.63	1215.79	0.62	0.98	1.36	-25719.79	38347.71	344072.90
<i>{Non-informative priors}</i>									
BRS Esplendor	1222.38	1469.55	1739.78	0.57	0.97	1.36	-29171.54	36328.46	424710.20
BRS Campeiro	948.10	1491.20	2041.77	0.09	0.94	1.77	-11779.31	282631.45	1957688.00
IPR Uirapuru	660.03	1192.23	1757.28	-0.04	0.82	1.67	-10887.67	294901.35	2068675.20
CNFP10104	969.06	1323.19	1702.62	0.48	1.05	1.61	-23903.36	111240.08	905142.30
CNFP10794	468.83	1417.00	2330.49	-0.10	1.34	2.80	34193.02	907456.08	5660614.90
CNFP15171	896.49	1651.20	2388.87	0.07	1.22	2.38	8727.72	565877.15	3596649.80
CNFP15174	981.01	1284.29	1612.11	0.56	1.05	1.52	-26694.69	71472.97	652694.00
CNFP15177	945.03	1295.65	1671.26	0.59	1.15	1.70	-24105.87	108137.35	886282.70
CNFP15178	910.56	1408.08	1924.56	0.49	1.28	2.05	-14696.87	241732.56	1729024.90
CNFP15188	1009.33	1423.86	1864.33	0.47	1.14	1.80	-20207.25	164212.86	1234219.00
CNFP15193	729.98	1266.16	1832.23	0.02	0.89	1.74	-10705.13	297473.83	2079723.10
CNFP15194	809.00	1405.57	2010.12	-0.26	0.67	1.59	-6961.36	349702.04	2374330.60
CNFP15198	712.82	1166.45	1651.94	0.25	0.99	1.71	-17255.08	205783.78	1509536.90
CNFP15207	1003.16	1276.71	1577.36	0.22	0.66	1.10	-28013.13	52820.24	532980.10
CNFP15208	840.26	1214.33	1615.10	0.39	0.99	1.58	-22708.54	127906.24	1014552.80

Considering the results obtained using Model 2 (M2), the genotypes BRS Esplendor, BRS Campeiro, IPR Uirapuru, CNFP15193, CNFP15194, CNFP15198, CNFP15207 and CNFP15208 were considered to have an unfavorable specific adaptability to environments ( $\beta_{1i} < 1$ ) (Table 3). Only 5 (CNFP10794, CNFP15171, CNFP15177, CNFP15178 and CNFP15188) genotypes were classified as of specific adaptability to favorable environments ( $\beta_{1i} > 1$ ) and two lines (CNFP10104 and CNFP15174) were classified as having general adaptability

The estimates of adaptability and stability parameters ( $\beta_{1i}$  and  $\sigma_{di}^2$ ) presented in the analysis using little informative priors (M3) were equivalent to those found in the analysis considering model M2. With respect to the Bayes Factor, a method that compares the two models in terms of quality of fit, the obtained values for both comparisons between models M1 and M3 and between M2 and M3 indicated that the entry of *a priori* information elevates the quality of fit of the model (Table 4).

Table 4. Bayes factor estimates obtained 406 through the comparison between models 407 using informative (i) and non-informative 408 priors (j) for black beans genotypes

Genotypes	FB <sub>ij</sub> (M1 vs M3)
BRS Esplendor	10.18
BRS Campeiro	9.51
IPR Uirapuru	9.20
Genotypes	FB <sub>ij</sub> (M2 vs M3)
BRS Esplendor	16.35
BRS Campeiro	15.42
IPR Uirapuru	15.36
CNFP10104	15.85
CNFP10794	14.82
CNFP15171	15.09
CNFP15174	16.04
CNFP15177	15.86
CNFP15178	15.49
CNFP15188	15.67
CNFP15193	15.37
CNFP15194	15.30
CNFP15198	15.53
CNFP15207	16.17
CNFP15208	15.77

Bayes-factor values ranged from 9.20 to 16.35, indicating substantial ( $3 \leq BF < 10$ ) to strong ( $10 \leq BF < 30$ ) evidence in favor of the model considering *a priori* information. Specifically, considering M2, *i.e.*, *a priori* information originating from the frequentist approach.

