Updating Knowledge in The Estimation of The Genetics Parameters Multi-trait and Multi-Environment Bayesian Analysis in Rice (Oryza Sativa L.)

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Updating knowledge in the estimation of the genetics parameters Multi-trait and Multi-Environment Bayesian analysis in rice (Oryza sativa L.)

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Abstract
Among the multi-trait models used to jointly study several traits and environments, the Bayesian framework has been a preferable tool for using a more complex and biologically realistic model. In most cases, the non-informative prior distributions are adopted in studies using the Bayesian approach. Still, the Bayesian approach tends to present more accurate estimates when it uses informative prior distributions. The present study was developed to evaluate the efficiency and applicability of multi-trait multi-environment (MTME) models under a Bayesian framework utilizing a strategy for eliciting informative prior distribution using previous data from rice. The study involved data pertained to rice genotypes in three environments and five agricultural years (2010/2011 until 2014/2015) for the following traits: grain yield (GY), flowering in days (FLOR) and plant height (PH). Variance components and genetic and non-genetic parameters were estimated by the Bayesian method. In general, the informative prior distribution in Bayesian MTME models provided higher estimates of heritability and variance components, as well as minor lengths for the highest probability density interval (HPD), compared to their respective non-informative prior distribution analyses. The use of more informative prior distributions makes it possible to detect genetic correlations between traits, which cannot be achieved with the use of non-informative prior distributions. Therefore, this mechanism presented for updating knowledge to the elicitation of an informative prior distribution can be efficiently applied in rice genetic selection.

Keywords: Selection, Genetic Correlation, Genetic Improvement, Heritability.

Declarations

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Conflicts of interest/Competing interests
The authors have no conflicts of interest to declare that are relevant to the content of this article.

Availability of data and material
Not applicable.

Code availability
Not applicable.
Introduction

Rice is one of the most important sources of the global population’s daily caloric and nutritional requirement (FAO, 2020). The global population is increasing, but the available area of suitable wetland is decreasing (Ray et al., 2013). Therefore, the need to increase crop productivity rather than expand agricultural land has grown over the years (Lobell et al., 2011; Phalan et al., 2011; Ray et al., 2013). It is estimated that by 2050 the agricultural production of rice should be between 60 and 110% (Hunter et al., 2017; Juliana et al., 2019). Thus, in rice cultivation, the evaluation of multiple traits aims to maximize grain yield potential (Liang et al., 2021).

In general, in a plant breeding program aimed to identify the most genetically superior genotypes, selection is based on only one trait (Suela et al., 2019; Parimala et al., 2020; Sabri et al., 2020). While interesting, this approach can cause problems if its performance in the other trait desired is not evaluated (Cruz et al., 2014). The genetic evaluation of multiple traits is relevant because superior varieties combine optimal attributes for several traits simultaneously in plant breeding (Torres et al., 2018). In these cases, the selection can be made indirectly, based on secondary traits of low environmental influence, easy to measure and genetically correlated with the target trait, which is a very interesting alternative to maximize accuracy (Santos et al., 2018).

Among the multi-trait models used for modeling jointly several traits and environment, the Bayesian framework has been a preferable tool for using a more complex and biologically realistic model (Dunson, 2001). In addition, Bayesian estimates tend to be less biased and produce more precise interval estimates when there are few observations (Sorensen and Gianola, 2002). Some studies have demonstrated the potential of the Bayesian approach for genetic evaluation in plant breeding considering multi-trait evaluation (Torres et al. 2018, Azevedo et al., 2019, Volpato et al., 2019, Peixoto et al., 2021). However, in most of these studies, non-informative prior distributions are used. In these situations, despite the bayesian advantages over interpretations, the estimates are close to frequentist analysis (Gamerman and Lopes, 2006). In addition, the Bayesian approach tends to present more accurate estimates than the
frequentist when it uses informative prior distributions (van de Schoot et al., 2021). Thus, informative prior
distributions should be preferable for breeding purposes to improve the accuracy of the selection process.

Silva et al. (2013) and Azevedo et al. (2022) presented a system, respectively, for updating
knowledge about the hyperparameters from the prior distributions of the variance components in the
univariate analysis in maize and white oat breeding, using the phenotypic data collected in different years.
However, these procedures for eliciting informative prior distributions have not been presented yet for
multi-trait analysis. Furthermore, although multi-trait and multi-environment studies in rice have already
been reported in the literature (Bhandari et al., 2019, Yu et al., 2019, Ahmadi et al., 2021, Sharma et al.,
2021), the combination of multi-trait models under a multi-environment under a Bayesian framework with
informative prior, so far, has not been investigated.

