Bayesian approach increases accuracy when selecting cowpea genotypes with high adaptability and phenotypic stability

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ABSTRACT. This study aimed to verify that a Bayesian approach could be used for the selection of upright cowpea genotypes with high adaptability and phenotypic stability, and the study also evaluated the efficiency of using informative and minimally informative *a priori* distributions. Six trials were conducted in randomized blocks, and the grain yield of 17 upright cowpea genotypes was assessed. To represent the minimally informative *a priori* distributions, a probability distribution with high variance was used, and a meta-analysis concept was adopted to represent the informative *a priori* distributions. Bayes factors were used to conduct comparisons between the *a priori* distributions. The Bayesian approach was effective for selection

of upright cowpea genotypes with high adaptability and phenotypic stability using the Eberhart and Russell method. Bayes factors indicated that the use of informative *a priori* distributions provided more accurate results than minimally informative *a priori* distributions.

Key words: *Vigna unguiculata* L.; Bayes factor; Informative prior; Genotype x environment interaction

INTRODUCTION

Owing to the growing diversity of the cowpea [*Vigna unguiculata* (L.) Walp.], which is currently cultivated in three regions of Brazil, it is very important to investigate the magnitude of genotype x environment interactions (G x E) when choosing the best selection strategy and cultivar recommendations (Santos et al., 2014a,b). Therefore, some studies have been conducted in order to select cowpea genotypes with upright and prostrate sizes that are superior in adaptability and yield stability (Torres et al., 2015a). Several methodologies are used, including the Eberhart and Russell (1966) (based on linear regression) as well as Yates and Cochran (1938) (traditional) and Wricke (1965), which are both based on ANOVA (Freire Filho et al., 2002; Rocha et al., 2007; Barros et al., 2013; Santos et al., 2015).

Despite the large number of methodologies for the detailed study of G x E, all make use of *a priori* information when estimating the parameters. The inclusion of *a priori* information can be performed using Bayesian inference. This approach uses three basic concepts: i) initial information (*a priori* probability), which is generally assumed to be a joint probability law on the parameters before obtaining the particular sample y_1, ..., y_n from random variables; ii) the probabilistic model of the random response variable y, which is used to obtain the sample likelihood, and iii) Bayes' theorem (Cotes et al., 2006). Thus, in a Bayesian context, the parameters are interpreted as random variables with a probability law (*a priori* distribution) that reflect the original information (or the lack of information) associated with them, regardless of what the data may show (Molina et al., 2011). In addition, the homogeneity of variance and the appropriateness of residues to a normal distribution are assumptions for many methodologies, but these are not required with the Bayesian approach (Cotes et al., 2006).

Despite being a robust statistical procedure with several possible applications, the use of Bayesian inference in genetic breeding is still limited. Mora et al. (2009) used the Bayesian approach to predict the heritability values of forest species, and concluded that this method made it possible to obtain low standard deviation values associated with heritability, which makes it an important tool for genetic breeding. Silva et al. (2013) used the Bayesian approach to select sugarcane families (*Saccharum officinarum* L.), and found that the informative *a priori* not only influenced the genetic effects, but it also influenced variance and heritability. Nascimento et al. (2011) formulated a Bayesian approach using the Eberhart and Russell (1966) method, and concluded that the selection of genotypes in different environments was most accurate when *a priori* information was used.

Thus, in order to generate relevant information regarding the genetic breeding of cowpeas, this study aimed to verify if the Bayesian approach could be employed for the selection of upright cowpea genotypes with high adaptability and phenotypic stability. Moreover, it also aimed to evaluate the efficiency of using informative and minimally informative *a priori* distributions.

MATERIAL AND METHODS

Six trials using cowpea genotypes were conducted during the 2005 and 2006 agricultural years in the municipalities of Chapadão do Sul and Dourados, and the soil and climate features of the region are shown in Table 1. The experimental design included a randomized block design with 17 treatments and four replications. The experimental unit consisted of four 5.0 m rows with 0.5 m between each row, and the plants in each row were spaced 0.25 m apart. For each experimental unit, grain yield (YIE) was evaluated in two central rows, and it was corrected to 13% moisture and extrapolated to kg/ha.

Table 1. Number of trials (NT), agricultural year, site, latitude, longitude, altitude, Köppen's classification, and sowing date of cowpea [*Vigna unguiculata* (L.) Walp.] genotypes that were evaluated in the State of Mato Grosso do Sul.

