# Adaptability and stability analysis of new popcorn simple hybrids evaluated using additive main effects and multiplicative interaction Bayesian approaches

Camila Rodrigues Castro<sup>1</sup>, Carlos Alberto Scapim<sup>1</sup>, Ronald José Barth Pinto<sup>1</sup>, Solenir Ruffato<sup>2</sup>, Douglas Mariani Zeffa<sup>1</sup>, Suzana Tiemi Ivamoto<sup>3</sup>, Gustavo Henrique Freiria<sup>3</sup>, Leandro Simões Azeredo Gonçalves<sup>3,\*</sup>

1. Universidade Estadual de Maringá Ron – Departamento de Agronomia – Maringá (PR), Brazil.

2. Universidade Federal de Mato Grosso 🔅 – Departamento de Agronomia – Cuiabá (MT), Brazil.

3. Universidade Estadual de Londrina 🔅 – Departamento de Agronomia – Londrina (PR), Brazil.

\*Corresponding author: leandrosag@uel.br Received: Nov. 9, 2020 | Accepted: Nov. 3, 2021

Section Editor: Luciana Carlini Garcia

How to cite: Castro, C. R., Scapim, C. A., Pinto, R. J. B., Ruffato, S., Zeffa, D. M., Ivamoto, S. T., Freiria, G. H. and Gonçalves, L. S. A. (2022) Adaptability and stability analysis of new popcorn simple hybrids evaluated using additive main effects and multiplicative interaction Bayesian approaches. Bragantia, 81, e1321. https://doi.org/10.1590/1678-4499.20200467

**ABSTRACT:** The development of new popcorn cultivars that include wide adaptation, high stability and superior performance characteristics is one of the main alternatives to mitigate the effects of the genotype × environment interaction. In this sense, our main goal was to evaluate the adaptability and stability of new popcorn hybrids using Bayesian additive main effects and multiplicative interaction (BAMMI) method for grain yield (GY) and popping expansion capacity (PE) traits. We evaluated GY and PE from 45 new popcorn hybrids and three commercial cultivars (IAC–125, Pop Top and Top Ten) as checks in six different environments. Genotype × environment interaction, correlation and stability analyses were performed using Bayesian approaches. The full models tested presented the lowest deviance information criterion (DIC) values when compared to null models, indicating the presence of the genotype × environment interaction for both evaluated agronomic traits. Negative correlations were observed between GY and PE (r = -0.24, 95% highest posterior density [HPD] = -0.31; -0.17) and confirm the difficulty to perform selection simultaneously for both characteristics. UEM–3 and UEM–7 hybrids showed wide stability and high *a posteriori* averages for GY and PE. Both cultivars can be registered and recommended for cultivation in popcorn producing regions. **Key words:** *Zea mays* var. *everta*, grain yield, popping expansion, genotype-environment interaction.

# INTRODUCTION

Popcorn (*Zea mays* var. *everta*) is a food snack widely appreciated in Brazilian market in different social classes. Brazil is the second largest consumer, behind only from the United States. In 2018, Brazil produced approximately 260 thousand tons of popcorn and generated a movement of US\$ 628 million dollars. In addition, there is a production growth projection of 48% in 2024 (Pereira Filho and Borghi 2019). In this context, the development and release of new popcorn cultivars is essential to avoid the dependence of foreign genotypes, to be able to attend producers and consumers demand as well to avoid the genetic vulnerability (Guimarães et al. 2018).

Before release new cultivars in the market, plant breeders need to perform experiments and investigate cultivars performance under different environmental conditions. Field experiments allow adaptation, stability and performance analysis of genotypes in facing different environmental conditions (Resende et al. 2019). Several statistical methods to study adaptability and stability have been developed and widely used in plant breeding programs (Annicchiarico 2002; Fasahat

et al. 2015). Additive main effects and multiplicative interaction analysis (AMMI) method stands out for its power to explain genotype × environment interaction, since it has greater capacity to capture the sum of the genotype × environment interaction squares compared to other methods (Gauch Junior 2013).

Some of the main methods used to evaluate adaptability and stability of new cultivars using Bayesian approaches are Eberhart and Russel (Couto et al. 2015; Euzebio et al. 2018), segmented regression (Nascimento et al. 2020), genotype plus genotype-by- environment interaction (GGE) biplot (Oliveira et al. 2016) and AMMI (Crossa et al. 2011; Freiria et al. 2020; Viele and Srinivasan 2000) methodologies. In general, Bayesian approaches to determine adaptability and stability show some advantages like the possibility to use data containing unbalanced structures, and/or under residual heterogeneity (Aczel et al. 2020). In addition, it allows to incorporate *a priori* information to obtain more accurate *a posteriori* estimation (Cotes et al. 2006; Silva et al. 2019).

The presence of credibility intervals for genotypic and environment scores is also considered an important advantage of AMMI Bayesian method in relation to AMMI frequentist (Oliveira et al. 2016). These credibility intervals lead to a greater precision to infer genotypic and environmental stability, since the subjectivity of the mean scores in relation to the proximity to the central point of the biplot (coordinates 0 and 0) is eliminated. Although there are no studies using Bayesian AMMI (BAMMI) model in popcorn, this method has been widely used to analyze adaptability and stability in several other crops (Bernardo Júnior et al. 2018; Corrêa et al. 2016; Teodoro et al. 2019; Zeffa et al. 2020).

In this study, our main goal was to evaluate adaptability and stability parameters using BAMMI approaches for grain yield and popping expansion capacity (PE) of new popcorn hybrids.

#### MATERIAL AND METHODS

# **Plant material**

We evaluated 45 simple popcorn hybrids developed by Breeding Program of Special Corn from Universidade Estadual de Maringá (UEM) and three commercial hybrids used as checks (IAC 125, Pop Top and Pop Ten). UEM's popcorn hybrids were originated from crosses between inbred lines obtained from eight commercial cultivars: Zélia (triple hybrid), UEM-M2 (open pollination variety), Zaeli (simple hybrid), IAC-112 (modified simple hybrid), IAC-125 (topcross hybrid), BRS Angela (open pollination variety), Maradona (open pollination variety) and Colombina (open pollination variety).

#### Environment localization and experimental design

We analyzed 48 popcorn hybrids in six different environments during 2016 and 2017 seasons (Table 1). Experiments were arranged in a complete randomized block design with three replications. Each plot consisted of two lines of 4 m and the spaced between lines was 0.90 m. Sowing was carried out with plants spaced 0.20 m apart, totaling 40 plants in a useful area of 7.2 m<sup>2</sup>. Base fertilization was applied using formulated fertilizer 8–20–20 (N–P<sub>2</sub>O<sub>2</sub>–K<sub>2</sub>O) in a proportion of 280 kg·ha<sup>-1</sup>.

