Bayesian approach, traditional method, and mixed models for multienvironment trials of soybean

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Abstract – The objective of this work was to compare the Bayesian approach and the frequentist methods to estimate means and genetic parameters in soybean multienvironment trials. Fifty-one soybean lines and four controls were evaluated in a randomized complete block design, in six environments, with three replicates, and soybean grain yield was determined. The half-normal prior and uniform distributions were used in combination with parameters obtained from data of 18 genotypes collected in previous and related experiments. The genotypic values of the genotypes of high- and low-grain yield, clustered by the Bayesian approach, differed from the means obtained by the frequentist inference. Soybean assessed through the Bayesian approach showed genetic parameter values of the mixed model (REML/Blup) close to those of the following variables: mean heritability (h^2mg), accuracy of genotype selection (Acgen), coefficient of genetic variation (CVgi%), and coefficient of environmental variation (CVe%). Therefore, the mixed model methodology and the Bayesian approach lead to similar results for genetic parameters in multienvironment trials.

Index terms: *Glycine max*, mathematical modeling, prior distribution in plant breeding.

Abordagem bayesiana, método tradicional e modelos mistos para experimentos multiambientes na cultura da soja

Resumo – O objetivo deste trabalho foi comparar a abordagem bayesiana e os métodos frequentistas para estimar as médias e os parâmetros genéticos em experimentos multiambientes de soja. Cinquenta e uma linhagens de soja e quatro testemunhas foram avaliadas em delineamento de blocos ao acaso, em seis ambientes, com três repetições, e a produtividade de grãos foi determinada. As distribuições "half-normal" a priori e uniformes foram utilizadas em combinação com parâmetros obtidos de dados de 18 genótipos coletados em experimentos anteriores e relacionados. Os valores genotípicos de genótipos com alta e baixa produção de grãos, agrupados pela abordagem bayesiana, diferiram das médias obtidas pela inferência frequentista. A soja avaliada pela abordagem bayesiana apresentou valores de parâmetros genéticos de modelos mistos (REML/Blup) próximos daqueles das seguintes variáveis: herdabilidade média (h^2mg), acurácia da seleção dos genótipos (Acgen), coeficiente de variação genético (CVgi%) e coeficiente de variação ambiental (CVe%). Portanto, em experimentos multiambientes, a metodologia de modelos mistos e a abordagem bayesiana produzem resultados similares de parâmetros genéticos.

Termos para indexação: *Glycine max*, modelagem matemática, distribuição a priori no melhoramento genético.

Introduction

Multienvironmental statistical analyses have been the frequentist methodology adopted in soybean breeding programs because it loses previous experimental data information (Omer et al., 2014a). Therefore, analyses based on the frequentist approach and on variance components are treated as constants that ignore any prior information (Gelman, 2006). Additionally, based on previous studies, the Bayesian approach improves the data accuracy and provides statistic-inference information that is more realistic (Singh et al., 2015).

The Bayesian approach can be applied to several fields such as cluster definition analyses (Priolli et al., 2013), phenological calculation changes (Shen &

Liu, 2015), and Bayesian network to study the relation between traits (Valentim et al., 2007). Moreover, to our knowledge, there are no Bayesian methods available to find the genotypic values in soybean breeding programs, so far.

Genotype value prediction for superior materials is the core problem in plant breeding programs because an accurate knowledge of the true variance component value is necessary, which is only found through adequate methods (Borges et al., 2010). Accordingly, the Bayesian approach emerged as an alternative method to estimate the genotype value in the plant breeding field.

Prior information on phenotypic data is often available in ongoing crop improvement programs, and it can be used to estimate the variance component and the genetic parameters through the application of the Bayesian methodology. There is no elucidating Bayesian study based on the use of prior information to estimate variance components and genetic parameters to be used in soybean breeding programs.

The objective of this work was to compare the Bayesian approach and the frequentist methods to estimate means and genetic parameters in soybean multienvironment trials.

Materials and Methods

Grain yield (kg ha^{-1}) of soybean (*Glycine max* L.) advanced lines was assessed. The experiment followed a randomized complete block design with three replicates. The plots consisted of 4 m long rows, spaced at 0.45 m from each other. For the analyses, only the two rows in the middle of the plot were taken into account. A total of 51 soybean lines resulting from simple, double, quadruple, and octuple crosses, by using different genitors CD-216 and Conquista (MG-BR46) cultivars, were tested. Checks were commercial cultivars Potência and V-Max.