NT	Year	Site	Latitude	Longitude	Altitude (m)	Köppen's classification	Sowing date
1	2005	Aquidauana	22º01'S	54º05'W	430	Aw	March 21, 2005
2	2005	Chapadão do Sul	18º05'S	52º04'W	790	Aw	March 14, 2005
3	2005	Dourados	20º03'S	55º05'W	147	Cwa	April 7, 2005
4	2006	Aquidauana	22º01'S	54º05'W	430	Aw	March 2, 2006
5	2006	Dourados	20º03'S	55º05'W	147	Cwa	February 27, 2006
6	2006	Primavera	15º33'S	54°17'W	636	Aw	March 15, 2006

Treatments consisted of 14 lines (MNC99-537F-1, MNC99-537F-4, MNC99-541-F5, MNC99-541-F8, IT93K-93-10, MNC99-519D-1-1-5, MNC00-544D-10-1-2-2, MNC00-544D-14-1-2-2, MNC00-553D-8-1-2-2, MNC00-553D-8-1-2-3, MNC00-561G-6, EV X 63-10E, EV X 91-2E-2, and MNC99-557F-2) and three cowpea cultivars (BRS Guariba, Patativa, and Vita-7), which were obtained from Embrapa Meio-Norte cowpea genetic breeding program.

Data were subjected to individual ANOVA, and fixed and other treatment effects were considered random. The results indicated that the relationship between the highest and lowest mean square of the individual ANOVA of the residues did not exceed the 7:1 ratio, which allowed the implementation of joint analysis of trials (Banzatto and Kronka, 2006). The data were subsequently subjected to adaptability and stability analyses using the Eberhart and Russell (1966) method.

The adopted linear regression model of Eberhart and Russell (1966) was:

$$Y_{ij} = \beta_{0i} + \beta_{1i} I_j + \Psi_{ij} \quad \text{(Equation 1)}$$

where Y_{ij} is the observed mean of genotype i in environment j; β_{0i} is the linear coefficient related to i^{th} genotype; β_{1i} is the regression coefficient of genotype i; I_j is the environmental index j; and Ψ_{ij} represents the random errors that are compounded by the regression deviation of genotype i in environment j and by the mean error associated with the mean. The environmental index was estimated using the following equation:

$$I_j = \bar{Y}_j - \bar{Y}_m, \text{ with } \sum_{j=1}^{n} I_j = 0 \quad \text{(Equation 2)}$$

where $\bar{Y}_m$ is the overall mean; $\bar{Y}_j$ is the mean of environment j; and n is the number of environments.

According to the Eberhart and Russell (1966) method, genotype adaptability was measured using the parameter β_{1i}, while the stability of behavior was evaluated using the variance

of the regression deviations (σ^2_{di}) and the coefficient of determination (R^2), which is an auxiliary measure for stability assessment (Cruz and Regazzi, 2007). The R^2 value indicates acceptable predictability when σ^2_{di} is significant and R^2 is higher than 80%. Using this frequentist approach, the hypotheses of interest are: H_0: $\beta_{1i} = 1$ versus H_1: $\beta_{1i} \neq 1$ and H_0: $\sigma^2_{di} = 0$ versus H_1: $\sigma^2_{di} > 0$, which are assessed using *t* and F statistics, respectively.

For the Bayesian analysis, we only considered genotypes that were evaluated in either Carvalho et al. (2006) or Valadares et al. (2010), which were used as references for the specification of *a priori* distributions (Table 2).

Table 2. Estimates and means (β_{0i}) associated with adaptability (β_{1i}) and stability (σ^2_{di}), which were obtained using the Eberhart and Russell method (1966) as described in Freire Filho et al. (2002), Carvalho et al. (2006), and Valadares et al. (2010).

Genotype	Reference	β_{0i} (kg/ha)	β_{1i}	σ^2_{di}
MNC99-537F-1	Valadares et al. (2010)	1,198	0.486	47,972.1
MNC99-537F-4	Valadares et al. (2010)	1,009	0.626	18,000.7
MNC99-541-F5	Valadares et al. (2010)	1,135	1.050	101,781.9
MNC99-541-F8	Valadares et al. (2010)	982	0.523	78,858.2
IT93K-93-10	Valadares et al. (2010)	992	0.826	35,027.7
MNC99-519D-1-1-5	Carvalho et al. (2006)	1,335	1.110	64,962.3
MNC00-544D-10-1-2-2	Carvalho et al. (2006)	1,341	1.280	174,507.1
MNC00-544D-14-1-2-2	Carvalho et al. (2006)	1,269	1.000	25,059.8
MNC00-553D-8-1-2-2	Carvalho et al. (2006)	1,257	1.190	89,750.1
MNC00-553D-8-1-2-3	Carvalho et al. (2006)	1,113	0.860	143,440.1
MNC00-561G-6	Carvalho et al. (2006)	1,307	1.140	47,269.3
EV X 63-10E	Carvalho et al. (2006)	1,456	1.170	48,760.7
EV X 91-2E-2	Carvalho et al. (2006)	1,387	1.220	68,953.7
MNC99-557F-2	Carvalho et al. (2006)	1,117	0.730	81,749.1
BRS Guariba	Carvalho et al. (2006)	1,377	1.190	19,336.7
Patativa	Carvalho et al. (2006)	1,311	0.970	97,943.2
Vita-7	Carvalho et al. (2006)	1,468	1.170	181,246.8

