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REVIEW

The Eberhart and Russel's Bayesian method used as an instrument to select maize hybrids

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Abstract Adaptability and stability analysis methods that use a priori information allow identifying and selecting potentially productive genotypes with greater accuracy. The aim of the current study is to use the Eberhart and Russel' Bayesian method as an instrument to analyze the adaptability and stability of hybrid maize cultivars and to assess the efficiency of using the distribution of informative and non-informative priors to select cultivars. Twenty-five (25) hybrid maize cultivars were assessed in 11 environments located in the Brazilian Northeastern region, during 2012 and 2013, according to a complete randomized block design, with two repetitions. The Eberhart and Russel's methodology was performed in the GENES software, whereas the Bayesian procedure was implemented in the free software R, by using the MCMCregress function of the MCMCpack package. The adaptability and stability parameters values and the credibility intervals have shown that the Eberhart and Russel's method via Bayesian technique has shown greater stability-estimation accuracy and greater efficiency in recommending cultivars adapted to favorable and unfavorable environments. The Bayesian methods using priories informative (M1) and few informative (M2) distributions have presented the same genotype classifications in the comparison between a priori distributions; however, according to the Bayes Factor, the M1 was the most adequate distribution to help finding more reliable estimates.

Keywords Bayes factor · Genotype × environment interaction · Informative priori · Zea mays *L.*

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Introduction

The main goal of a hybrid maize breeding program is to identify hybrid combinations showing high productive potential, as well as good adaptability and stability.

However, the genotype × environment interaction is one of the major challenges faced during selection, since it makes it difficult to identify effectively

superior genotypes. The diversity of cultivation environments is often responsible for the significant effect of the interaction between genotypes and environments (G×E) (Engelsing et al. 2012).

Estimating this interaction is extremely important, because it reduces the probability of errors in genotype selection or recommendation (Backes et al. 2005; Mendes et al. 2012). Several frequentist methods estimate genotype adaptability and stability based on different principles; among them, the mixed models (REML/BLUP), as well as the models based on simple linear regression (Eberhart and Russell 1966; Cruz et al. 1989) and on segmented linear regression (Verma et al. 1978), and the non-parametric methods (Lin and Binns 1988) stand out.

Issues concerning the accuracy and precision of predictions and estimates cannot be completely solved through REML/BLUP, since the distribution and variance of the estimators are not known, thus generating approximate confidence intervals for the genetic parameters (Resende et al. 2001). On the other hand, the other frequentist methods predict the performance of the genotypes based on parameter estimates derived from a set of estimators.

Unlike these methods, the Bayesian inference has a single estimator that leads to estimates able to maximize the probability density function a posteriori. It makes it possible generating exact credible intervals for genetic parameter estimates and provides more rigor to the analyses; consequently, the genotype selection shows greater accuracy (Resende 2000).

Thus, on the Bayesian procedure, the parameters are interprets as random variables, where the probability models may shows initial information about these parameters, independent of what the data may show (Molina et al. 2012). Studies have shown the Bayesian methodology superiority to select genotypes in different environments, in comparison to frequentist methods (Silva and Benavides 2001; Cotes et al. 2006; Couto et al. 2015; Teodoro et al. 2015).

The Bayesian analysis have been used in plant breeding for present itself as a robust statistical procedure that shows information richness and the possibility of several applications (Bastiaansen et al. 2012; Almeida et al. 2016; Macedo et al. 2017).

In light of the foregoing, the aim of the current study was to use the Eberhart and Russel' Bayesian method as an instrument to analyze the adaptability and stability of maize hybrids and to assess the efficiency of using informative and non-informative a priori distributions to select cultivars.

Materials and methods

The experiments were carried out in Maranhão (Balsas, Brejo, Colinas and São Raimundo das Mangabeiras counties), Piauí (Nova Santa Rosa, Teresina and Uruçuí counties) and Sergipe states (Nossa Senhora das Dores, Frei Paulo and Umbaúba counties), during the agricultural years 2012 and 2013.