Code	Location	State	Season	Coordinates	Altitude	<b>Climate</b> <sup>1</sup>
Env1	Londrina	Paraná	2016	23° 22´ 51° 22´	566 m	Cfa
Env2	Campo Novo dos Parecis	Mato Grosso	2016	13° 40´ 57° 53´	572 m	Aw
Env3	Maringá	Paraná	2016	23° 25´ 51° 57´	550 m	Cfb
Env4	Sabáudia	Paraná	2016	23° 19´ 51° 33´	725 m	Cfa
Env5	Londrina	Paraná	2017	23° 22´ 51° 22´	566 m	Cfa
Env6	Campo Novo dos Parecis	Mato Grosso	2017	13° 40´ 57° 53´	572 m	Aw

Table 1. Identification and characterization of six environments analyzed in this study

<sup>1</sup> Köppen climate classification= Cfa: humid subtropical climate; Cfb: Oceanic Temperate climate; Aw: Tropical savanna climate with dry-winter.

Nitrogen top-dressing fertilization with urea (250 kg·ha<sup>-1</sup>) was carried out at V6 development stage. Additional cultural treatments were carried out in accordance with the practices commonly adopted for popcorn crop.

#### Agronomic trait analysis

Grain yield (GY, kg·ha<sup>-1</sup> with moisture of 13.5%) values was obtained by measuring grain mass of each plot using Schmildt et al. (2001) methodology for stand correction. Popping expansion capacity ( $mL\cdot g^{-1}$ ) was determined from the average value of two samples composed by 30 g of grains (moisture of 13.5%) obtained from the central part of ears. Grain samples were expanded in an electric popcorn maker using a constant temperature of 280 °C for 2 min and 10 s. Expanded popcorn volume were evaluated in a 2,000 mL graduated beaker.

#### Statistical analyses

The presence of genotype × environment interaction was evaluated for GY and PE comparing the following models: (i) full model (considering double interaction between genotype × environment); and (ii) null model (considering interaction absence between genotype × environment). The full model follows the mathematical model shown in Eq. 1:

$$y_{ijk} = \mu + g_i + b_{j/k} + e_k + ge_{ik} + \varepsilon_{ijk} \tag{1}$$

where:  $\mu$  is the overall mean,  $g_i$  is the fixed effect of genotype *i*,  $b_{j/k}$  is the random effect of block *j* within environment *k*,  $e_k$  is the fixed effect of environment *k*,  $ge_{ik}$  is the fixed effect of genotype × environment interaction, and  $\varepsilon_{ijk} \sim N(0, \sigma^2)$  is the fandom effect of error associated with each experimental plot.

The marginal *a posteriori* distributions were performed considering noninformative *a priori* distributions for all model parameters using software R (https://www.r-project.org/) through the 'MCMCglmm' package (Hadfield 2010). A total of 1,000,000 values were generated by Markov Chain Monte Carlo (MCMC) process, assuming a burn-in period and thinning interval of 100,000 and 5 iterations, respectively. The MCMC convergence was verified using Heidelberger and Welch (1983) criteria through 'coda' package (Plummer et al. 2006).

All tested models were compared using deviance information criterion (DIC) as proposed by Spiegelhalter et al. (2002) (Eq. 2):

$$DIC = D(\bar{\theta}) + 2p_D \tag{2}$$

where:  $D(\overline{\theta})$  is a point estimate of the deviance obtained by replacing parameters with their respective *a posteriori* mean estimates in the likelihood function, while  $p_D$  is the effective number of parameters in the model. Models with smaller DIC should be preferred over models with higher DIC. However, differences (*D*) between DIC values of models *a* and *b* are given by  $D - |DIC_a - DIC_b|$ , and thus, if D < 5, there is no significant difference between compared models; if  $5 \le D \le 10$ , the difference is significant; and D > 10, the difference is highly significant.

Simple linear correlations analysis between GY and PE were performed using software R through the package 'BayesianFirstAid' (Bååth 2014). Median scores were reported with their respective 95% highest posterior density (HPD) intervals. Correlation estimates were considered significant when the HPD intervals did not overlap zero. The marginal *a posteriori* distributions were performed considering noninformative *a priori* distributions for all model parameters. A total of 100,000 values were generated by MCMC process, assuming a burn-in period and thinning interval of 10,000 and 10 iterations, respectively. The MCMC convergence diagnosis were verified using Heidelberger and Welch criteria (1983) through 'coda' package (Plummer et al. 2006).

Adaptability and stability of new popcorn hybrids were verified for GY and PE using BAMMI method following Eq. 3:

$$y = 1_n \mu + X_1 \tau + X_2 \delta + \sum_{k=1}^t \lambda_k \operatorname{diag}(X_1 \alpha_k) X_2 \gamma_k + \varepsilon$$
(3)

where:  $1_n$  is the vector of order  $n \times 1$ ,  $\mu$  is the overall mean,  $X_1$  is the genotypes matrix of order  $n \times g$ ,  $\tau$  is the effect vector  $g \times 1$  for genotypes,  $X_2$  and  $\delta$  are the matrices for environments of order  $n \times a$  and the effect vector  $a \times 1$  for environments, respectively.  $\lambda_k$  is the singular value for k<sup>th</sup> principal component, t is the number of multiplicative terms [ $t \le \min(g, a) - 1$ ),  $\alpha_k$  and  $\gamma_k$  are the singular vectors of k for genotypes and environments, respectively; and  $\varepsilon$  is the vector n of error effect. Vector  $\varepsilon$  has a multivariate normal distribution with zero mean and variance–covariance matrix  $\sigma_{\varepsilon}^2 I_n$ . In this way, vector y also has a multivariate normal distribution.