Thus, the present study aimed to evaluate different strategies for eliciting informative prior
distribution using previous data from rice. For such, phenotypic data of four traits associated with eighteen
genotypes of rice evaluated in five agricultural years were used.

Materials and methods

Experimental data

The field experiment was carried out in the experimental area of the Empresa de Pesquisa
Agropecuária de Minas Gerais (EPAMIG) in the municipalities of Janaúba (15° 48’ 77” S, 43° 17’ 59.09”
W), Lambari (21° 58’ 11.24” S, 45° 20’ 59.6” W) and Leopoldina (21° 31’ 55” S, 42° 38’ 35” W). In this
experiment, eighteen rice genotypes were evaluated for the flood irrigated rice breeding program. Among
these genotypes, five cultivars were used as experimental controls (Rubelita, Seleta, Ourominas, Predileta,
and Rio Grande). Grain yield (kg ha\(^{-1}\) - GY), flowering in days (FLOR) and plant height (cm - PH) were
also evaluated from the agricultural year 2010/2011 to 2014/2015. All experiments were arranged in
randomized block design with three replications.

The useful area consisted of 4 m of three internal rows (4 × 0.9 m, 3.60 m\(^2\)). The experiments were
conducted on floodplain soils with continuous flood irrigation. The cultural treatments were carried out
according to the recommendations for irrigated rice cultivation in the evaluated regions (Soares et al., 2005).

Model and Bayesian inference

The fitted multi-trait statistical model was given by:

\[ y = Xb + Z_1r + Z_2u + e \]

Which can be rewritten as:
\begin{align*}
\begin{bmatrix}
  y_{11} \\
  y_{12} \\
  y_{13} \\
  \vdots \\
  y_{21} \\
  y_{22} \\
  y_{23} \\
  \vdots \\
  y_{31} \\
  y_{32} \\
  y_{33}
\end{bmatrix}
= X
\begin{bmatrix}
  b_{11} \\
  b_{12} \\
  b_{13} \\
  \vdots \\
  b_{21} \\
  b_{22} \\
  b_{23} \\
  \vdots \\
  b_{31} \\
  b_{32} \\
  b_{33}
\end{bmatrix}
+ Z_1
\begin{bmatrix}
  r_{11} \\
  r_{12} \\
  r_{13} \\
  \vdots \\
  r_{21} \\
  r_{22} \\
  r_{23} \\
  \vdots \\
  r_{31} \\
  r_{32} \\
  r_{33}
\end{bmatrix}
+ Z_2
\begin{bmatrix}
  u_{11} \\
  u_{12} \\
  u_{13} \\
  \vdots \\
  u_{21} \\
  u_{22} \\
  u_{23} \\
  \vdots \\
  u_{31} \\
  u_{32} \\
  u_{33}
\end{bmatrix}
+ \begin{bmatrix}
  e_{11} \\
  e_{12} \\
  e_{13} \\
  \vdots \\
  e_{21} \\
  e_{22} \\
  e_{23} \\
  \vdots \\
  e_{31} \\
  e_{32} \\
  e_{33}
\end{bmatrix}
\end{align*}

where \( y_{ij} \) is the vector of phenotypic values of the \( i \)-th trait \((i = 1, 2, 3)\) in the \( j \)-th environment \((j = 1, 2, 3)\); \( b_{ij} \) is the vector of systematic effects of \( j \)-th environment in the \( i \)-th trait, \( r_{ij} \) is the block effects of the \( i \)-th trait in the \( j \)-th environment and \( e_{ij} \) is the residual vector of the \( i \)-th trait in the \( j \)-th environment. \( X \) is the incidence matrix of systematic effects, \( Z_1 \) is the incidence matrix of block effects and \( Z_2 \) is the incidence matrix of genotype effects.