#### 4. Discussion

The significant differences between the sources of variation show the existence of differentiated behavior between genotypes, environments and genotypes in the face of environmental changes (Table 2). These results corroborate many studies evaluating bean genotypes in different regions of Brazil (Barili et al., 2015; Torres et al., 2016; Torres Filho et al., 2017).

According to the estimations of the adaptability and stability parameters, the BRS Esplendor, BRS Campeiro and IPR Uirapuru cultivars presented general adaptability and low predictability, considering the Bayesian analysis whose *a priori* information was obtained from previous studies in the literature (Table 3).

Results found for cultivar BRS Esplendor agreed with those found by Rocha et al. (2010) and Barili et al. (2015) for adaptability and with those reported by Oliveira et al. (2011) for stability (Table 5). BRS Campeiro obtained the same results for adaptability found in the studies of Bertoldo et al. (2009) and agreed with Oliveira et al. (2011) for stability. With respect to cultivar IPR Uirapuru, only its adaptability agreed with the classification found by Barili et al. (2015), and only stability corroborated the results found by Oliveira et al. (2011). The determinations made by Bertoldo et al. (2009), in turn, were equal for both adaptability and stability.

Considering the results obtained using Model 2 (M2), except for BRS Esplendor, all genotypes showed stability ( $\sigma_{\alpha_i}^2$ ) values greater than zero, indicating low predictability in the limits of the 95% credibility interval (Table 3). These results disagreed with those of six genotypes for adaptability and of 13 genotypes for stability, in comparison with the frequentist analysis.

The line BRS Esplendor showed that the estimate of stability parameter presented in the analysis using little informative priors (M3) disagreed with those found in the analysis considering model M2. Similar results were also found by Nascimento et al. (2011), Couto et al. (2015) and Oliveira et al. (2018).

With respect to the BF, it showed a lower value for genotype CNFP10794 (14.82) and the highest when considering cultivar BRS Esplendor (16.35) (Table 4). In the comparison considering M1, however, the BF values were lower than those obtained considering M2. This finding indicates that the *a priori* information obtained from previous literature studies did not contribute to the process of estimation when compared with the use of information from the frequentist approach. This result is corroborated by Resende et al. (2014), who stated

that depending on the *a priori* information entered in the model, Bayesian inference can yield equal or even inferior results when compared with those provided by the ‘classical’ approach.

In studies of adaptability and stability, because of the reduced information used in the estimation process, which is given by the number of environments assessed, *a priori* information has a great impact. Additionally, because of the environmental differences in which genotypes are evaluated in the studies used for obtaining previous information, it is extremely important to evaluate the *a priori* information. Thus, the Bayesian approach provides greater precision of the data, allowing greater security in the indication of the genotypes, which can result in increased yields and reduced economic losses by producers.

Table 5. Estimates of the stability and adaptability found through the methodology by Eberhart and Russel (1966) based on the studies by Bertoldo et al. (2009), Rocha et al. (2010), Carvalho et al. (2011), Carvalho et al. (2012) and Barili et al. (2015)

Genotypes	Grain yield											
	Bertoldo et al. (2009)			Rocha et al. (2010)			Oliveira et al. (2011)			Barili et al. (2015)		
	$\sigma^2$	$\beta_0$	$\beta_1$	$\sigma^2$	$\beta_0$	$\beta_1$	$\sigma^2$	$\beta_0$	$\beta_1$	$\sigma^2$	$\beta_0$	$\beta_1$
BRS Esplendor	-	-	-	5248.30	1682.40	1.21	36337**	2357	0.95**	0.00	3380	0.90
BRS Campeiro	0	49.85	0.75	-	-	-	18502**	2726	1.07**	35393.00	3341	1.14**
IPR Uirapuru	28.65*	53.85	1.24	-	-	-	63883**	2340	1.20**	7910.57	3135	1.27

*Note.* Negative  $\sigma^2$  values were considered to be equal to zero; dashes indicate estimates that were not found in the literature consulted.

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