The genotypes were assessed in three municipalities of São Paulo state, in different crop seasons: Pindorama (2013/2014), Jaboticabal (2013/2014, 2014/2015, and 2015/2016), and Piracicaba (2013/2014 and 2014/2015). The crop seasons and locations were combined and taken as environments for all the inferences, as recommended by Omer et al. (2015).

As to the frequentist approach, the grain yield and multiple environment model, including the environment

block, the block within environment effect, genotypes and the genotypes by environment interaction, can be described as, $Y_{ijk} = \mu + E_j + R_{k(j)} + G_i + (GE_{ij}) + \varepsilon_{ijk}$, in which: Y_{ijk} is the observed yield data vector of the ith genotype, in the kth block of the jth environment; μ is the general mean; E_j is the jth environment effect; $R_{k(j)}$ is the kth block effect from the jth environment; G_i is the ith genotype effect; GE_{ij} is the ith genotype and the jth environment interaction; and ε_{ijk} is the error. The environments were fixed; the replicate within environments, genotypes, GE interaction, and error were the random effect. In general, the following assumption was taken into consideration:

$$R_{k(j)} \sim N(0, \sigma_R^2),\ G_i \sim N(0, \sigma_G^2),\ GE_{ij} \sim N(0, \sigma_{GE}^2),$$
$$\text{and } \varepsilon_{ijk} \sim N(0, \sigma_e^2),$$

in which: $N(0, \sigma^2)$ is the normal distribution with zero mean and σ^2 variance.

The genotype variance components, genotypes x environment and rep/environment effects, and the interaction in the Bayesian approach were random variables with known parameters in the prior distribution. These half-normal, uniform, prior distributions have been studied and recommended to calculate the variance components, the corresponding standard deviation components, or the scalar parameters (Gelman, 2006).

Monte Carlo via Markov chain (MCMC) was used to find the a posteriori distribution and the studied parameters. Computational analyses were composed of three chains, each one comprising 10,000 iterations (the first 5,000 ones were discarded) spaced by 15 point samples (thinning), and 1,002 iteration number simulations. The Gibbs sampler is a necessary iterative algorithm to verify the convergence through the Gelman-Rubin ($\hat{R}$) statistics, which is used to assess the variance ratio between the chain and the variance within the chain. $\hat{R}$ values below 1.1 confirmed the iteration convergence (Gelman & Rubin, 1992).

Two prior distributions were tested. Type 1 was the positive half-normal to the σ_E^2, σ_G^2, σ_R^2, and σ_{GE}^2 variances; its prior distribution values were calculated based on the inversed variance of previous trials by using 18 lines from the total of 51 evaluated ones, namely: Jab 4, Jab 5, Jab 6, Jab 7, Jab 8, Jab 10, Jab 12, Jab 15, Jab 16, Jab 17, Jab 19, Jab 20, Jab 22, Jab 23, Jab 24, Jab 39, Jab 40, and Jab 41. These genotypes were previously assessed in tree experiments

conducted in Jaboticabal (2011/2012 and 2012/2013), and in Piracicaba (2012/2013) (Di Mauro et al., 2014).

Type 2 prior distribution was tested through uniform distribution [0, and 5,000,000]. These values were used according to related studies (Di Mauro et al., 2014). The selection of the best prior distribution to be used in the Bayesian analyses was achieved through -2 x log-likelihood to the mean of the posterior parameters, the posterior mean of -2 x log-likelihood, the effective number of parameters and the deviance information criteria (DIC) (Spiegelhalter et al., 2002).

The mean genotype was calculated through the Bayesian approach, mixed models, adjusted mean (lsmeans: least-squares means) and arithmetic mean. The correlation coefficient between mean and mean rank of the evaluated methods, and the genotype means were estimated. The Spearman correlation between ranks was estimated ranks.

The random effect on the model used in unbalance experiments (data) was assessed through the deviance analyses according to Resende (2007), and through the analysis of variance.

All the Bayesian analyses were conducted in the R software (R Core Team, 2016) package R2WinBUGS (Sturtz et al., 2005). Blups (genotypic value) and variances were analyzed through REML by using the lme4 package. Deviance analyses were assessed via lmtest package (Zeileis & Hothorn, 2002).

Results and Discussion

All the variation sources were significant for F and for the likelihood ratio test (LRT) (Table 1).