The experimental area in Nossa Senhora das Dores County was divided in two environments, which were characterized according to fertilization differences. The trials using high fertilization range comprised 180.00 kg ha^{-1} N, 149.80 kg ha^{-1} P_2O_5 and 85.60 kg ha^{-1} K_2O, whereas the trials using low fertilization range comprised 45.00 kg ha^{-1} N, 37.80 kg ha^{-1} P_2O_5 and 21.60 kg ha^{-1} K_2O, in the form of 535 and 135 kg ha−1 of 8 − 28 − 16 + Zn at sowing time; both treatments received nitrogen cover in the form of urea 21 days after emergence. Twenty-two (22) environments, in total, were taken into consideration according to the edaphoclimatic differences in the different years, in the same sites.

Twenty-five (25) maize hybrids coming from public and private companies were assessed (Table 1). The experimental design was based on randomized blocks, with two repetitions, and the plots comprised four rows (5.0 m long), 0.70 m interrow spacing and 0.20 m spacing between holes within the rows. The fertilization was performed according to the results of the soil analysis performed in each experimental area. Irrigation was not carried out, whereas the weed and pest control was done according to the crop's need in each region.

The productivity data were subjected to analysis of variance. The joint analysis of variance was performed in the GENES software (Cruz 2006), after the homogeneity of the residual variances was found through the F maximum test by Hartley (1950). The joint analysis of variance has adopted the model $Y_{ijk} = \mu + R/E_{k(j)} + G_i + E_j + GE_{ij} + \varepsilon_{ijk}$, wherein: Y_{ijk} is the mean phenotypic value of the plot; μ is the general constant; $R/E_{k\,(j)}$ is the effect of kth repetition in the jth environment; G_i is the fixed effect of the ith genotype; E_j is the effect of the jth environment NID $(0, \sigma^2_E)$, GE_{ij} is the effect of the ith genotype

Table 1 List of hybrid maize cultivars and their respective origins, types, cycles, colors, grain textures and companies

Cultivar	Transgenic/conventional	Type	Cycle	Grain color	Grain texture	Company
30 A 95 HX	Transgenic	TH	E	OR	SMHARD	MORGAN
30 A 68 HX	Transgenic	SH	EE	OR	SMHARD	MORGAN
BM 820	Conventional	SH	E	R	HARD	BIOMATRIX
DKB 330 YG	Conventional	SH	EE	R/OR	SMDENT	DEKALB
AS 1596 R2	Transgenic	SH	E	R	SMDENT	AGROESTE
P 4285 H	Transgenic	SH	E	Y/OR	HARD	DU PONT
2 B 710 HX	Transgenic	SH	E	Y/OR	SMHARD	DOW
30 A 16 HX	Transgenic	SH	E	OR	SMHARD	MORGAN
DKB 370	Conventional	SHm	E	Y/OR	SMHARD	DEKALB
AG 8041 YG	Transgenic	SH	E	Y/OR	SMHARD	SEMENTES
20 A 55 HX	Transgenic	TH	E	OR	SMHARD	MORGAN
30 F 53 HR	Transgenic	SH	E	OR	SMHARD	DU PONT
30 A 37 HX	Transgenic	SH	EE	Y/OR	SMHARD	MORGAN
30 A 91 HX	Transgenic	SHm	E	Y/OR	SMHARD	MORGAN
2 B 587 HX	Transgenic	SH	E	Y/OR	SMDENT	DOW
2 B 433 HX	Transgenic	TH	EE	Y/OR	SMDENT	DOW
AS 1555 YG	Transgenic	SH	E	OR	SMHARD	AGROESTE
BRS 2022	Conventional	DH	E	OR	SMDENT	EMBRAPA
STATUSVIP	Transgenic	SH	E	OR	HARD	SYNGENTA
BRS 2020	Conventional	DH	E	OR	SMHARD	EMBRAPA
2 B 707 HX	Transgenic	SH	E	OR	SMHARD	DOW
20 A 78 HX	Transgenic	SH	E	OR	SMHARD	DOW
2 B 604 HX	Transgenic	SHm	E	OR	SMHARD	DOW
30 K 73 H	Transgenic	SH	E	Y/OR	SMHARD	DU PONT
2 B 688 HX	Transgenic	TH	E	OR	SMHARD	DOW

Type: *DH* double hybrid, *TH* triple hybrid, *SHm* modified single hybrid; Cycle: *EE* extra early, *E* early; Grain color: *OR* orange, *R* reddish, *Y* yellow; Grain texture: *SMDENT* semi-dent, *SMHARD* semi-hard

interaction in the jth environment NID (0, σ^2_{GE}) and, ε_{ijk} is the experimental error NID (0, σ^2).