The parameters estimations of the equation model previously presented assume that the conditional distribution of *y*, given that  $\mu$ ,  $\tau$ ,  $\delta$ ,  $\lambda$ ,  $\alpha$ ,  $\gamma$ , and  $\sigma_s^2$  is a multivariate normal distribution:

$$y \mid \mu, \tau, \delta, \lambda, \alpha, \gamma, \sigma_{\varepsilon}^{2} \sim N\left(1_{n}\mu + X_{1}\tau + X_{2}\delta + \sum_{k=1}^{t}\lambda_{k} \operatorname{diag}(X_{1}\alpha_{k})X_{2}\gamma_{k}I_{n}\sigma_{\varepsilon}^{2}\right)$$
(4)

where:  $I_n$  is the identity matrix of order *n*. The *a priori* distributions used for the parameters were the same as proposed by Crossa et al. (2011):

$$\mu \mid \mu_{\mu}, \sigma_{\mu}^2 \sim N(\mu_{\mu}, \sigma_{\mu}^2) \tag{5}$$

$$\tau \mid \mu_{\tau}, \sigma_{\tau}^2 \sim N(\mu_{\tau}, I_g \sigma_{\tau}^2) \tag{6}$$

$$\delta \mid \mu_{\delta}, \sigma_{\delta}^2 \sim N(\mu_{\delta}, I_g \sigma_{\delta}^2) \tag{7}$$

 $\lambda_k \mid \mu_{\lambda_k}, \sigma_{\lambda_k}^2 \sim N^+ (\mu_{\lambda_k}, I_e \sigma_{\lambda_k}^2) \text{ and } \lambda_k > 0 \text{ and } \lambda_{k-1} \ge \lambda_k$ 

 $\sigma_k \sim$  spherical uniform distribution on the corrected subspace;  $\gamma_k \sim$  spherical uniform distribution on the corrected subspace; and

$$\sigma_e^2 \mid v_{e'}, \ s_e^2 \sim Inv - Scale - \chi^2 \left( v_e, \ S_e^2 \right)$$
(8)

where: *N* represents the normal distribution, *N*<sup>+</sup> is the positive normal distribution, and *Inv* – Scale –  $\chi^2$  is the inverse chisquare distribution. In our study, *a priori* distributions were noninformative, with zero being used as *a priori* distribution for the mean in all genotypic and environmental effects, and high values for the variances, which resulted in:  $\mu_{\mu} = 0$ ,  $\mu_{\tau} = 1_g \times 0$ ,  $\mu_{\delta} = 1a \times 0$  and  $\mu_{\lambda k} = 0$ , and for the variances  $\sigma_{\mu}^2, \sigma_{\tau}^2, \sigma_{\delta}^2$  and  $\sigma \lambda_k^2 = 1 \times 10^{15}$ . The *a posteriori* distribution was estimated as follows:

$$p(\mu,\tau,\lambda,\alpha,\gamma,\sigma_{\varepsilon}^{2}|y)$$
(9)

$$\propto \exp\left[-(1/2\,\sigma_{\mu}^{2})(\mu_{\mu}-\mu)'(\mu_{\mu}-\mu)
ight]$$
 (10)

$$x \exp \left[ -(1/2 \sigma_{\tau}^2)(\mu_{\tau} - \tau)'(\mu_{\tau} - \tau) \right]$$
(11)

$$x \exp\left[-\left(1/2\,\sigma_{\delta}^{2}\right)(\mu_{\delta}-\delta)'(\mu_{\delta}-\delta)\right]$$
(12)

$$x \prod_{k=1}^{t} \exp\left[-\left(1/2 \sigma_{\lambda}^{2}\right)(\mu_{\lambda} - \lambda_{k})'(\mu_{\lambda} - \lambda_{k})\right]$$
(13)

$$x \exp \{ -(1/2 \sigma_{\varepsilon}^{2}) [y - 1_{n}\mu + X_{1}\tau + X_{2}\delta + \sum_{k=1}^{t} \lambda_{k} \operatorname{diag}(X_{1}\alpha_{k})X_{2}\gamma_{k})' [y - 1_{n}\mu + X_{1}\tau + X_{2}\delta + \sum_{k=1}^{t} \lambda_{k} \operatorname{diag}(X_{1}\alpha_{k})X_{2}\gamma_{k})$$

$$(14)$$

$$\times \left\{ \left(\sigma_{\varepsilon}^{2}\right)^{-\left\{ \left[\frac{(n+\nu_{\varepsilon})}{2}\right] - 1 \right\}} \exp\left[-\left(1/2 \, \sigma_{\varepsilon}^{2}\right) \nu_{\varepsilon} s_{\varepsilon}^{2}\right] \right\}$$
(15)

A total of 1,000,000 values were generated by MCMC process, assuming a burn-in period and thinning interval of 100,000 and 5 iterations, respectively. The MCMC convergence was verified using Heidelberger and Welch (1983) criterion through 'coda' package (Plummer et al. 2006). The statistical analyses of BAMMI method were performed using R script developed by Crossa et al. (2011).

### **RESULTS AND DISCUSSION**

Based on our DIC values, genotype × environment interaction was observed for both evaluated agronomic traits, since full models presented lower DIC values when compared to null models for GY and PE (Table 2). The presence of genotype × environment interaction for GY and PE has been reported in several popcorn studies, corroborating with this study and indicating that differential behavior of genotypes is environment-dependent (Gerhardt et al. 2019; Paula et al. 2010; Pena et al. 2012; Peterlini et al. 2020). In addition, these results confirm that adaptability and stability evaluation are important to mitigate the effects of the genotype × environment interaction (Resende et al. 2019).

Correlation coefficients (*r*) between GY and PE was negative and showed low magnitude (r = -0.24, 95% HPD = -0.31; -0.17) (Table 2). The negative relationship between GY and PE was already reported in previous popcorn studies where authors reported the difficulty to simultaneously select the two most important agronomic traits for the popcorn breeding programs (Bombonato et al. 2020; Brocolli and Burak 2004; Cabral et al. 2016; Dofing et al. 1991). Dofing et al. (1991) reported a low phenotypic correlation coefficient ( $r_p = -0.34$ ; p < 0.01) between GY and PE in popcorn when they were evaluating this relationship. However, it was already reported a moderate magnitude of correlation between GY and PE (-0.67; p < 0.05) in a study using 90 popcorn hybrids (Cabral et al. 2016).

A posteriori means of environmental effects ( $\delta$ ) and their respective HPD intervals are shown in Table 3. Overall means ( $\mu$ ) of GY and PE were 2,024 kg·ha<sup>-1</sup> (95% HPD = 1,993.4; 2,054.4 kg·ha<sup>-1</sup>) and 28.6 mL·g<sup>-1</sup> (95% HPD = 27.5; 29.7 mL·g<sup>-1</sup>), respectively, emphasizing the high potential of some evaluated new popcorn hybrids. Regarding environmental effects, only Env1 and Env2 environments were considered as being favorable environments for GY, since their *a posteriori* means were positive and above overall average (Table 3). Env3 and Env4 environments were classified as favorable for PE trait, while Env1 and Env6 were considered as unfavorable environments. Env2 and Env5 environments did not have a defined classification, since their HPD intervals overlapped zero. These results indicate that environments favorable

**Table 2.** Deviance information criterion (DIC) for full model (considering interactions between genotype [G] × environment [E]) and null model (considering only additive effects between G and E) for grain yield and popping expansion capacity evaluated in 48 genotypes of popcorn in six environments and correlation between both traits.