The prior distributions for the parameters of the model were given by:

\begin{align*}
  \beta &\sim N(\mu, I \otimes \Sigma_b) \\
  \tau &\sim N(0, I \otimes \Sigma_r) \\
  \nu &\sim N(0, I \otimes \Sigma_u) \\
  \epsilon &\sim N(0, I \otimes \Sigma_e)
\end{align*}

where \( I \) is the identity matrix, \( \Sigma_b, \Sigma_r, \Sigma_u, \) and \( \Sigma_e \) are the (co)variance matrix estimates with prior distributions given by:

\begin{align*}
  \Sigma_b &\sim IW(I, 0.002) \\
  \Sigma_r &\sim IW(\mathbf{V}_r, \eta_r) \\
  \Sigma_u &\sim IW(\mathbf{V}_u, \eta_u) \\
  \Sigma_e &\sim IW(\mathbf{V}_e, \eta_e)
\end{align*}

where \( IW \) is the inverted Wishart distribution, \( \mathbf{V}_r, \mathbf{V}_u, \) and \( \mathbf{V}_e \) are matrices with known values and \( \eta_r, \eta_u \) and \( \eta_e \) are known constants called hyperparameters. The \( j \)-th value of the chain of additive genetic heritability associated with \( i \)-th trait, \( h^2_{i(j)} \), is given by:

\[ h^2_{i(j)} = \frac{\sigma_{u(i)}^{2(j)}}{\sigma_r^{2(j)} + \sigma_u^{2(j)} + \sigma_e^{2(j)}} \]

where \( \sigma_r^{2(j)}, \sigma_u^{2(j)} \) and \( \sigma_e^{2(j)} \) are, respectively, block, genetic and residual variances of \( j \)-th iteration and \( i \)-th trait. The \( j \)-th value of the chain of genetic correlation between traits \( i \) and \( k \), \( r_{ik}^{(j)} \), is given by:
\[ r_{lk}^{(j)} = \frac{\sigma_{u(ik)}^{(j)}}{\sqrt{\sigma_{u(i)}^{2(j)} \sigma_{u(k)}^{2(j)}}} \]

where \( \sigma_{u(ik)}^{(j)} \) is the genetic covariance between traits i and k, \( \sigma_{u(i)}^{2(j)} \) is the genetic variance of i-th trait and \( \sigma_{u(k)}^{2(j)} \) is the genetic variance of k-th trait. The j-th value of the chain of genetic correlation between environments \( l \) and \( h \), \( r_{lh}^{(j)} \), is given by:

\[ r_{lh}^{(j)} = \frac{\sigma_{u(lh)}^{(j)}}{\sqrt{\sigma_{u(l)}^{2(j)} \sigma_{u(h)}^{2(j)}}} \]

where \( \sigma_{u(lh)}^{(j)} \) is the genetic covariance between environments \( l \) and \( h \), \( \sigma_{u(i)}^{2(j)} \) is the genetic variance of \( l \)-th environment and \( \sigma_{u(h)}^{2(j)} \) is the genetic variance of \( h \)-th environment.

The relative variation index is the ratio of the coefficient of genotypic variation to the coefficient of residual variation, this is \( CV_g / CV_e \).

The informativeness of prior distribution is associated with the values of the hyperparameters and, consequently, in this study, with the (co)variance matrices of the normal distribution (van de Schoot et al., 2021). Thus, we consider \( V_r = V_u = V_e = 1 \) and \( \eta_r = \eta_u = \eta_e = 2 \) (Hadfield, 2010) for analyses using non-informative prior distributions. Furthermore, we know that, if \( \Sigma \sim IW(V, \eta) \) (the dimension of \( \Sigma \) is 3x3), then the expected value of \( \Sigma \) is given by \( \frac{V \eta}{\eta - 10} \) where \( \eta \geq 10 \) and the mode of \( \Sigma \) is given by \( \frac{V \eta}{\eta + 10} \).

Thus, the average of (co)variance components \( \langle \Sigma \rangle \) and its respective mode \( \langle M_o \rangle \) were calculated from a set of values reported in these studies and equalized to the expectation and mode of \( \Sigma \sim IW(V, \eta) \) distribution. Through these expressions, it is possible to find the following equality: \( \eta = \frac{10(\Sigma_{11} + M_{o11})}{\Sigma_{11} - M_{o11}} \) and

\[ V = \frac{\eta - 10}{\eta}. \]

A similar procedure was used by Silva et al. (2013) to select hyperparameters for inverse gamma prior distributions (mean and variance) in univariate Bayesian inference of mixed models in quantitative genetics of crop species, while Azevedo et al. (2022) used it to select hyperparameters for inverse gamma prior distributions (mean and mode) in univariate Bayesian inference in white oat.