The Bayesian analysis considered the values resulting from the frequentist analysis as a priori information, wherein the hypotheses H_0: $\beta_{1i} = 1$ and $H_1 : \beta_{1i} \neq 1$, for adaptability; and H_0: $\sigma^2_{di} = 0$ and H_1: $\sigma^2_{di} >$, for stability, were assessed through t and F statistics, respectively (Teodoro et al. 2015). The use of values resulting from the frequentist analysis as a priori information was necessary since the genotypes evaluated in this work does not present any information about the regression parameters in the literature. This approach, called Empirical Bayes, was used by Kitada et al. (2000) and Wang et al. (2016). However, if this information have been available, as Nascimento et al. (2011) and Couto et al. (2015), we should use information from previous studies.

The method by Eberhart and Russell (1966) is based on simple regression analysis, in which adaptability, or the linear response to the environments, is given by the β_{1i} parameter estimate and by the mean productivity β_{0i}, whereas stability is found through the regression deviation δ_{ij}, according to the statistical model used in experiments involving g genotypes, e environments and r repetitions: $Y_{ij} = \beta_{0i} + \beta_{1i}I_j + \delta_{ij} + \overline{\varepsilon}_{ij}$, wherein Y_{ij} is the response of genotype i in the environment j; β_{0i} is the response of genotype i; β_{1i} is the regression coefficient measuring the ith genotype response to the environment variation; I_j is the

coded environmental index; δ_{ij} is the regression deviation and $\bar{\varepsilon}_{ij}$ is the mean experimental error.

If one considers the statistical model $Y_{ij} = \beta_{0i} + \beta_{1i}I_j + \delta_{ij} + \bar{\varepsilon}_{ij}$ in the Bayesian approach, and assumes that each Y_{ij} observation 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):

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

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

It is necessary assigning the a priori distributions to the parameters in order to estimate their adaptability and stability. The following distributions were taken into consideration for β_{0i}, β_{1i} and σ_i^2: $\beta_{0i} \sim N(\mu_{0i}, \sigma_{0i}^2)$, $\beta_{1i} \sim N(\mu_{1i}, \sigma_{1i}^2)$, $\sigma_i^2 \sim GamaInv(\alpha_i, \beta_i)$; the $\sigma_i^2 \sim GamaInv(\alpha_i, \beta_i)$ distribution comprised an inverse range with mean and variance equal to $\frac{\beta_i}{\alpha_i}$ and $\frac{\beta_i^2}{(\alpha_i-1)^2(\alpha_i-2)}$, respectively (Nascimento et al. 2011).

If one assumes independence between the parameters of these distributions, the a priori joint distribution for each genotype is given through (Nascimento et al. 2011):

$$P_i(\beta_0, \beta_{1i}, \sigma_i^2) = \frac{1}{\sqrt{2\pi\sigma_{0i}^2}} exp\left\{-\frac{1}{2\sigma_{0i}^2}(\beta_{0i}, \mu_{0i})^2\right\} \times \frac{1}{\sqrt{2\pi\sigma_{1i}^2}}$$

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

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

It is necessary finding the marginal a posteriori distributions of the parameters of interest in order to make inferences about them. If one denotes the parameter vector for each genotype i through $\theta_{pi} = (\beta_{1i}, \beta_{2i}, \sigma_i^2)$—wherein p = 1,2,3—then, the marginal a posteriori distribution for the θ_{pi} parameter is found through the following integral: $P(\theta_{pi}|x) = \int P(\theta_{pi}|x)d\theta_{pi}$, which refers to the integral of all vector parameters, except for the pth component.