As to the assessed environments, two of them were favorable and 4 were unfavorable; the checked environmental index signal was positive and negative (I_j). Besides, the coefficient of variation varied from 21.04% up to 51.47% (Table 2).

The half-normal was the most appropriate prior distribution to find the genetic value through MCMC method. This prior distribution showed the smallest information deviance criterion (DIC), deviance of posterior mean parameters ($\hat{D}$), and deviance of posterior mean ($\bar{D}$), but the effective number of parameters (P_D) in positive half-normal was higher than in the uniform distribution. The larger the effective number of parameters, the easier the data fit by the model (Table 3). The half-normal distribution has been used to set the number of replicates in plant breeding experimental designs because it has been showing the smallest deviance criteria (DIC) (Omer et al., 2014b), as well as heritability and genetic gain estimates through the Bayesian approach (Omer et al., 2014a). The DIC is an estimated error prediction; the lower value indicates a better adjusted model. The DIC from half-normal distribution was lower than the distribution uniform value. It indicates that the half-normal prior distribution should be taken into consideration rather than the uniform distribution. Therefore, all the variance components were found through the half-normal prior distribution. Previous experimental data information in genetic experiments lead to better variance estimates and decrease the residual variance (Carneiro Júnior et al., 2005). Moreover, the chosen of priors to calculate posteriors, conducted through the Bayesian approach, was generated according to the inverse variance of 18 genotypes, collected from 55 genotypes in the present study.

The genotype behavior was estimated in percentiles of the previous values, and in their ranks, according

Table 1. Deviance analyses and F-test to measure the random and fixed effects, respectively, on soybean grain yield (kg ha^{-1}).

Variation source	Bayesian analysis			Analysis of variance			
	Deviance	Statistic test	p-value	DF	Mean square	F-value	p-value
Environment	[1]	F=29.38	<0.0001	5	124,875,061.1	94.87	<0.0001
Replicate/environment	15,935.10[2]	LRT=10.22	0.0014	12	3,896,104.0	2.96	0.0005
Genotypes	15,937.48[2]	LRT=12.59	0.0004	54	3,453,633.5	2.62	<0.0001
Genotypes x environment	15,932.09[2]	LRT=7.20	0.0073	264	1,711,109.2	1.30	0.0052
Complete model and Error[3]	15,924.89			601	1,316,272.0		

[1]Fixed effect was not calculated. F, F-test calculated; LRT, likelihood ratio test conducted through chi-square at 1 degree of freedom. Chi-square table value at 1% equals 3.83, and, at 5%, equals 6.63. [2]Adjusted deviance model without the referred effect. [3]Complete model for Bayesian analysis and error for analysis of varinace.

to the posterior mean by using the Bayesian approach (Table 4). Moreover, the mean national soybean grain yield is 2,870 kg ha^{-1} (Conab, 2017). Thus, taking into account the credibility interval, the genotypes Jab 42, Jab 44, Jab 32, Jab 31, Conquista, Jab 27, Jab 41, and Jab 5 showed higher values of the limit credibility interval that were above the mean national grain yield; therefore, they were considered the most productive genotypes. Besides, the Jab 42 line remains in the breeding process, and it was herein highlighted as a potential genotype that shows grain yield values above the national mean (Table 4).

Genotypes Jab 48, Jab 15, Jab 26, Jab 24, Jab 6, and Jab 25 did not reach a high rank, taking into consideration the percentiles 2.5 and 5%; therefore, they should not be selected. According to the ranks, the percentiles 95 and 97.5% would show the predictions of the most unproductive genotypes, if it was selected based on the mean. Genotype Jab 42 may decrease to the 2nd position (percentile 97.5%), or remain in the 1st one (percentile 95%, and others).

Means obtained through the Bayesian approach, lsmeans, and genotypic mean were the least discrepant ones for magnitude and rank (Tables 4 and 5) because they are methods based on experimental designs used to adjust the means whenever necessary. The posterior distribution in the Bayesian method is generated for the studied parameters (genotype, heritability etc.) as a random effect. Genotypes are treated as fixed effect in lsmeans or in marginal mean predictions, and mean adjustment is done according to the factor found in the linear model (genotype, replicate/environment, and environment). Genotypes are treated as random effects in the mixed model method, and the same genotype

mean in multi-environment experiments is equal to the general mean + Blup of the genotype + Blup in GxE interaction (Resende, 2007).