Based on phenotypic databases containing several years of collection, it is possible to update the hyperparameters and, consequently, our knowledge regarding the (co)variance matrices. Azevedo et al. (2022) demonstrated in univariate analyses with ten years of data that the procedure for updating knowledge for the year \( k \)-th should be carried out only with information from the (k-1)-th year. Thus, the hyperparameters were calculated by analyzing the \( (k - 1) \)-th year with the expression above. Therefore, in this work, two approaches were performed aiming to evaluate different strategies for eliciting informative prior distribution: i) five analyses considering year by year separately and non-informative prior distributions; ii) five analyses considering year by year separately for the construction of informative prior distributions.
The following parameters were calculated to assess the impact of prior knowledge insertion: i) the posterior coefficient of variation (CV) of the estimates of the components of variance, heritability, genetic correlation and additive genetic values; ii) length of the Highest Posterior Density intervals (HPD) of the parameter estimates; iii) the deviance information criterion (DIC), when possible, since the quality of the fit can only be compared using the DIC when the model uses the same data; iv) agreement between genetic estimates by non-informative and informative prior distribution, considering 30% of the selection differential (total of 6 genotypes).

All computational implementations of the analysis were performed using the R software program (R Core Team, 2021). The model was fitted in the MCMCglmm package (Hadfield, 2010) through the MCMCglmm function from the R software system (R Core Team, 2021). A total of 3,000,000 samples were generated, assuming a burnin period and sampling interval of 100,000 and 10 iterations, respectively, which resulted in 290,000 samples. The convergence of MCMC was assessed by the Geweke’s diagnostic (Geweke, 1992), which was performed using the CODA R package (Plummer et al., 2006).

Results and discussion

Model selection and convergence of parameters

Overall, except for the agricultural years 2012-2013, the full model (model with the interaction effect) presented lower DIC values, compared with those obtained from the reduced model (model without the interaction effect) (Table 1). The smaller values of DIC indicates better goodness-of-fit of the full model (Spiegelhalter et al., 2014).

Insert Table 1

For all parameters, the p-values of Geweke’s Z statistics were greater than 1% significance (Tables 2 and 3), which indicates that the convergence was achieved, and the inferences can be performed.

Insert Table 2

Insert Table 3

Comparison between informative and non-informative prior distributions

The smaller posterior coefficient of variation (CV) values of the genetic variance and heritability (Table 2) and genetic correlation (Table 3) were observed considering the informative prior to the estimation process. In this approach, the hyperparameters from the prior distributions were obtained by analyzing the previous year. Therefore, the length of the HPD interval is also smaller due to the higher precision provided by this informative prior (Tables 2 and 3). The same results were found by Azevedo et al. (2022) considering univariate analyses in white oat (Avena sativa L.). However, the same was not observed for genetic values. In most analyses, the CV of genetic value presented increased amplitude in the informative priors. Despite these amplitude values, considering a selection differential of 30%, the agreement between the selected genotypes in both prior distributions is above 50% (Table 4).
Considering the results obtained by the informative priors, the estimates of heritability for GY, FLOR and PH were low to high, respectively, with 0.27 [0.25;0.29], 0.47 [0.21; 0.74] and 0.79 [0.77; 0.80] for the locality of Janaúba, 0.21 [0.20;0.23], 0.62 [0.60; 0.64] and 0.43 [0.40; 0.45] for locality of Lambari and 0.14 [0.13;0.15], 0.77 [0.76; 0.79] and 0.58 [0.56; 0.60] for the locality of Leopoldina (Table 2). It is worth to emphasize that the low heritability values observed depend on the number of evaluated genotypes, since the used Bayesian approach is essentially recommended for small sample sizes (Torres et al., 2018). In addition, GY is quantitative and highly affected by the environment (Rao et al., 2017; Li et al., 2018; Kumar et al., 2019; Zhang et al., 2020).

It was observed increased additive genetic variance and heritability with the use of informative prior about the results of the non-informative prior distribution for all traits, except for PH, in the locality of Lambari, and FLOR, in the locality of Janaúba (Table 2). Among the 18 rice genotypes evaluated, the trait GY in the Janaúba locality obtained the highest additive genetic variance, while the smallest value was found for PH in the Lambari locality. It was also observed the highest heritability value of 0.79 in the Janaúba locality for PH and the lowest heritability for GY, with a value of 0.14 in the Leopoldina locality. Guimarães et al. (2021) used ANOVA and found heritability values of 0.48 for GY, 0.94 for FLOR, and 0.73 for PH. Sari et al. (2020) found heritability values of 0.35 for GY, 0.77 for FLOR, and 0.76 for PH, using ANOVA and 36 upland rice genotypes. Catolos et al. (2017), considering different years, seasons, and treatments, found heritability values ranging from 0.44-0.87 for GY, 0.46-0.94 for FLOR and 0.45-0.96 for PH, using ANOVA and recombinant inbred lines. For FLOR, Sangaré et al. (2017), using the ANOVA method, found heritability results of 0.76, while Bhandari et al. (2019), using the mixed model, found heritability results of 0.88. In this study, heritability values ranging from 0.47 to 0.77 were found. As for the GY trait, Bhandari et al. (2019) found heritability values of 0.71, and Xu et al. (2018), values from 0.30, while in this study, values from 0.14 to 0.27 were found.