With the Bayesian approach, we considered the following statistical model:

$$Y_{ij} = \beta_{0i} + \beta_{1i}I_j + \Psi_{ij} \quad \text{(Equation 3)}$$

where each Y_{ij} observation was assumed to have the following distribution:

$$Y_{ij} \sim N(\beta_{0i} + \beta_{1i}I_j;\ \sigma^2_{di}) \quad \text{(Equation 4)}$$

where the likelihood function for each genotype i is given by:

$$L_i(\beta_{0i}, \beta_{1i}, \sigma^2_i, y_{ij}) = \prod_{j=1}^{n} \frac{1}{\sqrt{2\pi\sigma^2_i}} \exp\left\{-\frac{1}{2\sigma^2_i}\left[y_{ij} - (\beta_{0i} + \beta_{1i}I_j)\right]^2\right\} = \frac{1}{\left(\sqrt{2\pi\sigma^2_i}\right)^n} \exp\left\{-\frac{1}{2\sigma^2_i}\sum_{j=1}^{n}\left[y_{ij} - (\beta_{0i} + \beta_{1i}I_j)\right]^2\right\}, \forall_i \quad \text{(Equation 5)}$$

To estimate the adaptability and stability parameters, *a priori* distributions were assigned for the parameters. The following distributions were considered for β_{0i}, β_{1i}, and σ^2_{di}:

$$\beta_{0i} \sim N(\mu_{0i},\ \sigma^2_{0i}),\ \beta_{1i} \sim N(\mu_{0i},\ \sigma^2_{1i}) \quad \text{(Equation 6)}$$

$$\sigma^2_{di} \sim GamaInv(\alpha_i;\beta_i). \quad \text{(Equation 7)}$$

The equal mean and variance for the reverse gamma values were calculated as follows, respectively:

$$\frac{\beta_i}{\alpha_i - 1} \quad \text{(Equation 8)}$$

$$\frac{\beta_i^2}{(\alpha_i - 1)^2(\alpha_i - 2)}. \quad \text{(Equation 9)}$$

When we assumed independence between the parameters of these distributions, the joint *a priori* distributions for each genotype were given by:

$$P_i(\beta_{oi},\beta_{ai},\sigma_i^2,y_{ij}) = \frac{1}{\sqrt{2\pi\sigma_{oi}^2}}\exp\left\{-\frac{1}{2\sigma_{oi}^2}[(\beta_{oi}+\mu_{oi})^2]\right\}\times\frac{1}{\sqrt{2\pi\sigma_{ai}^2}}\exp\left\{-\frac{1}{2\sigma_{ai}^2}[(\beta_{ai}+\mu_{ai})^2]\right\}\times\sigma_{0i}^2 \quad \text{(Equation 10)}$$

$$\frac{1}{[\beta_i^{\alpha_i}G(\alpha_i)]}\left(\frac{1}{\sigma_i^2}\right)^{\alpha_i+1}\exp\left\{-\frac{1}{\beta_i\sigma_i^2}\right\}\infty\exp\left[-\frac{1}{2\sigma_i^2}(\beta_{oi}+\mu_{oi})^2\right]\times\frac{1}{\sqrt{2\pi\sigma_{ai}^2}}\exp\left[-\frac{1}{2\sigma_{ai}^2}(\beta_{ai}+\mu_{ai})^2\right]\times\left(\frac{1}{\sigma_i^2}\right)^{\alpha_i+1}\exp\left\{-\frac{1}{\beta_i\sigma_i^2}\right\}. \quad \text{(Equation 11)}$$

To make inferences about the parameter of interest, the marginal *a posteriori* distributions must be obtained. When we denoted the parameter vectors for each genotype i using the following equation:

$$\theta_{pi} = (\beta_{1i},\beta_{2i},\sigma_{3i}^2) \quad \text{(Equation 12)}$$

where p = 1, 2, 3, the marginal *a posteriori* distribution for the parameter θ_{pi} was obtained using the following integral:

$$P(\theta_{pi} \mid x) = \int P(\theta_{pi} \mid x)d\theta_{pi} \quad \text{(Equation 13)}$$

(i.e., the integral in relation to all vector parameters with the exception of the p^{th} component).