The methodology adopted in the present study was implemented in the R software (The R Foundation 2010), whereas the joint distribution sample was obtained through the MCMCregress function of the MCMCpack package. The Bayes Factor was calculated using the BayesFactor function of the MCMCpack package. This factor may vary from less than 1 to more than or equal to 100, wherein BFij < 1 shows evidence in favor of model j; 1 ≤ BFij < 3 shows moderate evidence in favor of model i; 3 ≤ BFij < 10 shows substantial evidence in favor of model i; 10 ≤ BFij < 30 shows strong evidence in favor of model i; 30 ≤ BFij < 100 shows very strong evidence in favor of model i; and BFij ≥ 100 shows decisive evidence in favor of model i (Jeffreys 1961).

Informative a priori distributions, whose information derived from the frequentist analysis considering all the assessed genotypes, were used in the first model (M1) to perform the Bayesian analysis. The information was inserted in the analysis through the values assumed for the a priori distribution parameters, named hyperparameters.

These values were found through the mean and variance of the sample composed of the parameter estimates found in the frequentist analysis, which resulted in the following distributions: $\beta_{0i} \sim N\left(\mu_{0i} = \overline{\beta}_{0i}, \sigma_{0i}^2 = Var(\overline{\beta}_{0i})\right)$, $\beta_{1i} \sim N\left(\mu_{1i} = \overline{\beta}_{1i}, \sigma_{1i}^2 = Var(\overline{\beta}_{1i})\right)$ and $\sigma_i^2 \sim GamaInv(\alpha_i, \beta_i)$, wherein: $\overline{\beta}_{0i}$ is the β_{0i} estimates; $\overline{\beta}_{1i}$ is the β_{1i} estimates; $Var(\overline{\beta}_{0i})$ is the variance of β_{0i} values; $Var(\overline{\beta}_{1i})$ is the variance of β_{1i} values; and α_i and β_i are values obtained from the system equation:

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

$$Var(\overline{\sigma}_i^2) = \frac{\beta_i^2}{(\alpha_i-1)^2+(\alpha_i-2)}, \text{ which were:}$$

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

The second model (M2) used slightly informative a priori distributions, which represented probability distributions showing great variance. The following distributions were herein adopted: $\beta_{0i} \sim N(\mu_{0i} = 0, \sigma^2_{0i} = 1{,}000{,}000)$, $\beta_{1i} \sim N(\mu_{1i} = 0, \sigma^2_{1i} = 1{,}000{,}000)$ and $\sigma^2_i \sim GamaInv(\alpha_i = 0.0001; \beta_i = 5.000)$.

The comparison between M1 and M2, i.e., between informative and non-informative a priori distributions, was based on the Bayes Factor (BF) (Kass and Raftery 1995).

The Bayes Factor was calculated through the BayesFactor function of the MCMCpack package. According to Jeffreys (1961), the Bayes Factor may be interpreted as follows: $BF_{ij} < 1$ shows 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.

The marginal distribution samples of the stability parameter (σ^2_{di}) were indirectly obtained, since this parameter represents a σ^2_i function. If one indirectly finds σ^2_{di} values in each interaction, it is possible finding σ^2_{di} values through the following expression: $\widehat{\sigma}^2_{di} = \widehat{\sigma}^2_i - \left(MSR/r\right)$, wherein: MSR is the mean square residue provided by the analysis of variance, and r is the number of repetitions in the experiment.

The hypotheses of interest were tested through the construction of credible intervals for the parameters. The intervals were directly obtained from the marginal a posteriori distribution of parameters.

Since the Gibbs sampler is an iterative algorithm, it is necessary checking its convergence. Such convergence was confirmed in the current study by applying the criteria by Heidelberger and Welch (1983) and Raftery and Lewis (1992), which were implemented in the Bayesian Output Analysis (BOA) package of the R software (The R Foundation 2017).