The GY, FLOR and PH traits presented coefficients of variation ($CV_g$) from 0.95% to 2.58%, 3.25% to 3.84% and 1.06% to 2.48%, respectively, for informative prior distributions for each place studied. These can be considered adequate when compared to the method for the classification of coefficients of variation for rice cultivation, proposed by Costa et al. (2002), which determine that the coefficients of variation should be below 51.36%, 7.62%, and 17.27% for grain yield, flowering in days and plant height, respectively. The relative variation indices ($CV_g/ CV_e$) that are greater than the unit suggest that genetic variation is more influential than residual variation (Torres et al., 2018). This was observed in this study for FLOR, in Lambari and Leopoldina, and for PH, in Janaúba and Leopoldina.
between environments (Table 5). The genetic correlations between environments were positive for all traits. Leopoldina was the environment that presented the highest correlations with other locations. Considering the genetic correlations below 0.30 as low and above 0.60, (Oliveira et al., 2020) suggest, respectively, the occurrence of high (0.14-0.22) and moderate (0.34-0.47) G × E, i.e., the performance of genotypes changed across environments.

**Insert Table 5**

The percentage of agreement considering a selection differential of 30% was calculated to compare the ranking of genotypes between the three environments for each trait, as described above (Table 5). For the trait GY, 83.33%, 0.00% and 16.67% of coincidence between the environments were observed. For the trait FLOR, 83.33%, 50.00% and 66.67% of coincidence between the environments were observed. For the trait PH, all coincidences observed were 16.67%. This result suggests that the traits PH and GY are more influenced by environments than FLOR.

**Genetic correlation between the traits**

In Figures 1, 2, and 3, it is possible to verify that the HPD lengths of genetic correlation, using the informative prior distribution, have decreased over the years. In addition, for four pairs of the traits and environment (GY × FLOR in the Lambari and Leopoldina locality and GY × PH), they are not significant in the first years. With the accumulation of information over the years, these correlations have presented significance. In contrast, all the correlations obtained using the non-informative model were not significant. The correlations obtained, using the informative model, for GY and PH traits, were significant for all locations. For the localities of Lambari and Leopoldina, the correlations were 0.14 [0.09, 0.20] and 0.15 [0.10, 0.21], respectively, while for Janaúba, the correlation was -0.50 [-0.54, -0.46]. Similar results were observed by Lakshmi et al. (2014) and Oladosu et al. (2018), in their study on rice genotypes under tropical conditions, who found correlations of 0.18 and -0.34, respectively. This divergence can be explained by the effect of the environment on the expression of these traits, as observed in the results of Table 5. The estimated correlation values for GY and FLOR were 0.11 [0.05, 0.16] for Lambari and 0.13 [0.07, 0.18] for Leopoldina, which corroborates the correlation of 0.11 estimated by Lakshmi et al. (2014).

The Bayesian estimation of parameters such as genetic correlation is advantageous, compared to the classical estimation using the maximum likelihood method (Nustad et al., 2018). In classical statistics, confidence intervals are only possible through Bootstrap and delta method procedures (Manichaikul et al., 2006). These intervals generally have great amplitudes (Beyene and Moineddin, 2005). In the Bayesian approach, it is possible to estimate credibility intervals (in general, they are smaller than the confidence intervals). Thus, with a shorter length of intervals, it is easier to detect correlations between traits and even between environments.