Trait	DIC			
Trait	Full	Null	Correlation (95% HPD) <sup>1</sup>	
Grain yield (kg∙ha⁻¹)	13882.17	13933.44	0.24 ( 0.21, 0.17)	
Popping expansion (mL·g <sup><math>-1</math></sup> )	4507.95	4455.10	-0.24 (-0.31; -0.17)	

<sup>1</sup>Correlation coefficients are considered as significant when highest posterior density (HPD) intervals do not overlap the value of zero.

Parameter <sup>1/</sup>	Mean (95% HPD)		Environments		
Parameter	GY	PE	GY	PE	
$\delta_1$ (Env1)	651.8 (640.8; 662.7)	-3.1 (-4.3; -1.9)	Favorable	Unfavorable	
δ <sub>2</sub> (Env2)	1061.0 (1050.1; 1072.0)	– 0.1 (–1.3; 1.15)	Favorable	Undefined	
$δ_3$ (Env3)	–779.1 (–790.1; –768.1)	1.5 (0.3; 2.8)	Unfavorable	Favorable	
$\delta_4$ (Env4)	–728.9 (–739.8; –717.9)	4.2 (3.0; 5.4)	Unfavorable	Favorable	
δ <sub>5</sub> (Env5)	–102.7 (–113.7; –91.7)	0.9 (-0.3; 2.1)	Unfavorable	Undefined	
δ <sub>6</sub> (Env6)	-102.2 (-113.3; -91.3)	-3.4 (-4.7; -2.2)	Unfavorable	Unfavorable	
μ (mean)	2024.0 (1993.4; 2054.4)	28.6 (27.5; 29.7)			

**Table 3.** A posteriori mean of Bayesian additive main effects and multiplicative interaction (BAMMI) for grain yield (GY, kg·ha<sup>-1</sup>) and popping expansion capacity (PE, mL·g<sup>-1</sup>) of 48 popcorn genotypes in six environments for overall mean ( $\mu$ ) and environment effect ( $\delta$ ).

<sup>1/</sup>Environment description is showed in Table 2.

to GY can be classified as unfavorable for PE, emphasizing the difficulty of simultaneously select both interesting agronomic traits.

The *a posteriori* means of genotypic effects ( $\tau$ ) with their respective HPD intervals are shown in Table 4. Twenty-three popcorn hybrids presented *a posteriori* positive means with HPD intervals that did not overlap the zero value for GY, showing means above the overall average. Five new hybrids stood out: UEM–2 (428.6 kg·ha<sup>-1</sup>, 95% HPD = 416.6; 440.7 kg·ha<sup>-1</sup>), UEM–3 (493.9 kg·ha<sup>-1</sup>, 95% HPD = 481.9; 505.9 kg·ha<sup>-1</sup>), UEM–5 (639.6.6 kg·ha<sup>-1</sup>, 95% HPD = 627.6; 651.5 kg·ha<sup>-1</sup>), UEM–7 (390.8 kg·ha<sup>-1</sup>, 95% HPD = 378.8; 402.8 kg·ha<sup>-1</sup>) and UEM–39 (403.2 kg·ha<sup>-1</sup>, 95% HPD = 391.3; 415.17 kg·ha<sup>-1</sup>). In addition, 13 new hybrids (UEM–2, UEM–3, UEM–4, UEM–5, UEM–6, UEM–7, UEM–9, UEM–18, UEM–19, UEM–24, UEM–26, UEM–27 and UEM–39) showed *a posteriori* means higher than the best commercial check IAC–125 (195.0 kg·ha<sup>-1</sup>, 95% HPD = 183.2; 207.1 kg·ha<sup>-1</sup>).

For PE, 12 hybrids presented *a posteriori* positive means of genotypic effect ( $\tau$ ) with HPD intervals that did not overlap zero (Table 4). The hybrids that stood out the most were: IAC–125 (3.4 mL·g<sup>-1</sup>, 95% HPD = 2.1; 4.7 mL·g<sup>-1</sup>), Pop Top (2.9 mL·g<sup>-1</sup>, 95% HPD = 1.6; 4.3 mL·g<sup>-1</sup>), Pop Ten (6.1 mL·g<sup>-1</sup>, 95% HPD = 4.8; 7.5 mL·g<sup>-1</sup>), UEM–1 (2.9 mL·g<sup>-1</sup>, 95% HPD = 1.7; 4.3 mL·g<sup>-1</sup>), UEM–7 (2.7 mL·g<sup>-1</sup>, 95% HPD = 1.4; 4.0 mL·g<sup>-1</sup>) and UEM–38 (2.4 mL·g<sup>-1</sup>, 95% HPD = 1.1; 3.8 mL·g<sup>-1</sup>). Although the three commercial checks stood out in relation to PE, nine new hybrids (UEM–1, UEM–3, UEM–7, UEM–11, UEM–16, UEM–34, UEM–36, UEM–38 and UEM–43) presented *a posteriori* means statistically equivalent to IAC–125 and Pop Top cultivars, since their HPD intervals were overlapped.

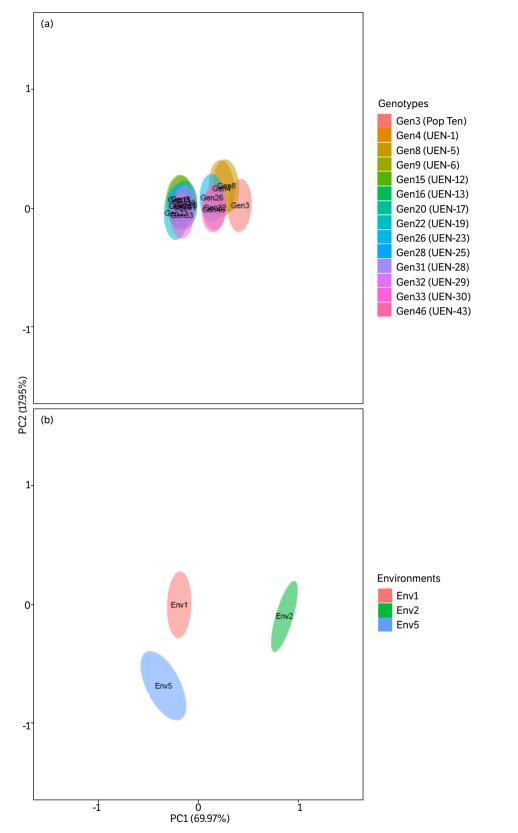
Genotypic and environmental scores with their respective HPD intervals for GY and PE traits are shown in Figs. 1 and 2, respectively. The first two principal components (PC1 and PC2) explained together 87.92 and 59.26% for GY and PE, respectively, of the total variation observed. The HPD intervals overlapping in the central point indicate the presence of genotypic or environmental stability. In addition, HPD intervals overlapping between genotypes or environments indicates similar responses between genotypes (Crossa et al. 2011; Oliveira et al. 2016). In relation to GY, the genotypic scores showed that 34 hybrids presented high stability since their HPD intervals overlapped with zero values on both axes (Fig. 1a). Wide behavioral stability was also observed for PE, since only UEM–24 and UEM–28 new hybrids were classified as unstable (Fig. 2a).