The Bayesian adaptability and stability analysis applied to each parameter of the herein adopted regression model took into consideration 250.000 iterations in the Gibbs sampler algorithm based on a burn-in period of 10.000 iterations. The spacing between points sampled from five iterations (thinning) was taken into consideration to find an uncorrelated sample, and it resulted in samples of the marginal a posteriori distributions of each parameter; the inference of each parameter was based on such distributions.

Results and discussion

Overall, all chains achieves convergence, since the Raftery and Lewis (1992) dependency factor provided values lower than five, and the p value of the Heidelberger and Welch test Heidelberger and Welch (1983), which to test if the length of the sample is enough to estimate the mean with sufficient accuracy, was always higher than the 5% level of significance.

The significance of the variation sources has shown substantial differences between genotypes and environments (Table 2). The significant result between genotypes and environments (GxE) has indicated different cultivar behaviors in different environments. Significant GxE interaction effects were also reported in several studies about maize genotypes in different Brazilian regions (Engelsing et al. 2012; Carvalho et al. 2013; Storck et al. 2014). This significant interaction is one of the greatest challenges for genotype selection, since it makes it difficult identifying effectively superior genotypes. The occurrence of these variations has led to the need of conducting a detailed study about genotypes' behavior in different environments, based on adaptability and stability analyses.

The adaptability and stability parameters were found by considering values derived from the frequentist analysis as a priori information, along with their respective credible intervals, as shown in Table 3.

Table 2 Estimates of the mean yield squares of 25 hybrid maize genotypes assessed in 22 environments

Sources of variation	df	Mean square
Genotypes (G)	24	16,241,031.01**
Environments (E)	21	114,448,699.64**
Genotypes × environments (GxE)	504	2,454,247.71**
Residue	528	708,660.56
MS >/MS <	–	5.92

**Significant at 0.01 probability levels by F test

Table 3 Stability and adaptability estimates found through the methodology by Eberhart and Russell (1966)

Genotypes	Mean	Eberhard and Russell (1966)		R^2
		β1i	δ^2d	
30 A 68 HX	9402a	1.03	850,431.38**	70
2 B 707 HX	9301a	1.20*	684,693.98**	78
30 A 16 HX	9287a	1.49**	597,704.35**	86
2 B 587 HX	9192a	1.29**	314,451.11**	87
2 B 710 HX	9150a	1.02	103,367.25**	85
2 B 604 HX	9146a	1.19*	495,764.81**	81
30 A 37 HX	9124a	1.13	255,791.43	85
30 A 95 HX	8992a	1.21*	786,791.73**	77
2 B 433 HX	8932b	1.06	− 27,025.11**	90
P 4285 H	8907b	0.70**	484,829.04**	61
20 A 55 HX	8853b	1.13	119,157.46	87
30 F 53 HR	8833b	0.80*	131,892.45**	50
AG 8041YG	8743b	0.82*	444,286.36*	69
30 A 91 HX	8737b	1.18*	131,312.58	88
2 B 688 HX	8736b	1.20*	649,181.43*	79
20 A 78 HX	8730b	1.11	681,658.41	76
DKB 370	8640b	0.88	521,731.59**	70
30 K 73 H	8591b	1.00	394,714.43**	78
DKB 330 YG	8579b	1.00	669,348.74**	72
AS 1596 R2	8401c	0.92	658,136.68**	69
Statusvip	8345c	0.77**	649,673.59**	61
BM 820	8275c	0.80*	611,926.64**	64
AS 1555 YG	8098c	0.95	467,038.09**	74
BRS 2022	7428d	0.65**	500,842.29**	57
BRS 2020	7354d	0.47**	737,313.21**	35

* and **significant at 0.05 and 0.01 probability levels, respectively

Only 2 (30A16HX and 2B587HX) out of the 25 genotypes assessed according to the Bayesian methodology in model M1 (informative priors) were classified as of specific adaptability to favorable environments ($\beta_{1i} > 1$) (Table 4). The hybrids P4285HX, BRS2022, 30A91HX and BRS2020 were classified as of specific adaptability to unfavorable environments ($\beta_{1i} < 1$). The other genotypes were considered of general adaptability and showed adaptability parameters within the 95% credible interval range. All genotypes have presented stability parameter $\left(\sigma^2_{di}\right)$ values higher than 0 and were considered of low predictability within the 95% credible interval range.