**Conclusion**
We demonstrated the feasibility of the proposed multi-trait multi-environment Bayesian model for plant breeding involving a low number of genotypes that are evaluated for multiple traits across a range of environments. In addition, we presented a knowledge-updating mechanism for eliciting an informative prior distribution. The use of more informative prior distributions makes it possible to detect genetic correlations between traits, which was not feasible with the use of non-informative prior distributions.
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Table 1. Deviance information criteria for the full (considering G×E interaction) and null (not considering the interaction).

| Prior distribution | Agricultural Year | DIC | Full model | Null model |
|--------------------|-------------------|-----|------------|------------|
|                    | 2010-2011         |     | 4257.48    | 4482.73    |
|                    | 2011-2012         |     | 4770.29    | 4862.28    |
| Non-informative    | 2012-2013         |     | 4790.47    | 4788.56    |
|                    | 2013-2014         |     | 4553.67    | 4653.66    |
|                    | 2014-2015         |     | 4610.33    | 4676.94    |
|                    | 2010-2011         |     | 4257.48    | 4482.73    |
|                    | 2011-2012         |     | 4953.24    | 4972.15    |
| Informative        | 2012-2013         |     | 5126.80    | 5134.15    |
|                    | 2013-2014         |     | 4668.30    | 4724.78    |
|                    | 2014-2015         |     | 4720.88    | 4774.18    |
Table 2. Mean, 95% highest probability density interval (HPD) and coefficient of variation (CV) of the posterior densities of the genetic parameters for traits relative to 2014-2015, considering non-informative and informative prior distributions, the statistics of convergence and DIC (Deviance information criterion).

| Trait | Env. | Prior | Par. | Mean   | CV(%) | HPD              | HPD length | Z-Geweke p-value |
|-------|------|-------|------|--------|-------|------------------|------------|------------------|
|       |      |       |      |        |       |                  |            |                  |
|       |      | Non-informative | $\sigma_u^2$ | 73490.27 | 215.93 | [0.65, 360190.57] | 360189.92 | 0.02             |
|       |      |       | $h^2$ | 0.05   | 173.92 | [0.01, 0.25]     | 0.24       | 0.02             |
|       |      |       | $u^i$ | -157.90, 146.26 | -4289.26, 3217.16 |                  |            |                  |
|       |      | Informative | $\sigma_u^2$ | 344808.35 | 4.04   | [317919.21, 372412.33] | 54493.12 | 0.42             |
|       |      |       | $h^2$ | 0.27   | 3.25   | [0.25, 0.29]     | 0.04       | 0.43             |
|       |      |       | $u^i$ | -633.45, 554.98 | -1558.94, 7797.58 |                  |            |                  |
|       |      | Non-informative | $\sigma_u^2$ | 35268.97 | 254.67 | [0.61, 177287.83] | 177287.21 | 0.21             |
|       |      |       | $h^2$ | 0.03   | 211.09 | [0.01, 0.14]     | 0.13       | 0.17             |
|       |      |       | $u^i$ | -84.49, 67.25 | -4798.25, 1335.09 |                  |            |                  |
|       |      | Informative | $\sigma_u^2$ | 252771.77 | 4.06   | [232867.49, 272951.33] | 40083.84 | 0.41             |
|       |      |       | $h^2$ | 0.21   | 3.52   | [0.20, 0.23]     | 0.03       | 0.50             |
|       |      |       | $u^i$ | -672.79, 676.69 | -531.31, 660.67 |                  |            |                  |
|       |      | Non-informative | $\sigma_u^2$ | 17281.16 | 253.05 | [0.75, 82190.60] | 82189.86 | 0.18             |
|       |      |       | $h^2$ | 0.01   | 218.95 | [0.00, 0.07]     | 0.06       | 0.13             |
|       |      |       | $u^i$ | -13.13, 13.68 | -16649.59, 4632.50 |                  |            |                  |
| Location   | Type       | $\sigma_{u}^2$ | $h^2$ | [Lower, Upper] | $u^t$ | $[Lower, Upper]$ | $p$-value |
|------------|------------|----------------|-------|----------------|-------|-----------------|------------|
| Informative | 151921.97  | 0.14           | 3.84  | [0.13, 0.15]   | -247.54, 368.66 | -744.00, 6979.67 | 0.02, 1.00 |
| Non-informative | 25.36     | 0.47           | 29.61 | [0.21, 0.74]   | -4.50, 5.32     | -1364.57, 408.16 | 0.02, 0.92 |
| FLOR       | Informative | 18.89          | 4.04  | [17.42, 20.40] | -4.53, 4.99     | -13476.08, 4827.68 | 0.02, 0.85 |
| Janaúba    | Non-informative | 13.43          | 0.33  | [0.08, 0.59]   | -2.69, 4.46     | -7116.56, 346.96  | 0.11, 0.90 |
| Informative | 35.20      | 0.47           | 2.48  | [0.44, 0.49]   | -4.26, 3.94     | -4207.17, 409.63  | 0.02, 0.82 |
| Lambari    | Non-informative | 63.88          | 0.69  | [15.85, 133.92]| -8.58, 8.35     | -453.60, 242.41   | 0.02, 0.95 |
| Leopoldina | Non-informative | 63.88          | 0.69  | [0.48, 0.89]   | -8.58, 8.35     | -453.60, 242.41   | 0.02, 0.95 |
| Region     | Type       | $\sigma_u^2$ | $h^2$ | $u^t$ | 95% CI | $\hat{\beta}_1$ | 95% CI | 95% CI |
|------------|------------|--------------|-------|-------|--------|----------------|--------|--------|
| Janaúba    | Informative| 73.38        | 4.03  | -9.46, 8.67 | [67.70, 79.28] | 11.57 | 0.92   |
|            | Non-informative| 3.79        | 0.77  | -1.32, 0.90 | [0.38, 9.33] | 8.95 | 0.36   |
|            | Informative| 37.07        | 7.24  | -4.10, 2.84 | [31.87, 42.38] | 10.52 | 0.53   |
| PH         | Non-informative| 19.58        | 0.52  | -4.44, 3.60 | [3.28, 43.58] | 40.30 | 0.95   |
| Lambari    | Informative| 18.29        | 6.64  | -3.66, 3.84 | [15.93, 20.68] | 4.75 | 0.79   |
| Leopoldina | Non-informative| 17.01        | 2.865 | -5.74, 3.58 | [2.58, 38.05] | 35.48 | 0.78   |
\( \sigma^2_u \) is the additive genetic variance, \( h^2 \) is the heritability and \( u \) is the additive genetic value. Minimum and maximum additive value and average SD. Grain yield (GY), in kg ha\(^{-1}\); Flowering (FLOR) in days and Plant Height (PH), in cm.