For the environment scores, Env1, Env2 and Env5 for GY, and Env2 and Env3 for PE were the environments which contributed more to genotype × environment interaction, since their HPD intervals did not overlap zero value on the axis of PC1 and PC2 simultaneously (Figs. 1b and 2b). These environments can be classified as being unstable environments and with low predictability (Crossa et al. 2011; Teodoro et al. 2019). Environmental stability refers to the reliability of the genotypes ordering in a given environment in relation to the classification of overall means (Bernardo Júnior et al. 2018; Lin and Binns 1994). In this context, Env3, Env4 and Env6 for GY and Env1, Env4, Env5 and Env6 for PE can be classified as stable environments, since they presented genotypes ranking with low discordance in relation to the classification of overall means.

**Table 4.** A posteriori mean of Bayesian additive main effects and multiplicative interaction (BAMMI) for grain yield (GY) and popping expansion capacity (PE) of 48 popcorn genotypes in six environments for overall mean ( $\mu$ ) and genotypic effects ( $\tau_i$ ) with their respective 95% highest posterior density (HPD).

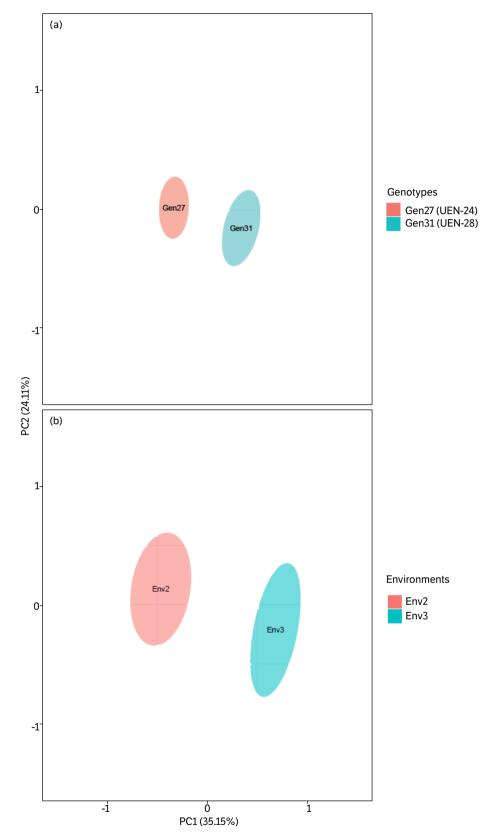
Parameter	Mean (959	% HPD)	Wide st	ability <sup>1/</sup>
Falametel	GY (kg·ha⁻¹)	PE (mL·g⁻¹)	GY	PE
τ <sub>1</sub> (IAC–125)	195.0 (183.2; 207.1)	3.4 (2.1; 4.7)	+	+
$\tau_2$ (Pop Top)	-314.3 (-326.3; -302.4)	2.9 (1.6; 4.3)	+	+
$\tau_{_3}$ (Pop Ten)	-66.2 (-78.1; 54.2)	6.1 (4.8; 7.5)	-	+
τ <sub>4</sub> (UEM–1)	-334.6 (-346.6; 322.5)	2.9 (1.7; 4.3)	-	+
τ <sub>5</sub> (UEM–2)	428.6 (416.6; 440.7)	-3.2 (-4.6; -1.9)	+	+
τ <sub>6</sub> (UEM–3)	493.9 (481.9; 505.9)	1.4 (0.1; 2.7)	+	+
τ <sub>7</sub> (UEM–4)	268.4 (256.37; 280.3)	-1.2 (-2.5; 0.1)	+	+
τ <sub>s</sub> (UEM–5)	639.6 (627.6; 651.5)	0.4 (-0.9; 1.7)	_	+
τ <sub>0</sub> (UEM–6)	470.1 (458.2; 481.9)	-1.4 (-2.8; -0.1)	_	+
τ <sub>10</sub> (UEM–7)	390.8 (378.8;402.8)	2.7 (1.4; 4.0)	+	+
τ <sub>11</sub> (UEM–8)	-46.5 (-58.4; 34.6)	1.2 (-0.1; 2.6)	+	+
τ <sub>12</sub> (UEM–9)	229.1 (217.1; 241.26)	-1.8 (-3.1; -0.5)	+	+
τ <sub>13</sub> (UEM–10)	70.8 (58.9; 82.8)	-0.7 (-2.1; 0.6)	+	+
τ <sub>14</sub> (UEM–11)	-43.7 (-55.7; 31.8)	1.5 (0.2; 2.9)	+	+
$\tau_{14}$ (UEM–12)	-942.9 (-954.8; -930.9)	-0.5 (-1.9; 0.8)	-	+
$\tau_{15}$ (UEM–13)	70.5 (58.5; 82.5)	1.2 (-0.1; 2.5)	_	+
τ <sub>17</sub> (UEM–13) τ <sub>17</sub> (UEM–14)	-257.1 (-268.9; -244.9)	0.7 (-0.6; 2.0)	+	+
$\tau_{17} (UEM-14)$ $\tau_{18} (UEM-15)$	-582.1 (-594.1; -570.1)	1.1 (-0.2; 2.5)	+	+
τ <sub>18</sub> (UEM–15) τ <sub>19</sub> (UEM–16)			+	+
15	-358.5 (-370.4; -346.6)	2.1 (0.8; 3.5)	т	
τ <sub>20</sub> (UEM–17)	-273.8 (-285.8; -261.8)	-0.4 (-1.7; 1.0)		+
τ <sub>21</sub> (UEM–18)	254.1 (242.1; 266.1)	-2.3 (-3.6; 0.9)	+	+
τ <sub>22</sub> (UEM–19)	309.2 (297.3; 321.2)	-3.8 (-5.1; -2.4)		+
τ <sub>23</sub> (UEM–20)	103.4 (91.3; 115.4)	-0.5 (-1.8; 0.9)	+	+
τ <sub>24</sub> (UEM–21)	-57.6 (-69.6; -45.7)	-3.9 (-5.3; -2.6)	+	+
τ <sub>25</sub> (UEM–22)	-40.7 (-52.6; -28.6)	0.6 (–0.7; 2.0)	+	+
τ <sub>26</sub> (UEM–23)	66.1 (54.2; 78.1)	–1.3 (–2.7; –0.0)	-	+
τ <sub>27</sub> (UEM–24)	343.4 (331.4; 355.2)	-2.8 (-4.12; -1.5)	+	-
τ <sub>28</sub> (UEM–25)	-6.3 (-18.3; 5.7)	-2.0 (-3.3; -0.7)	-	+
τ <sub>29</sub> (UEM–26)	264.6 (252.7; 276.5)	0.9 (–0.4; 2.3)	+	+
τ <sub>30</sub> (UEM–27)	359.8 (347.8; 371.7)	-0.8 (-2.2; 0.5)	+	+
τ <sub>31</sub> (UEM–28)	25.6 (13.7; 37.5)	-0.9 (-2.2; 0.4)	-	_
τ <sub>32</sub> (UEM–29)	113.6 (101.7; 125.7)	–1.3 (–2.7; –0.0)	-	+
τ <sub>33</sub> (UEM–30)	-88.8 (-100.7; -769)	-3.0 (-4.3; -1.7)	-	+
τ <sub>34</sub> (UEM–31)	-304.4 (-316.3; -292.5)	-0.4 (-1.8; 0.9)	+	+
τ <sub>35</sub> (UEM–32)	-61.5 (-73.6; -49.6)	–1.6 (–2.9; –0.2)	+	+
τ <sub>36</sub> (UEM–33)	11.4 (-0.1; 23.3)	1.3 (–0.0; 2.6)	+	+
τ <sub>37</sub> (UEM–34)	-255.8 (-267.8; -243.8)	1.6 (0.3; 2.9)	+	+
τ <sub>38</sub> (UEM–35)	-239.1 (-251.1; 227.2)	-1.9 (-3.2; -0.6)	+	+
τ <sub>39</sub> (UEM–36)	-411.8 (-423.9; 399.8)	1.9 (0.5; 3.2)	+	+
τ <sub>40</sub> (UEM–37)	-379.4 (-391.4; -367.5)	0.5 (-0.8; 1.9)	+	+
τ <sub>41</sub> (UEM–38)	106.3 (94.4; 118.4)	2.4 (1.1 3.8)	+	+
τ <sub>42</sub> (UEM–39)	403.2 (391.3; 415.1)	-1.6 (-2.9; -0.2)	+	+
τ <sub>43</sub> (UEM–40)	-338.0 (-349.9; -326.1)	0.5 (-0.8; 1.9)	+	+
τ <sub>44</sub> (UEM-41)	143.9 (131.8; 155.8)	0.5 (-0.8 1.9)	+	+
τ <sub>45</sub> (UEM-42)	-127.2 (-139.3; 115.3)	-1.9 (-3.3; -0.6)	+	+
τ <sub>45</sub> (UEM-43)	154.9 (142.9; 166.9)	2.2 (0.9; 3.6)		+
τ <sub>46</sub> (UEM–43) τ <sub>47</sub> (UEM–44)	-7.9 (-19.9; 4.1)	-0.3 (-1.7; 1.0)	+	+
τ <sub>47</sub> (UEM–44) τ <sub>48</sub> (UEM–45)			+	+
LAD (ULIVI-49)	–378.1 (–390.1; –366.3)	–0.6 (–1.9; 0.7)	Ŧ	Ť