In most cases, these integrals were complex and did not have exact solutions. To work around this problem, we used other methodologies. For example, we obtained a sample of the joint *a posteriori* distribution using the Markov chain and Monte Carlo (MCMC) method, which was used to determine the moments associated with the marginal distributions of interest (Cassela and George, 1992). In this study, the methodology was implemented using the R software (R Development Core Team, 2015), and the joint distribution sample was obtained using the MCMC regression function of the MCMC package.

To evaluate the influence of *a priori* information when estimating the adaptability and sta-

bility parameters, we utilized two different models: informative *a priori* distributions and minimally informative *a priori* distributions. In Model 1, the informative *a priori* information was derived from the application of meta-analysis techniques, which were characterized using information from Carvalho et al. (2006) and Valadares et al. (2010).

The 17 genotypes evaluated in the trials were used as references for *a priori* specification. Therefore, all of the genotypes presented in Table 2 were considered for Bayesian analysis. Information was inserted into the analysis using the assumed values for *a priori* distribution parameters (i.e., hyperparameters). These values were based on the mean and variance values of the samples that were composed using the parameter estimates obtained from the cited references (Table 2), which resulted in the following distributions:

$$\beta_{0i} \sim N(\mu_{0i}=\bar{\beta}_{0i}, \sigma^2_{1i} = Var(\bar{\beta}_{0i})) \quad \text{(Equation 14)}$$

$$\beta_{1i} \sim N(\mu_{1i}=\bar{\beta}_{1i}, \sigma^2_{1i} = Var(\bar{\beta}_{0i})) \quad \text{(Equation 15)}$$

$$\sigma^2_{di} \sim GamaInv(\alpha_i, \beta_i) \quad \text{(Equation 16)}$$

where $\bar{\beta}_{0i}$ represents the means of the β_{0i} estimates; $\bar{\beta}_{1i}$ represents the means of the β_{1i} estimates; $Var(\bar{\beta}_{0i})$ is the variance of the mean $\bar{\beta}_{0i}$ values; $Var(\bar{\beta}_{1i})$ is the variance of the mean $\bar{\beta}_{1i}$ values; and α and β_i represent values obtained using the following system resolution equations:

$$\bar{\sigma}^2_i = \frac{\beta_i}{\alpha_i - 1} \quad \text{(Equation 17)}$$

$$Var(\bar{\sigma}^2_i) = \frac{\beta^2_i}{(\alpha_i - 1)^2(\alpha_i - 2)} \quad \text{(Equation 18)}$$

$$\alpha_i = \frac{(\bar{\sigma}^2_i)^3}{Var(\bar{\sigma}^2_i) \times \bar{\sigma}^2_i} \quad \beta_i = \frac{(\bar{\sigma}^2_i)^3}{Var(\bar{\sigma}^2_i) + \bar{\sigma}^2_i} \quad \text{(Equation 19)}$$

In Model 2, minimally informative *a priori* distributions were used, and these distributions represented probability distributions with large variance. The following distributions were adopted:

$$\beta_{0i} \sim N(\mu_{0i}=\beta_{0i}, \sigma^2_{0i} = 1{,}000{,}000) \quad \text{(Equation 20)}$$

$$\beta_{1i} \sim N(\mu_{0i}=\beta_{0i}, \sigma^2_{1i} = 100{,}000) \quad \text{(Equation 21)}$$

$$\beta_{1i} \sim N(\mu_{0i}=\beta_{0i}, \sigma^2_{1i}=100{,}000) \quad \text{(Equation 22)}$$

The comparisons between Models 1 and 2 (i.e., between informative and minimally informative *a priori* distributions) were performed using the Bayes factor calculation (Kass and Raftery, 1995), which was conducted using the BayesFactor function of the MCMC package. According to Jeffreys (1961), Bayes factors can be interpreted as follows: FBij < 1 provides evidence in favor of model j; 1 ≤ FBij < 3 provides moderate evidence in favor of model i; 3 ≤ FBij < 10 indicates substantial evidence in favor of model i; 10 ≤ FBij < 30 demonstrates strong evidence in favor of model i; 30 ≤ FBij < 100 provides very strong evidence in favor of model i; and FBij ≥ 100 indicates decisive evidence in favor of model i.

Regarding the stability parameter (σ^2_{di}), samples of its marginal distributions were obtained indirectly, because this parameter represents a function. When values for σ^2_i were obtained indirectly in each iteration, we acquired values for σ^2_{di} using the following expression:

$$\hat{\sigma}^2_{di} = \hat{\sigma}^2_i - (MSR/r) \quad \text{(Equation 23)}$$

where MSR is the mean square of the residue provided by ANOVA; and r is the number of repetitions in the trial.