The M2 (non-informative priors) analysis has applied the same criteria used to classify the genotypes in M1, i.e., the 95% CI range.

The β_{1i} and σ^2_{di} estimates for all hybrids in M2 were equivalent to the M1 analysis results. These results do not corroborate those reported by Nascimento et al. (2011), Couto et al. (2015) and Teodoro et al. (2015), whose priors' information derived from the application of the meta-analysis technique, i.e., the data used in the analysis came from previous studies. However, Nascimento et al. (2011) have stated that more accurate results can be found in adaptability and stability studies that have more information available for meta-analysis.

The Bayes factor, which is a method that compares model 1 to model 2, has presented the lowest estimate value (18.36) in the analysis of the Statusvip genotype, as well as the highest estimate value (20.59) in the analysis of the 2B433HX genotype (Table 5).

These results have shown that, although the adaptability and stability parameter estimates of the two models presented similar results, M1 has shown the highest fit quality because it met the $10 \leq BF_{ij} < 30$ intervals. Thus, the Bayes factor has shown that higher accuracy can be achieved when informative priors are used to build the Model. In addition, the insertion of a priori information in Model 1 has generated smaller credible interval ranges in comparison to Model 2, fact that reinforced the greater accuracy in the estimation of parameters and, consequently, in a more reliable genotype selection.

The results of the frequentist analysis, which enabled the a priori inferences, has shown great divergence from the Bayesian approach results. Among the genotypes classified as of specific adaptability to favorable environments ($\beta_{1i} < 1$)—30A68HX, 2B707HX, 2B587HX, 2B604HX, 2B710HX, 2B710HX, 2B710HX, 2B433HX, 20A55HX, 20A78HX, 2B688HX, 30K73H and DKB330YG—only 2B587HX complied with the adaptability results found through the Bayesian procedure. It has also disagreed with the stability classification, which was high for this genotype, according to the frequentist analysis.

The 30A16HX cultivar was considered of great adaptability and high predictability, fact that disagree with the Bayesian approach, which classified it as of specific adaptability to favorable environments and of

Table 4 Estimates of the a posteriori mean ($\overline{\beta}_{0i}$) and of the credible intervals (95%) of the adaptability ($\overline{\beta}_{1i}$) and stability ($\overline{\sigma}^2_{di}$) parameters, by taking into consideration informative and non-informative priors for maize hybrids