 $^{\mbox{\tiny 1/}}$  Genotypes considered with (+) and without (–) wide stability based on Figs. 1 and 2.



<sup>1</sup>Hybrids and environment not plotted on the graphs showed HPD intervals overlapping with zero value in both principal components (PC1 and PC2). Env1 = Londrina (2016). Env2 = Campo Novo dos Parecis (2016). Env5 = Londrina (2017). Source. Elaborated by the authors.

Figure 1. Genotype (a) and environment (b) scores with their respective 95% highest posterior density (HPD) intervals of 48 popcorn hybrids evaluated for grain yield (kg·ha<sup>-1</sup>) in six environments.



<sup>1</sup>Hybrids and environment not plotted on the graphs showed HPD intervals overlapping with zero value in both principal components (PC1 and PC2). Env2 = Campo Novo dos Parecis (2016). Env3 = Maringá (2016). Source. Elaborated by the authors.

**Figure 2.** Genotype (a) and intervals environment (b) scores with their respective 95% highest posterior density (HPD) of 48 popcorn hybrids evaluated popping expansion capacity ( $mL\cdot g^{-1}$ ) in six environments.

Through the coordinates of PC1 and PC2 it is possible to infer about the specific adaptation of hybrids to certain environments (Figs. 1 and 2). In this sense, considering only hybrids and environments that showed significant contribution for genotype × environment interaction to GY, eight new hybrids (UEM–6, UEM–12, UEM–13, UEM–17, UEM–25, UEM–28, UEM–29 and UEM–33) showed specific adaptation to Env1, while six hybrids (Pop Ten, UEM–1, UEM–5, UEM–23, UEM–29 and UEM–43) showed specific adaptation to Env2 (Fig. 1b). In relation to PE, hybrids UEM–24 and UEM–28 showed specific adaptation to Env3 environments, respectively (Fig. 2b).

Although the selection of genotypes is carried out for specific environments, usually the plant breeders select stable genotypes that also showed high GY and PE overall means (Amaral Júnior et al. 2016; Bombonato et al. 2020; Scapim et al. 2010; Silva et al. 2013). In this way, the hybrids UEM–3 and UEM–7 stood out being highly stable and showing high GY and PE values (Table 4). For GY, both hybrids presented *a posteriori* means higher than the other three commercial checks, while for PE the *a posteriori* means of these hybrids were did not differ statistically to IAC–125 and Pop Top commercial checks. Therefore, UEM–3 and UEM–7 new hybrids have the potential to be registered as a cultivar in the Ministry of Agriculture, Livestock and Supply (MAPA – Ministério da Agricultura, Pecuária e Abastecimento) and recommended to popcorn producers.

#### CONCLUSION

Our results indicated the presence of genotype × environment interaction for GY and PE traits. Negative correlations were observed between GY and PE, confirming the difficulty to select popcorn genotypes with high GY and PE at the same time. In addition, we also observed that the favorable environments for GY were not always favorable for PE. UEM–3 and UEM–7 new hybrids are promising options to recommend for popcorn-producing regions, since they showed wide stability and high GY and PE values.