The hypotheses of interest were tested by constructing credibility ranges for the parameters, and the intervals were obtained directly from the marginal *a posteriori* distribution of the parameters. Thus, the credibility interval (CI) for θ_i, with a probability of covering δ, is given by:

$$\int_{-\infty}^{\theta*} P_i(\theta_i = (\beta_{0i}\, \beta_{1i} : \sigma^2_{di}) \mid y_{ij}) d\theta_i = \alpha/2 \quad \text{(Equation 24)}$$

$$\int_{\theta^*}^{-\infty} P_i(\theta_i = (\beta_{0i}\, \beta_{1i} : \sigma^2_{di}) \mid y_{ij}) d\theta_i = \alpha/2 \quad \text{(Equation 25)}$$

where θ_* and θ^* represent the lower and upper limits of the CI, respectively. Since the Gibbs sampler is an iterative algorithm, it is necessary to check its convergence. In this study, the convergence was checked by applying the Heidelberger and Welch (1983), Raftery and Lewis (1992), and Geweke (1992) criteria, which were implemented in the Bayesian Output Analysis package of the R program (R Development Core Team, 2015).

Regarding Bayesian analyses of adaptability and stability for each parameter of the adopted regression model, 110,000 iterations in the Gibbs sampler algorithm with a warm period ("burn-in") of 10,000 iterations were considered. To obtain a non-correlated sample, we considered the spacing between the sampling points of two iterations ("thinning"), which resulted in a final sample size of 50,000. The samples represented samples of marginal *a posteriori* distributions for each parameter under which the inference was conducted.

RESULTS AND DISCUSSION

In joint analyses, all of the effects were significant ($P \leq 0.01$) (Table 3), which indicated contrasts between the environments and the occurrence of genotypic differential responses to environmental effects. This can be confirmed by examining differences in the soil and climatic features of each environment, including altitude, latitude, longitude, climate type, soil type, rainfall, and temperature (Table 1). Similar results were obtained in previous studies that found significant differences associated with the effects of genotypes, environments, and G x E interactions when evaluating cowpea genotypes in multi-environment trials in the Brazilian Cerrado (Rocha et al., 2007; Barros et al., 2013; Santos et al., 2015; Torres et al., 2015b). The existence of significant G x E interactions for YIE that the stability and adaptability analyses were suitable, and this result was further supported by the fact that edaphoclimatic factors had the greatest influence on the adaptability and stability of genotypes.

Table 3. Summary of joint ANOVA for grain yield (kg/ha) of 17 upright cowpea genotypes that were evaluated in six environments in the State of Estado do Mato Grosso do Sul.

Sources of variation	d.f.	Mean square
Blocks/Environment	18	230,431.83
Genotypes	16	237,309.26*
Environment	5	10,921,770.95*
Genotypes x Environment	57	189,533.11*
Error	190	47,623.88
Mean (kg/ha)	-	664.43
Coefficient of variation (%)	-	25.32

*Significant at a 0.01 probability level using the F test.

Regarding the convergence for all simulated chains, the dependency factor of Raftery and Lewis (1992) gave values lower than five, and P values based on the criteria of Geweke (1992) were higher than the prefixed significance level ($P \leq 0.05$) (i.e., both criteria indicated convergence of the chains generated by the Gibbs sampler). In order to confirm this convergence, we also used the criteria of Heidelberger and Welch (1983), which determined whether the chain values were derived from a stationary distribution.

The adaptability and stability parameter estimated values were obtained by calculating the *a posteriori* means, which are presented together with their respective CIs in Table 4. In Model 1 (informative *a priori*), of the 17 genotypes evaluated by the Bayesian approach, only the EV X 63-10E, BRS Guariba, and Vita-7 genotypes were classified as having specific adaptability to favorable environments ($\beta_{1i} > 1$) (CI limits at 95%). The other genotypes were classified as having general adaptability and stability, since the value of 1 fell within a CI of 95%. However, when considering the analysis of genotypes under Model 2 conditions (minimally informative *a priori*), all genotypes showed specific adaptability to favorable environments ($\beta_{1i} > 1$). Therefore, it is possible to infer that the use of the frequentist model, in which *a priori* information is not taken into account, tends to conclude that the genotypes exhibit stability and adaptability to different environments, but this does not favor reliable genotype recommendations. Nascimento et al. (2011) and Couto et al. (2015) obtained similar results after evaluating the adaptability and phenotypic stability of alfalfa and popcorn genotypes, respectively.