| Informative | \( \sigma^2_u \) | 52.72 | 4.04 | [48.63, 56.96] | 8.33 | 0.57 |
|-------------|-----------------|-------|------|---------------|------|------|
|             | \( h^2 \)      | 0.58  | 1.88 | [0.56, 0.60]  | 0.04 | 0.29 |
|             | \( u \)        | -7.00, 3.42 | -5999.53, 2215.48 | 0.13, 1.00 |
Table 3. Mean, 95% highest probability density interval (HPD) and coefficient of variation (CV) of the posterior densities of the genetic correlation ($r_g$) for traits relative to 2014-2015, considering non-informative and informative prior distributions and the statistics of convergence.

| Prior      | Environment | Pair of traits | Mean  | CV(%) | HPD                  | HPD length | Z-Geweke pvalue |
|------------|-------------|----------------|-------|-------|----------------------|------------|-----------------|
| Non-Informative | Janaúba   | GY, FLOR       | -0.14 | -366.96 | [-0.96, 0.80]       | 1.77       | 0.58            |
|            |             | GY, PH         | -0.04 | -1068.84 | [-0.85, 0.78]      | 1.63       | 0.50            |
|            |             | FLOR, PH       | 0.10  | 424.58   | [-0.69, 0.86]      | 1.56       | 0.24            |
| Informative | Janaúba   | GY, FLOR       | -0.03 | -110.32  | [-0.08, 0.03]      | 0.11       | 0.17            |
|            |             | GY, PH         | -0.50 | -4.31    | [-0.54, -0.46]     | 0.08       | 0.56            |
|            |             | FLOR, PH       | 0.04  | 76.50    | [-0.02, 0.09]      | 0.11       | 0.77            |
| Non-Informative | Lambari   | GY, FLOR       | -0.13 | -416.44  | [-0.95, 0.82]      | 1.76       | 0.28            |
|            |             | GY, PH         | -0.10 | -521.43  | [-0.94, 0.80]      | 1.73       | 0.39            |
|            |             | FLOR, PH       | 0.15  | 249.10   | [-0.57, 0.84]      | 1.41       | 0.83            |
| Leopoldina |             | GY, FLOR       | 0.06  | 1259.01  | [-0.95, 0.98]      | 1.93       | 0.45            |
|            |             | GY, PH         | 0.01  | 6134.78  | [-0.89, 0.91]      | 1.79       | 0.69            |
|            |             | FLOR, PH       | -0.43 | -70.93   | [-0.92, 0.17]      | 1.09       | 0.85            |
| Informative | Janaúba   | GY, FLOR       | 0.11  | 25.79    | [0.05, 0.16]       | 0.11       | 0.15            |
|            |             | GY, PH         | 0.14  | 19.35    | [0.09, 0.20]       | 0.11       | 0.28            |
|            |             | FLOR, PH       | 0.03  | 91.47    | [-0.02, 0.09]      | 0.11       | 0.23            |
| Leopoldina |             | GY, FLOR       | 0.13  | 22.01    | [0.07, 0.18]       | 0.11       | 0.87            |
|          | GY, PH | FLOR, PH |
|----------|--------|----------|
|          | 0.15   | 0.03     |
|          | 18.17  | 87.38    |
|          | [0.10, 0.21] | [-0.02, 0.09] |
|          | 0.11   | 0.15     |
|          | 0.03   |          |