Genotypes	LI $\overline{\beta}_{0i}$	$\overline{\beta}_{0i}$	LS $\overline{\beta}_{0i}$	LI $\overline{\beta}_{1i}$	$\overline{\beta}_{1i}$	LS $\overline{\beta}_{1i}$	LI $\overline{\sigma}^2_i$	$\overline{\sigma}^2_{di}$	LS $\overline{\sigma}^2_{di}$
Informative priors									
30A68HX	9416.08	9463.89	9511.36	0.73	1.04	1.34	311,899.62	887,359.99	1,935,057.20
30A16HX	9382.74	9430.41	9477.79	1.35	1.61	1.87	117,565.66	526,297.11	1,270,207.50
2B707HX	9238.99	9286.75	9334.20	0.93	1.21	1.49	225,864.34	727,687.02	1,640,833.00
2B587HX	9151.92	9199.34	9246.51	1.13	1.34	1.55	− 51,770.34	211,236.70	692,476.20
30A37HX	9146.36	9193.89	9241.16	0.97	1.20	1.43	10,629.24	327,298.87	904,565.90
2B604HX	9144.73	9192.48	9239.91	0.95	1.23	1.51	201,790.21	682,954.25	1,558,560.70
2B710HX	9133.03	9180.48	9227.66	0.85	1.06	1.27	− 43,194.16	227,209.23	721,929.40
30A95HX	9025.42	9073.28	9120.80	0.93	1.26	1.59	442,877.91	1,130,403.57	2,383,595.30
P4285H	9006.77	9054.46	9101.85	0.42	0.69	0.95	140,969.12	569,779.12	1,350,301.20
30F53HR	8959.88	9007.78	9055.33	0.43	0.78	1.14	609,719.54	1,439,328.15	2,950,703.90
2B433HX	8912.67	8959.75	9006.56	0.86	1.03	1.20	− 167,182.45	− 3612.86	295,831.70
20A55HX	8786.16	8833.55	8880.66	0.94	1.14	1.35	− 71,742.43	173,993.29	623,656.90
20A78HX	8768.06	8815.87	8863.34	0.84	1.14	1.44	310,156.49	884,139.39	1,929,113.10
DKB370	8708.17	8755.89	8803.31	0.61	0.88	1.15	169,379.90	622,651.69	1,447,705.50
2B688HX	8707.50	8755.21	8802.62	0.98	1.25	1.52	161,845.34	608682.56	1,421,914.60
AG8041YG	8696.20	8743.87	8791.23	0.59	0.85	1.11	119,565.53	529,657.49	1,277,164.00
30K73H	8682.75	8730.50	8777.94	0.81	1.09	1.37	201,007.43	681,462.55	1,555,662.60
DKB330YG	8426.20	8474.05	8521.56	0.72	1.05	1.38	427,583.11	1,102,070.29	2,331,325.70
AS1596R2	8314.25	8362.05	8409.51	0.59	0.89	1.19	291,091.25	848,739.54	1,863,742.80
BM820	8220.55	8268.32	8315.76	0.56	0.84	1.13	223,355.24	723,056.76	1,632,220.90
AS1555YG	7942.64	7990.41	8037.86	0.62	0.91	1.20	242,445.36	758,502.57	1,697,529.60
Statusvip	7729.26	7777.25	7824.89	0.49	0.96	1.44	1,564,416.33	3,204,913.43	6,183,297.30
BRS2022	7527.46	7575.03	7622.33	0.43	0.66	0.90	33,436.37	369,834.02	982,831.10
30A91HX	7437.66	7485.55	7533.10	0.12	0.47	0.83	605,087.04	1,430,747.35	2,934,813.60
BRS2020	7418.13	7465.68	7512.97	0.19	0.42	0.66	23,700.53	351,619.57	949,326.40
Non-informative priors									
30A68HX	8913.71	9407.22	9887.84	0.71	1.04	1.37	338,403.17	968,784.33	2,128,015.90
30A16HX	8976.40	9390.35	9795.92	1.33	1.61	1.88	135,996.96	581,887.80	1,401,014.20
2B707HX	8778.78	9238.29	9687.48	0.90	1.21	1.52	248,651.39	797,372.50	1,805,782.60
2B587HX	8843.71	9174.22	9500.04	1.12	1.34	1.57	− 40,243.16	245,598.89	770,422.60
30A37HX	8913.71	9407.22	9887.84	0.71	1.04	1.37	338,403.17	968,784.33	2,128,015.90
2B604HX	8696.873 + J8	9146.50	9586.56	0.93	1.23	1.53	223,436.49	749,391.27	1,716,256.30
2B710HX	8819.62	9154.71	9485.00	0.83	1.06	1.28	− 31,330.75	262,608.07	802,157.10
30A95HX	8468.50	9008.34	9533.29	0.90	1.26	1.62	475,026.41	1,229,569.04	2,615,132.80
P4285H	8590.30	9014.10	9429.46	0.41	0.69	0.97	160,247.10	628,201.21	1487562.40
30F53HR	8336.09	8929.92	9505.58	0.39	0.78	1.18	649,052.18	1,562,314.35	3,241,610.60
2B433HX	8684.77	8944.56	9201.53	0.85	1.03	1.20	− 160,363.61	17,063.95	342,653.70
20A55HX	8491.74	8811.01	9126.02	0.93	1.15	1.36	− 61,117.26	205,882.75	695680.50
20A78HX	8271.50	8763.24	9243.72	0.81	1.14	1.47	336,355.29	964,741.14	2120765.70
DKB370	8278.96	8714.64	9141.67	0.59	0.88	1.17	189,798.37	684,594.79	1593382.90
2B688HX	8281.95	8714.55	9138.65	0.97	1.25	1.54	181,918.21	669,653.25	1565143.20
AG8041YG	8329.97	8743.71	9149.69	0.57	0.85	1.13	136,819.85	583,467.75	1,403,600.10
30K73H	8238.08	8686.90	9126.67	0.79	1.09	1.39	222,851.07	747,507.70	1,711,321.20