Table 4. Estimates of *a posteriori* mean ($\bar{\beta}_{0i}$, in kg/ha) and credibility intervals (95%) of the adaptability ($\bar{\beta}_{1i}$) and stability ($\bar{\sigma}^2_i$) parameters when considering informative and minimally informative *a priori* distributions.

Genotype	LI $\bar{\beta}_{0i}$	$\bar{\beta}_{0i}$	LS $\bar{\beta}_{0i}$	LI $\bar{\beta}_{1i}$	$\bar{\beta}_{1i}$	LS $\bar{\beta}_{1i}$	$\bar{\sigma}^2_i$ x1000	LI $\bar{\sigma}^2_{di}$ x1000	$\bar{\sigma}^2_{di}$ x1000	LS $\bar{\sigma}^2_{di}$ x1000
Informative *a priori*										
MNC99-537F-1	649	962	1331	0.12	0.60	1.01	344.5	2.7	336.6	1738.1
MNC99-537F-4	740	837	1013	0.60	1.03	1.24	26.2	-6.9	18.3	159.6
MNC99-541-F5	662	825	1154	0.73	1.07	1.40	81.7	-4.6	73.7	479.6
MNC99-541-F8	544	788	1114	0.22	0.75	1.20	254.3	1.9	246.4	1280.1
IT93K-93-10	509	764	1105	0.36	0.76	1.19	235.7	6.6	227.8	1181.1
MNC99-519D-1-1-5	784	1159	1509	0.62	1.08	1.55	721.8	36.9	713.9	3348.1
MNC00-544D-10-1-2-2	581	873	1382	0.64	1.10	1.43	305.1	-7.6	297.2	1823.1
MNC00-544D-14-1-2-2	654	944	1451	0.88	1.24	1.66	293.6	-7.5	285.7	1772.1
MNC00-553D-8-1-2-2	753	1101	1440	0.69	1.16	1.63	800.6	63.0	792.7	3659.1
MNC00-553D-8-1-2-3	586	722	1108	0.63	1.01	1.26	71.8	-6.9	63.9	508.9
MNC00-561G-6	735	1090	1457	0.70	1.15	1.59	469.3	11.6	461.4	2288.1
EV X 63-10E	966	1311	1646	1.13	1.31	1.46	928.0	83.9	920.1	4187.1
EV X 91-2E-2	687	972	1498	0.84	1.23	1.61	297.7	-7.7	289.8	1831.1
MNC99-557F-2	539	721	1165	0.45	0.89	1.16	129.9	-7.1	121.9	869.6
BRS Guariba	819	1192	1545	1.03	1.15	1.26	651.2	29.3	643.3	3039.1
Patativa	620	945	1432	0.56	0.96	1.37	337.2	-7.4	329.3	1926.1
Vita-7	1036	1364	1687	1.27	1.35	1.43	1775.0	232.9	1767.1	7738.1
Minimally informative *a priori*										
MNC99-537F-1	318	633	939	0.14	0.87	1.60	238.8	-2.3	230.9	785.8
MNC99-537F-4	640	811	977	0.74	1.14	1.53	76.0	-6.3	68.1	229.9
MNC99-541-F5	450	705	952	0.50	1.09	1.68	160.4	-4.2	152.5	517.1
MNC99-541-F8	262	568	867	0.50	1.21	1.92	227.5	-2.5	219.6	747.8
IT93K-93-10	74	513	940	-0.41	0.61	1.63	448.5	3.3	440.6	1534.1
MNC99-519D-1-1-5	245	612	969	0.03	0.88	1.73	319.4	-0.1	311.5	1070.1
MNC00-544D-10-1-2-2	472	598	721	0.91	1.20	1.49	42.9	-7.0	35.1	122.7
MNC00-544D-14-1-2-2	542	671	799	0.91	1.21	1.51	45.6	-6.9	37.6	130.9
MNC00-553D-8-1-2-2	216	5289	1040	-0.29	0.94	2.16	634.0	8.4	626.1	2198.1
MNC00-553D-8-1-2-3	458	622	783	0.70	1.08	1.45	70.3	-6.4	62.4	212.2
MNC00-561G-6	291	667	1032	0.30	1.17	2.04	333.8	0.2	325.9	1119.1
EV X 63-10E	124	684	1220	-0.34	0.95	2.25	710.0	10.4	702.1	2466.1
EV X 91-2E-2	579	703	824	0.95	1.24	1.52	41.7	-7.1	33.8	118.4
MNC99-557F-2	411	567	721	0.61	0.98	1.34	64.9	-6.5	56.9	194.7
BRS Guariba	292	677	1050	0.12	1.01	1.90	348.8	0.6	340.9	1172.1
Patativa	501	635	767	0.63	0.94	1.25	48.5	-6.9	40.6	140.4
Vita-7	111	473	924	-0.41	0.67	1.74	495.7	4.6	487.8	1706.1