The Bayesian method and Blups were similar for correlation means; they recorded r = 0.9974. The lsmeans method used to calculate the mean genotype showed the second highest correlation values through the Bayesian method, r = 0.9678. And the simple arithmetic mean method showed correlation r = 0.9663 (Table 5). The REML/Blup method is the standard one to calculate the random effects on genotype selection in plant breeding (Oliveira et al., 2016). This method showed a high correlation with the Bayesian approach in partially unbalanced experimental situations.

In the present study, there were 5% missed plots, and the data set was restricted to six plots only. However, these missed plots did not significantly influence the genotype rank effect. Thus, it is necessary to assess the Bayesian approach in a larger number of missed plots, environments, and heterogeneous variance situations, in order to verify its efficiency. The Bayesian approach was used to model the heterogeneous variances in an experiment conducted to estimate the error and the genotype x environment interaction variances. The Bayesian approach was able to provide a more parsimonious answer to the question about whether the use of weighted, or unweighted means, in multi-environment trial modeling, properly sets the heterogeneous variances in the assessed experiments (Edwards & Jannink, 2006).

The genetic parameters estimated through the analysis of variance and through the mixed model were similar to all the assessed genetic parameters. The genetic parameters estimated through the

Table 2. Soybean grain yield, overall mean, and the environmental index of the assessed locations and crop seasons.

Location	Crop season	Grain yield (kg ha^{-1})	Coefficient of variation (%)	Environmental index (I$_j$)
Jaboticabal	2013/2014	1,901.36	44.24	-475.90
Jaboticabal	2014/2015	2,335.26	38.21	-42.00
Jaboticabal	2015/2016	2,169.60	51.47	-207.66
Piracicaba	2013/2014	3,383.12	21.04	1,005.86
Piracicaba	2014/2015	3,371.36	44.51	994.10
Pindorama	2013/2014	1,050.01	31.00	-1,327.25
Overall mean	-	2,377.26	48.26	-

Table 3. Discrepancy statistics to the prior selection in a soybean trial for grain yield (kg ha^{-1}) conducted in six environments.

Prior distribution model	$\bar{D}$	$\hat{D}$	P$_D$	DIC
P1	14,981.80	14,791.60	190.24	15,172.00
P2	15,951.60	15,901.30	50.34	16,001.90

$\bar{D}$, posterior mean of -2 x log-likelihood. $\hat{D}$, -2 x log-likelihood to posterior mean parameters. P$_D$, parameter effective number. DIC, deviance criteria information. P1, σ^2_E, σ^2_G, σ^2_R, and σ^2_{GE} independent distribution ~ positive half-normal with inverse variance = σ^2_E (0, 0,00028), σ^2_G.(0, 0,00304), σ^2_R .(0, 0,00001), and σ^2_{GE} .(0, 0,00170). P2, σ^2_E, σ^2_G, σ^2_R, and σ^2_{GE} independent ~ uniform (0, and 5,000,000).

Table 4. Genotype mean predicted were ordered by posterior means, and its ranks were measured by the Bayesian approach and the frequentist analyses based on predicted genotypic values (BLUPs), on adjusted mean, and on the arithmetic mean of 55 soybean lines for grain yield (kg ha^{-1}).