Table 4 continued

Genotypes	LI $\overline{\beta}_{0i}$	$\overline{\beta}_{0i}$	LS $\overline{\beta}_{0i}$	LI $\overline{\beta}_{1i}$	$\overline{\beta}_{1i}$	LS $\overline{\beta}_{1i}$	LI $\overline{\sigma}_i^2$	$\overline{\sigma}_{di}^2$	LS $\overline{\sigma}_{di}^2$
DKB330YG	7880.92	8414.58	8935.10	0.70	1.05	1.41	458,960.20	1,198,374.09	2,558,804.10
AS1596R2	7829.70	8313.57	8787.54	0.57	0.89	1.21	316,346.87	926,411.22	2,046,826.90
BM820	7767.90	8225.38	8673.86	0.54	0.85	1.15	246,014.87	791,742.77	1,793,407.30
AS1555YG	7483.03	7947.56	8403.25	0.60	0.91	1.22	265,974.04	829,505.07	1,864,084.20
Statusvip	6804.04	7644.35	8451.20	0.41	0.96	1.52	164,9167.25	3,474,136.65	6,841,080.20
BRS2022	7175.07	7548.57	7917.12	0.41	0.66	0.91	48,362.98	414,210.74	1,085,415.40
30A91HX	6831.42	7421.24	7997.40	0.08	0.48	0.87	643,672.46	1,550,486.30	3,218,416.80
BRS2020	7071.74	7440.27	7804.20	0.18	0.43	0.67	38,193.37	394,773.24	1,048,826.20

Table 5 Bayes factor estimates obtained through the comparison between models using informative (i) and non-informative priors (j) for maize hybrids

Genotypes	FB_{ij}
2B433HX	20.59
2B587HX	20.56
30A16HX	20.55
2B710HX	20.53
30A37HX	20.46
30A68HX	20.40
2B707HX	20.31
20A55HX	20.27
2B604HX	20.24
P4285H	20.18
30A95HX	19.94
AG8041YG	19.94
2B688HX	19.89
DKB370	19.88
30K73H	19.83
20A78HX	19.81
30F53HR	19.78
AS1596R2	19.44
DKB330YG	19.43
BM820	19.42
AS1555YG	19.17
BRS2022	19.07
BRS2020	19.01
30A91HX	18.53
Statusvip	18.36

low predictability. Only two (P4285H and BRS2022) out of the eight genotypes considered of specific adaptability to unfavorable environments ($\beta 1 > 1$) have shown results agreeing with the Bayesian inference ones. The 30A91HX and BRS2020 cultivars were considered of great adaptability, according to the frequentist analysis, and of specific adaptability to unfavorable environments, according to the Bayesian methodology.

The disagreement between results often derives from the frequentist model tendency to classify the genotypes as of specific adaptability to favorable or unfavorable environments, thus compromising the reliable recommendation of these genotypes.

Thus, the Bayesian approach provides more accuracy and allows producing more reliable results to indicate genotypes. Consequently, it allows producers to increase the yield and reduce economic losses.

Conclusions

Using the Bayesian approach in adaptability and stability studies provides greater accuracy to the selection of hybrid maize genotypes.

The 30A16HX and 2B587HX genotypes were classified as of specific adaptability to favorable environments, based on informative priors.

The P4285HX, BRS2022, 30A91HX and BRS2020 genotypes have shown specific adaptability to unfavorable environments.

The results derived from the use of informative a priori distributions have shown greater adjust accuracy than those derived from non-informative a priori distributions, according to the Bayes factor models.

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