By comparing the estimates of the parameters obtained using the two models, similar differences in magnitude between the parameters were observed. Thus, it is necessary to determine which of the two models exhibited a higher quality setting, and this answer was provided using Bayes factor calculations (Nascimento et al., 2011). With the exception of the MNC99-519D-1-1-5, MNC00-544D-10-1-2-2, MNC00-553D-8-1-2-2, MNC00-561G-6, EV X 91-2E-2, Patativa, and Vita-7 genotypes, all of the other genotypes exhibited Bayes factors that were greater than 10 (Table 5).

These results indicated that the use of informative *a priori* distributions provided more accurate results. Despite the *a priori* information for each genotype that was based on a single study, similar results were found in studies that evaluated the adaptability and phenotypic stability of the dry matter yield of alfalfa genotypes (Nascimento et al., 2011), popcorn grain yield (Couto et al., 2015) and cowpea YIE (Teodoro et al., 2015). Therefore, it is expected that the results will be more accurate in studies examining the stability and adaptability of other crops that have larger amounts of available information for meta-analysis.

The Bayesian approach, in conjunction with the Eberhart and Russell method (1966), was an effective method for the selection of upright cowpea genotypes with high adaptability and phenotypic stability. Moreover, Bayes factors indicated that the use of informative *a priori* distributions provided more accurate results compared to minimally *a priori* distributions.

Table 5. Values obtained for Bayes factors (BF) of models compared using informative *a priori* (i) and minimally informative *a priori* (j) distributions for the evaluated genotypes.

Genotype	BF_{ij}
MNC99-537F-1	11.20
MNC99-537F-4	14.90
MNC99-541-F5	13.80
MNC99-541-F8	11.80
IT93K-93-10	13.70
MNC99-519D-1-1-5	8.12
MNC00-544D-10-1-2-2	9.12
MNC00-544D-14-1-2-2	9.29
MNC00-553D-8-1-2-2	8.33
MNC00-553D-8-1-2-3	12.60
MNC00-561G-6	9.73
EV X 63-10E	10.80
EV X 91-2E-2	9.21
MNC99-557F-2	11.30
BRS Guariba	11.90
Patativa	9.02
Vita-7	2.29
MNC99-537F-1	11.20
MNC99-537F-4	14.90
MNC99-541-F5	13.80

Conflicts of interest

The authors declare no conflict of interest.

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REFERENCES

Banzatto DA and Kronka SN (2006). Experimentação agrícola. FUNEP, Jaboticabal.

Barros MA, Rocha MM, Gomes RLF, Silva KJD, et al. (2013). Adaptabilidade e estabilidade produtiva de feijão-caupi de porte semiprostrado. *Pesq. Agropec. Bras.* 48: 403-410. http://dx.doi.org/10.1590/S0100-204X2013000400008

Carvalho HWL, Brito Neto J, Freire Filho FR, Rocha MM, et al. (2006). Estabilidade de linhagens de feijão-caupi de porte ereto. In: Anais do Congresso Nacional de Feijão-caupi, Teresina.

Cassela G and George EI (1992). Explaining the Gibbs sampler. *Am. Stat.* 46: 167-174.

Cotes JM, Crossa A, Sanches PL and Cornelius A (2006). Bayesian approach for assessing the stability of genotypes. *Crop Sci.* 46: 2654-2665. http://dx.doi.org/10.2135/cropsci2006.04.0227

Couto MF, Nascimento M, Amaral AT, Silva FF, et al. (2015). Eberhart and Russel's bayesian method in the selection of popcorn cultivars. *Crop Sci.* 55: 571-577. http://dx.doi.org/10.2135/cropsci2014.07.0498

Cruz CD and Regazzi AJ (2007). Modelos biométricos aplicados ao melhoramento genético. Imprensa Universitária, Viçosa.

Eberhart SA and Russell WA (1966). Stability parameters for comparing varieties. *Crop Sci.* 6: 36-40. http://dx.doi.org/10.2135/cropsci1966.0011183X000600010011x

Freire Filho FR, Ribeiro VQ, Rocha MM and Lopes ACA (2002). Adaptabilidade e estabilidade da produtividade de grãos de linhagens de caupi de porte enramador. *Rev. Ceres* 49: 383-393.

Geweke J (1992). Evaluating the accuracy of sampling-based approaches to the calculation of posterior moments. In: Bayesian statistics (Bernardo JM, Berger JO, David AP and Smith AFM eds.). Oxford University, New York.