Rank of posterior means	Genotype	Posterior means	IC 95%[1] Lower	IC 95%[1] Upper	Rank of posterior means	Posterior ranks (quantile) 0.025	0.05	0.5	0.95	0.975	Genotypic values[2] (u+g+ge)	Phenotypic mean (lsmeans)	Arithmetic mean	N[3]
1	Jab 42	3,331.33	2,914	3,843	1.07	1	1	1	1	2	3,514.27	4,179.80	4,179.80	18
2	Jab 44	2,743.28	2,390	3,168	7.78	2	2	5	22.48	27	2,802.50	3,057.61	3,057.61	18
3	Jab 32	2,655.86	2,262	3,052	11.06	2	2	9	29	34	2,707.58	2,907.95	2,907.95	18
4	Jab 31	2,622.42	2,260	2,994	12.39	2	2	10	32	36	2,670.94	2,850.19	2,850.19	18
5	Conquista	2,620.53	2,255	3,004	12.56	2	2	10	32	36	2,666.00	2,842.40	2,842.40	18
6	Jab 27	2,619.51	2,225	2,991	12.72	2	2	10	33	36.98	2,670.05	2,848.78	2,848.78	18
7	Jab 41	2,594.81	2,180	2,970	13.81	2	2	11	34	38.49	2,652.07	2,907.69	2,827.45	17
8	Jab 5	2,590.56	2,205	2,986	14.03	2	2	11	35	39.98	2,636.43	2,795.77	2,795.77	18
9	Jab 30	2,567.34	2,159	2,934	15.25	2	3	13	37	40	2,594.21	2,723.61	2,820.76	17
10	Jab 45	2,563.80	2,213	2,976	15.59	2	3	14	36	39	2,606.41	2,737.20	2,835.76	17
11	Jab 39	2,527.19	2,189	2,955	17.39	2.03	3	15	39	42	2,565.91	2,684.60	2,684.60	18
12	Jab 1	2,506.70	2,099	2,856	18.49	3	3.5	16	40	43	2,557.47	2,671.29	2,671.29	18
13	Jab 7	2,506.69	2,085	2,857	18.53	3	4	17	41	44	2,539.33	2,642.69	2,642.69	18
14	Jab 43	2,498.92	2,090	2,913	19.14	2	3	17	41	45	2,530.52	2,597.47	2,651.90	17
15	Jab 35	2,489.26	2,088	2,862	19.47	3	4	18	41	44	2,503.67	2,540.52	2,609.15	17
16	Potência	2,486.78	2,126	2,876	19.60	3	4	18	42	45	2,513.25	2,601.56	2,601.56	18
17	Jab 2	2,439.57	2,022	2,813	22.49	4	5	21	44	47	2,452.12	2,488.70	2,446.42	17
18	Jab 11	2,439.03	2,100	2,855	22.78	4	5	22	44	46.98	2,448.51	2,510.01	2,437.05	17
19	Jab 47	2,429.59	2,020	2,778	23.14	4	6	22	44	47.98	2,454.61	2,482.74	2,574.31	16
20	Jab 3	2,420.53	2,055	2,788	23.55	4	6	23	44	47.98	2,436.79	2,481.02	2,481.02	18
21	Jab 10	2,419.02	2,033	2,821	23.87	4	5	23	45.98	49	2,419.94	2,470.63	2,428.62	17
22	Jab 49	2,410.54	2,050	2,807	24.20	4	6	23	45	48	2,417.66	2,450.87	2,450.87	18
23	Jab 36	2,398.55	2,016	2,772	25.00	5	6.05	24.25	45	49.98	2,416.74	2,420.38	2,464.28	17
24	Jab 23	2,391.44	1,989	2,749	25.68	4.03	6	25	47	49	2,404.65	2,430.35	2,430.35	18
25	Jab 38	2,383.61	2,007	2,750	26.05	4	6	25.25	47	49	2,392.75	2,411.59	2,411.59	18
26	Jab 19	2,358.46	1,947	2,712	27.54	5	7	27	49	50	2,363.68	2,364.64	2,439.82	17
27	Jab 4	2,357.72	1,976	2,728	27.73	5	7	28	47.48	49	2,352.26	2,313.35	2,433.90	17
28	Jab 46	2,355.90	1,957	2,718	27.78	5	7	27	48	50	2,344.65	2,327.44	2,416.70	17
29	Jab 29	2,355.75	2,008	2,763	27.94	5	7	29	47	49	2,356.50	2,341.90	2,401.11	17
30	Jab 34	2,351.34	1,960	2,728	28.22	5	7	29	48	50	2,341.81	2,279.17	2,263.80	16
31	Jab 18	2,340.73	1,912	2,671	28.57	6	9	28	49	50	2,344.21	2,335.06	2,335.06	18
32	Jab 51	2,329.56	1,997	2,717	29.52	7	9	30	48	50	2,337.37	2,324.28	2,324.28	18
33	Jab 40	2,303.98	1,889	2,657	30.97	6.03	10	32	50	51.49	2,296.39	2,259.66	2,259.66	18
34	Jab 50	2,294.55	1,943	2,680	31.76	7	11	33	49	51	2,267.20	2,206.48	2,255.05	17
35	Jab 28	2,293.54	1,927	2,659	31.54	9	11.5	32	50	52	2,287.64	2,245.86	2,245.86	18
36	Jab 33	2,277.31	1,925	2,683	32.53	7.01	11	33	51	52	2,258.88	2,200.53	2,200.53	18
37	Jab 9	2,276.19	1,868	2,670	32.82	7	10	34	51	52	2,250.81	2,182.33	2,191.63	16
38	Jab 20	2,276.16	1,876	2,629	32.76	8	12	34	51	52	2,263.70	2,227.69	2,221.25	17
39	Jab 21	2,253.82	1,854	2,629	34.10	9	13	35	51	53	2,231.06	2,156.66	2,156.66	18
40	Jab 22	2,233.35	1,859	2,620	35.37	10	13.05	37	52	53	2,214.37	2,130.35	2,130.35	18
41	CD-216	2,214.19	1,846	2,596	36.46	11	15.53	38	52	53	2,163.76	2,027.43	2,063.77	16
42	Jab 8	2,204.78	1,842	2,628	36.98	11.03	16	39	52	54	2,175.53	2,069.11	2,069.11	18
43	Jab 13	2,175.63	1,798	2,554	38.65	14.03	18	41	53	54	2,160.64	2,055.34	2,108.44	16
44	Jab 16	2,173.26	1,770	2,558	38.89	13	18	41	53	54	2,140.16	2,013.35	2,013.35	18
45	V-Max	2,148.40	1,651	2,722	38.56	7	11	42	55	55	2,244.82	2,234.26	2,174.49	16
46	Jab 37	2,139.46	1,696	2,492	40.57	15	20	42.75	54	55	2,092.06	1,905.08	1,954.90	17
47	Jab 17	2,112.46	1,622	2,591	40.85	12	16	44	55	55	2,063.98	1,103.34	1,103.34	6
48	Jab 14	2,107.45	1,708	2,476	42.34	18	24	44.75	54	55	2,058.68	1,884.88	1,884.88	18
49	Jab 12	2,105.07	1,598	2,541	41.19	13	17.53	44	55	55	2,056.02	1,614.92	1,614.92	7
50	Jab 48	2,098.04	1,683	2,485	42.53	19	23	45	54	55	2,041.42	1,857.68	1,857.68	18
51	Jab 15	2,037.59	1,668	2,451	45.45	23	28	48	55	55	1,984.18	1,767.43	1,767.43	18
52	Jab 26	2,015.36	1,615	2,368	46.09	25	29	49	55	55	1956.89	1,724.40	1,724.40	18
53	Jab 24	1,969.07	1,596	2,377	48.08	29	33	50.5	55	55	1,889.34	1,617.90	1,617.90	18
54	Jab 6	1,938.13	1,529	2,351	48.83	29.03	34	51	55	55	1,865.43	1,586.84	1,635.00	17
55	Jab 25	1,908.55	1,476	2,283	49.74	33	37	52	55	55	1,826.89	1,472.25	1,518.55	17