# **AUTHORS' CONTRIBUTION**

**Conceptualization:** Castro C. C., Scapim C. A., Zeffa D. M. and Gonçalves L. S. A.; **Investigation:** Castro C. C., Ruffato S., Barth Pinto R. J. and Scapim C. A.; **Writing – Original Draft:** Castro C. C., Zeffa D. M. and Gonçalves L. S. A.; **Writing – Review and Editing:** Scapim C. A., Ivamoto S. T. and Gonçalves L. S. A.; **Funding Acquisition:** Scapim C. A. and Barth Pinto R. J.; **Resources:** Scapim C. A. and Barth Pinto R. J.; **Supervision:** Scapim C. A. and Barth Pinto R. J.

### DATA AVAILABILITY STATEMENT

Data will be available upon request.

### FUNDING

Coordenação de Aperfeiçoamento de Pessoal de Nível Superior [https://doi.org/10.13039/501100002322] Finance Code 001

#### ACKNOWLEDGEMENTS

We acknowledge the Universidade Estadual de Maringá, Universidade Estadual de Londrina and Universidade Federal de Mato Grosso for the structure made available to carry out this research.

# REFERENCES

Aczel, B., Hoekstra, R., Gelman, A., Wagenmakers, E.-J., Klugkist, I. G., Rouder, J. N., Vandekerckhove, J., Lee, M. D., Morey, R. D., Vanpaemel, W., Dienes, Z. and van Ravenzwaaij, D. (2020). Discussion points for Bayesian inference. Nature Human Behaviour, 4, 561-563. https://doi.org/10.1038/s41562-019-0807-z

Amaral Júnior, A. T., Santos, A., Gerhardt, I. F. S., Kurosawa, R. N. F., Moreira, N. F., Pereira, M. G., Gravina, G. A. and Silva, F. H. L. (2016). Proposal of a super trait for the optimum selection of popcorn progenies based on path analysis. Genetics and Molecular Research, 15, 1-9. https://doi.org/10.4238/gmr15049309

Annicchiarico, P. (2002). Defining adaptation strategies and yield-stability targets in breeding programmes. In M.S. Kang (Ed.), Quantitative genetics, genomics and plant breeding (p. 365-383). Wallingford: CABI Publishing.

Bååth, R. (2014). Bayesian first aid: A package that implements Bayesian alternatives to the classical\*. test functions in R [Paper presentation]. Paper presented at the UseR!2014 – the International R User Conference.

Bernardo Júnior, L. A. Y., Silva, C. P., Oliveira, L. A., Nuvunga, J. J., Pires, L. P. M., Pinho, R. G. V. and Balestre, M. (2018). AMMI Bayesian Models to Study Stability and Adaptability in Maize. Agronomy Journal, 110, 1765-1776. https://doi.org/10.2134/agronj2017.11.0668

Bombonato, A. L., Carvalho, H. F., Rocha, D. S., Sawazaki, E., Barros, V. L. N. P. and Paterniani, M. E. A. G. Z. (2020). Selection Index and Genetic Parameters in Tropical Popcorn Hybrids. Tropical Plant Biology, 13, 382-388. https://doi.org/10.1007/s12042-020-09264-1

Broccoli, A. M. and Burak, R. (2004). Effect of genotype x environment interactions in popcorn maize yield and grain quality. Spanish Journal of Agricultural Research, 1, 85-92. https://doi.org/10.5424/sjar/2004021-64

Cabral, P. D. S., Amaral Júnior, A. T., Freitas, I. L. J., Ribeiro, R. M. and Silva, T. R. C. (2016). Relação causa e efeito de caracteres quantitativos sobre a capacidade de expansão do grão em milho-pipoca. Revista Ciência Agronômica, 47, 108-117. https://doi. org/10.5935/1806-6690.20160013

Corrêa, A. M., Teodoro, P. E., Gonçalves, M. C., Barroso, L. M. A., Nascimento, M., Santos, A. and Torres, F. E. (2016). Adaptability and phenotypic stability of common bean genotypes through Bayesian inference. Genetics and Molecular Research, 15, 1-11. https://doi.org/10.4238/qmr.15028260

Cotes, J. M., Crossa, J., Sanches, A. and Cornelius, P. L. (2006). A Bayesian Approach for Assessing the Stability of Genotypes. Crop Science, 46, 2654-2665. https://doi.org/10.2135/cropsci2006.04.0227

Couto, M. F., Nascimento, M., Amaral Júnior, A. T., Silva, F. F., Viana, A. P. and Vivas, M. (2015). Eberhart and Russel's Bayesian Method in the Selection of Popcorn Cultivars. Crop Science, 55, 571-577. https://doi.org/10.2135/cropsci2014.07.0498

Crossa, J., Perez-Elizalde, S., Jarquin, D., Cotes, J. M., Viele, K., Liu, G. and Cornelius, P. L. (2011). Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model. Crop Science, 51, 1458-1469. https://doi.org/10.2135/cropsci2010.06.0343

Dofing, S. M., D'Croz-Mason, N. and Thomas-Compton, M. A. (1991). Inheritance of Expansion Volume and Yield in Two Popcorn × Dent Corn Crosses. Crop Science, 31, 715-718. https://doi.org/10.2135/cropsci1991.0011183X003100030035x

Euzebio, M. P., Fonseca, I. C. B., Fonseca Júnior, N. S., Nascimento, M., Giordani, W. and Gonçalves, L. S. A. (2018). Adaptability and stability assessment of bean cultivars of the carioca commercial group by a Bayesian approach. Acta Scientiarum Agronomy, 40, e35015. https://doi.org/10.4025/actasciagron.v40i1.35272

Fasahat, P., Rajabi, A., Mahmoudi, S. B., Noghabi, M. A. and Rad, J. M. (2015). An overview on the use of stability parameters in plant breeding. Biometrics & Biostatistics International Journal, 2, 149-159. https://doi.org/10.15406/bbij.2015.02.00043

Freiria, G. H., Gonçalves, L. S. A., Zeffa, D. M., Lima, W. F., Fonseca Júnior, N. S., Prete, C. E. C. and Fonseca, I. C. B. (2020). Bayesian AMMI applied to food-type soybean multi-environment trials. Revista Ciência Agronômica, 51, e20207333. https://doi.org/10.5935/1806-6690.20200077

Gauch Junior, H. G (2013). A Simple Protocol for AMMI Analysis of Yield Trials. Crop Science, 53, 1860-1869. https://doi.org/10.2135/ cropsci2013.04.0241

Gerhardt, I. F. S., Amaral Junior, A. T., Pena, G. F., Guimarães, L. J. M., Lima, V. J., Vivas, M., Santos, P. H. A. D., Ferreira, F. R. A., Freitas, M. S. M. and Kamphorst, S. H. (2019). Genetic effects on the efficiency and responsiveness to phosphorus use in popcorn as estimated by diallel analysis. PLOS ONE, 14, e0216980. https://doi.org/10.1371/journal.pone.0216980

Guimarães, A. G., Amaral Júnior, A. T., Lima, V. J., Leite, J. T., Scapim, C. A. and Vivas, M. (2018). Genetic gains and selection advances of the UENF-14 popcorn population. Revista Caatinga, 31, 271-278. https://doi.org/10.1590/1983-21252018v31n202rc

Hadfield, J. D. (2010). MCMC Methods for Multi-Response Generalized Linear Mixed Models: The MCMCglmm R Package. Journal of Statistical Software, 33, 1-22.