Heidelberger P and Welch PD (1983). Simulation run length control in the presence of an initial transient. *Oper. Res.* 31: 1109-1144. http://dx.doi.org/10.1287/opre.31.6.1109

Jeffreys H (1961). Theory of probability. Claredon, Oxford.

Kass RE and Raftery AE (1995). Bayes factors. *J. Am. Stat. Assoc.* 90: 773-795. http://dx.doi.org/10.1080/01621459.1995.10476572

Molina LMR, Sanches A and Torres JMC (2011). Inferência bayesiana na análise de testes regionais de arroz em dois sistemas de cultivo. *Rev. Fac. Nac. Agro.* 64: 5883-5891.

Mora F, Scapim CA and Pinto RJB (2009). El análisis bayesiano y la precisión de los valores de la heredabilidad en especies perenes. *Cienc. Florest.* 19: 343-349. http://dx.doi.org/10.5902/19805098890

Nascimento M, Silva FF, Sáfadi T, Nascimento ACC, et al. (2011). Abordagem bayesiana para avaliação da adaptabilidade e estabilidade de genotipos de alfafa. *Pesq. Agropec. Bras.* 46: 26-32. http://dx.doi.org/10.1590/S0100-204X2011000100004

R Development Core Team R: a language and environment for statistical computing. Vienna: R Foundation for Statistical Computing. http://www.R- project.org. Accessed April 15, 2015.

Raftery AL and Lewis SM (1992). Practical markov chain monte carlo: comment: one long run with diagnostics: implementation strategies for Markov chain Monte Carlo. *Stat. Sci.* 7: 493-497. http://dx.doi.org/10.1214/ss/1177011143

Rocha MM, Freire Filho FR, Ribeiro VQ, Carvalho HWL, et al. (2007). Adaptabilidade e estabilidade produtiva de genótipos de feijão-caupi de porte semiereto na região Nordeste do Brasil. *Pesq. Agropec. Bras.* 42: 1283-1289. http://dx.doi.org/10.1590/S0100-204X2007000900010

Santos A, Ceccon G, Rodrigues EV, Teodoro PE, et al. (2015). Adaptability and stability of cowpea genotypes to Brazilian Midwest. *Afr. J. Agric. Res.* 10: 3901-3908.

Santos JAS, Teodoro PE, Correa AM, Soares CMG, et al. (2014a). Desempenho agronômico e divergência genética entre genótipos de feijão-caupi cultivados no ecótono Cerrado/Pantanal. *Bragantia* 73: 377-382. http://dx.doi.org/10.1590/1678-4499.0250

Santos JAS, Soares CMG, Corrêa AM, Teodoro PE, et al. (2014b). Agronomic performance and genetic dissimilarity among cowpea [*Vigna unguiculata* (L.) Walp.] genotypes. *Glob. Adv. Res. J. Agr. Sci.* 3: 271-277.

Silva MAG, Peternelli LA, Nascimento M and Silva FL (2013). Modelos mistos na seleção de famílias de cana de açúcar aparentados sob o enfoque clássico e bayesiano. *Rev. Bras. Biol.* 31: 1-12.

Teodoro PE, Nascimento M, Torres FE, Barroso LMA, et al. (2015). Perspectiva baysiana na seleção de genótipos de feijão-caupi em ensaios de valor de cultivo e uso. *Pesq. Agropec. Bras.* 50: 878-885. http://dx.doi.org/10.1590/S0100-204X2015001000003

Torres FE, Sagrilo E, Teodoro PE, Ribeiro LP, et al. (2015a). Número de repetições para avaliação de caracteres em genótipos de feijão-caupi. *Bragantia* 74: 161-168. http://dx.doi.org/10.1590/1678-4499.0393

Torres FE, Teodoro PE, Sagrilo E, Correa AM, et al. (2015b). Interação genótipo x ambiente em genótipos de feijão-caupi semiprostrado via modelos mistos. *Bragantia* 74: 255-260. http://dx.doi.org/10.1590/1678-4499.0099

Valadares RN, Moura MCCL, Silva AFA, Silva LS, et al. (2010). Adaptabilidade e estabilidade fenotípica em genótipos de feijão-caupi [*Vigna unguiculata* (L.) Walp.] de porte ereto/semiereto nas mesorregiões leste e sul maranhense. *Agropec. Cien. Semi-Árido* 6: 21-27.

Wricke G (1965). Zur berechnung der okovalenz bei sommerweizen und hafer. *Z. Pflanzenzuchtg* 52: 127-138.

Yates F and Cochran WG (1938). The analysis of group of experiments. *J. Agric. Sci.* 28: 556-580. http://dx.doi.org/10.1017/S0021859600050978