[1]Posterior of the credibility interval. [2]Genotypic value: general experimental mean + Blup + GE interaction mean. [3]Total of replicate number by which each genotype was evaluated.

Bayesian approach and the mixed model were similar to the heritability at mean level (h²mg), genotype selection accuracy (Acgen), and genetic variation coefficient (CVgi%) (Table 6). Besides, the heritability and genotypic correlation values between genotype behaviors corroborate the published literature if one takes into consideration the different grain yield (kg ha⁻¹) environments (Di Mauro et al., 2014). Accuracy values were classified as high in both the Bayesian and mixed model methodologies, as these methods showed values above 0.7 (Resende & Duarte, 2007).

The Bayesian approach showed the smallest GE interaction variance, showing the lowest determination coefficient of the GE interaction (c²int). Consequently, the genotypic correlation coefficient between genotypes in different environments (rgloc) increased up to the unit value. A rgloc value close to the unit in genotype selection implies a genotype-selection confidence increase in some tested environments (Resende, 2007).

The GE interaction defined that rgloc ≥ 0.80 in simulation studies, using the analysis of variance, indicates a simple interaction. A rgloc ≤ 0.20 evidences a complex interaction (Cruz & Castoldi, 1991). Thus, rgloc close to one indicates lesser complex GE interaction, adaptability, and stability because of the variation decrease of the environment (Rosado et al., 2012). The interaction effect is associated with two factors: the first simple one, which is the variability difference between genotypes in the environments;

and the second one (the complex factor), which is indicated by genotype superiority inconsistency with the environment variation. In other words, there are genotypes that shows a superior behavior in a certain environment, but the same genotype is not observed in another environment; so, it increases intricacy in the suggested selection (Cruz et al., 2012).