Heidelberger, P. and Welch, P. D. (1983). Simulation Run Length Control in the Presence of an Initial Transient. Operations Research, 31, 1109-1144. https://doi.org/10.1287/opre.31.6.1109

Lin, C. S. and Binns, M. R. (1994). Concepts and Methods for Analyzing Regional Trial Data for Cultivar and Location Selection. In J. Janick (Ed.), Plant Breeding Reviews, Volume 12 (p. 271-297). Hoboken: John Wiley & Sons. https://doi.org/10.1002/9780470650493.ch10

Nascimento, M., Nascimento, A. C. C., Silva, F. F., Teodoro, P. E., Azevedo, C. F., Oliveira, T. R. A., Amaral Junior, A. T., Cruz, C. D., Farias, F. J. C. and Carvalho, L. P. (2020). Bayesian segmented regression model for adaptability and stability evaluation of cotton genotypes. Euphytica, 216, 30. https://doi.org/10.1007/s10681-020-2564-5

Oliveira, L. A., Silva, C. P., Nuvunga, J. J., Silva, A. Q. and Balestre, M. (2016). Bayesian GGE biplot models applied to maize multienvironments trials. Genetics and Molecular Research, 15, gmr.15028612. http://doi.org/10.4238/gmr.15028612

Paula, T. O. M., Amaral Júnior, A. T., Gonçalves, L. S. A., Scapim, C. A., Peternelli, L. A. and Silva, V. Q. R. (2010). Pi statistics underlying the evaluation of stability, adaptability and relation between the genetic structure and homeostasis in popcorn. Acta Scientiarum. Agronomy, 32, 269-277. https://doi.org/10.4025/actasciagron.v32i2.7312

Pena, G. F., Amaral Júnior, A. T., Gonçalves, L. S. A., Candido, L. S., Vittorazzi, C., Ribeiro, R. M. and Freitas Júnior, S. P. (2012). Stability and adaptability of popcorn genotypes in the State of Rio de Janeiro, Brazil. Genetics and Molecular Research, 11, 3042-3050. https://doi.org/10.4238/2012.August.31.1

Pereira Filho, I. A. and Borghi, E. (2019). Milho-pipoca é um novo atrativo para o produtor? Campo & Negócios. [Accessed Ago. 09, 2021]. Available at: https://revistacampoenegocios.com.br/milho-pipoca-e-um-novo-atrativo-para-o-produtor/

Peterlini, E., Pinto, R. J. B., Scapim, C. A., Rizzardi, D. A., Bertagna, F. A. B. and Amaral Júnior, A. T. (2020). Diallel analysis of popcorn populations for yield, popping expansion and resistance to fall armyworm. Revista Ceres, 67, 288-295. https://doi.org/10.1590/0034-737x202067040006

Plummer, M., Best, N., Cowles, K. and Vines, K. (2006). CODA: convergence diagnosis and output analysis for MCMC. R news, 6, 7-11.

Resende, R. T., Piepho, H. P., Silva-Junior, O. B., Silva, F. F., Resende, M. D. V. and Grattapaglia, D. (2019). Enviromics in breeding: applications and perspectives on envirotypic-assisted selection. BioRxiv, 726513. https://doi.org/10.1101/726513

Scapim, C. A., Amaral Júnior, A. T., Vieira, R. A., Moterle, L. M., Texeira, L. R., Viganó, J. and Sandoval Júnior, G. B. (2010). Novos compostos de milho-pipoca para o Brasil. Semina: Ciências Agrárias, 31, 321-329. https://doi.org/10.5433/1679-0359.2010v31n2p321

Schmildt, E. R., Cruz, C. D., Zanuncio, J. C., Pereira, P. R. G. and Ferrão, R. G. (2001). Avaliação de métodos de correção do estande para estimar a produtividade em milho. Pesquisa Agropecuária Brasileira, 36, 1011-1018. https://doi.org/10.1590/S0100-204X2001000800002

Silva, C. P., Oliveira, L. A., Nuvunga, J. J., Pamplona, A. K. A. and Balestre, M. (2019). Heterogeneity of Variances in the Bayesian AMMI Model for Multienvironment Trial Studies. Crop Science, 59, 2455-2472. https://doi.org/10.2135/cropsci2018.10.0641Silva,

T. R. C., Amaral Júnior, A. T., Gonçalves, L. S. A., Candido, L. S., Vittorazzi, C. and Scapim, C. A. (2013). Agronomic performance of popcorn genotypes in Northern and Northwestern Rio de Janeiro State. Acta Scientiarum. Agronomy, 35, 57-63. https://doi.org/10.4025/actasciagron.v35i1.15694

Spiegelhalter, D. J., Best, N. G., Carlin, B. P., van der Linde, A. (2002). Bayesian measures of model complexity and fit. Journal of the Royal Statistical Society: Series B (Statistical Methodology), 64, 583-640. https://doi.org/10.1111/1467-9868.00353

Teodoro, P. E., Azevedo, C. F., Farias, F. J. C., Alves, R. S., Peixoto, L. A., Ribeiro, L. P., Carvalho, L. P. and Bhering, L. L. (2019). Adaptability of cotton (*Gossypium hirsutum*) genotypes analysed using a Bayesian AMMI model. Crop & Pasture Science, 70, 615-621. https://doi. org/10.1071/CP18318

Viele, K. and Srinivasan, C. (2000). Parsimonious estimation of multiplicative interaction in analysis of variance using Kullback–Leibler Information. Journal of Statistical Planning and Inference, 84, 201-219. https://doi.org/10.1016/S0378-3758(99)00151-2

Zeffa, D. M., Moda-Cirino, V., Medeiros, I. A., Freiria, G. H., Santos Neto, J., Ivamoto-Suzuki, S. T., Delfini, J., Scapim, C. A. and Gonçalves, L. S. A. (2020). Genetic Progress of Seed Yield and Nitrogen Use Efficiency of Brazilian carioca Common Bean Cultivars Using Bayesian Approaches. Frontiers in Plant Science, 11, 1168. https://doi.org/10.3389/fpls.2020.01168