The predicted error variance (PEV) in genotype values and the standard deviation in genotypic variance values (SEP) in the Bayesian approach were smaller than those in the mixed model, indicating a better adjustment in the mean soybean genotype calculated a posteriori. The smaller PEC and SEP values are desirable for plant breeding programs because they are directly linked to precision and accuracy maximization (Resende & Suarte, 2007).

The advantages of using the Bayesian method in experimental data lies on its methodology, which

Table 6. Genetic parameters estimated through the analysis of variance, likelihood method, and Bayesian approach for soybean grain yield (kg ha⁻¹).

Genetic parameter	Analysis of variance	REML	Bayesian	CI 95% [lower; upper]
σ^2_g	103,486.10	102,260.30	84,841.57	
σ^2_{ge}	136,711.50	142,192.01	4,433.44	
σ^2_e	1,316,272.10	1,312,588.37	1,269,348.00	
σ^2_f	1,556,469.70	1,557,040.68	1,354,189.60	
h²mg	0.52	0.51	0.53	(0.39; 0.68)
Acgen	0.72	0.72	0.73	
c²int	0.09	0.09	0.003	
Rgloc	0.43	0.42	0.95	
CVgi%	13.53	13.55	12.36	
CVe%	48.26	48.55	47.79	
PEV	49,777.46	49,680.15	18,544.99	
SEP	223.11	222.89	136.18	
$\overline{M}$	2,377.26	2,360.06	2,357.51	

$\sigma^2_f = \sigma^2_g + \sigma^2_{ge} + \sigma^2_e$, phenotypic variance; σ^2_g, genotypic variance; σ^2_{ge}, genotypic x environment interaction variance; $c^2 int = \sigma^2_{ge}/\sigma^2_f$, determination coefficient of the GE interaction effect; σ^2_e, residual variance; $h^2mg = \sigma^2_g/\left(\sigma^2_g + \sigma^2_{ge}/N.env + \sigma^2_e/\left(N.env \times N.rep\right)\right)$ is the heritability at mean level (genotype); $Acgen = \sqrt{\left(1 - PEV/\sigma^2_g\right)}$ is the genotype selection accuracy; $CVgi = \sqrt{\sigma^2_g/\overline{M}}$ is the genetic coefficient variation; $CVe = \sqrt{\sigma^2_e/\overline{M}}$ is the environmental variation coefficient; $rgloc = \sigma^2_g/\left(\sigma^2_g + \sigma^2_{ge}\right)$ is the genotypic correlation between genotype behavior in several environments; $PEV = \left(1 - Acgen^2\right) \times \sigma^2_g$ is the error variance prediction; $SEP = \sqrt{PEV}$ is the standard deviation of progeny genotypic value; $\overline{M}$ is the overall mean; CI is the credibility interval; N.env is the number of environments; N.rep is the number of replicates.

Table 5. Correlation coefficient between means and ranks of all the assessed methods. Superior diagonal, Pearson correlation between mean genotypes and the inferior diagonal, Spearman correlation coefficient between genotype ranks for soybean grain yield (kg ha⁻¹).

	Bayesian	Blups	Lsmeans	Arithmetic
Bayesian	-	0.99742 <0.0001*	0.96775 <0.0001	0.96627 <0.0001
Blups	0.99740 <0.0001	-	0.97256 <0.0001	0.96945 <0.0001
Lsmeans	0.98954 <0.0001	0.99430 <0.0001	-	0.99629 <0.0001
Arithmetic	0.98867 <0.0001	0.99091 <0.0001	0.99019 <0.0001	-

*Significant by the t-test at 5% probability.

allows of the use of previous data information, presents a lesser sensitive modeling to outliers than the frequentist methods, and works well with lesser assumptions (large sample numbers, balance experiments, etc.) in analysis processes (Singh et al., 2015).

It is worth highlighting that the Bayesian approach applied to complex agriculture experimental data, such as years, crops, location, and interaction in the model, takes a bit longer than the mixed model in computer processes. Besides, with regard to specific cases based on prior information, the Bayesian analysis could assemble a posterior distribution, which would be highly influenced by the prior information. In this case, it is recommended to use the prior information as parsimony (Gelman, 2006).

Conclusions

1. The mixed models and the Bayesian methodology show similar genetic parameters.

2. The mean genotypic values obtained through the Bayesian approach differ from those obtained through the frequentist method.

3. The Bayesian approach uses previous soybean experimental data information that can be used as tools in soybean breeding programs.

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