Grain yield (GY), in kg ha⁻¹; Flowering (FLOR) in days and Plant Height (PH), in cm.
Table 4. Agreement between genetic breeding values estimated via Bayesian approach with non-informative and informative prior distribution, considering each agricultural year, environment and trait.

| Trait | Agricultural Year | Janaúba | Lambari | Leopoldina |
|-------|-------------------|---------|---------|------------|
| GY    | 2010-2011         | 100.00  | 100.00  | 100.00     |
|       | 2011-2012         | 83.33   | 66.67   | 50.00      |
|       | 2012-2013         | 66.67   | 66.67   | 50.00      |
|       | 2013-2014         | 66.67   | 50.00   | 83.33      |
|       | 2014-2015         | 66.67   | 50.00   | 83.33      |
| FLOR  | 2010-2011         | 100.00  | 100.00  | 100.00     |
|       | 2011-2012         | 66.67   | 100.00  | 83.33      |
|       | 2012-2013         | 66.67   | 83.33   | 66.67      |
|       | 2013-2014         | 100.00  | 83.33   | 100.00     |
|       | 2014-2015         | 83.33   | 83.33   | 100.00     |
| PH    | 2010-2011         | 100.00  | 100.00  | 100.00     |
|       | 2011-2012         | 83.33   | 66.67   | 83.33      |
|       | 2012-2013         | 83.33   | 66.67   | 66.67      |
|       | 2013-2014         | 83.33   | 83.33   | 83.33      |
|       | 2014-2015         | 83.33   | 83.33   | 100.00     |

Grain yield (GY), in kg.ha-1; Flowering (FLOR) in days and Plant Height (PH), in cm.
Table 5. Mean and 95 % highest probability density (HPD) interval of the genetic correlation \( r_g \) between environment (upper diagonal), relative variation index (diagonal) and agreement between genetic breeding values estimated for each pair of environments relative to 2014-2015 (under diagonal).

| Trait | Environment | Janaúba     | Lambari     | Leopoldina   |
|-------|-------------|-------------|-------------|--------------|
| GY    | Janaúba     | 0.61 [0.58; 0.63] | 0.35 [0.30; 0.40] | 0.14 [0.09; 0.20] |
|       | Lambari     | 83.33       | 0.52 [0.50; 0.54] | 0.47 [0.43; 0.52] |
|       | Leopoldina  | 0.00        | 16.67       | 0.40 [0.39; 0.52] |
| FLOR  | Janaúba     | 0.96 [0.92; 1.01] | 0.14 [0.09; 0.20] | 0.36 [0.31; 0.41] |
|       | Lambari     | 83.33       | 1.31 [1.26; 1.37] | 0.22 [0.16; 0.27] |
|       | Leopoldina  | 50.00       | 66.67       | 1.90 [1.82; 1.98] |
| PH    | Janaúba     | 1.96 [1.86; 2.04] | 0.34 [0.29; 0.39] | 0.43 [0.38; 0.47] |
|       | Lambari     | 16.67       | 0.87 [0.84; 0.91] | 0.47 [0.43; 0.52] |
|       | Leopoldina  | 16.67       | 16.67       | 1.20 [1.15; 1.25] |

Grain yield (GY), in kg.ha⁻¹; Flowering (FLOR) in days and Plant Height (PH), in cm.
Figure 1. (a) Mean posterior (in bars) and Highest posterior density (in arrows) of genetic correlation (GY × FLOR), (b) absolute value of Coefficient of variation (CV) of genetic correlation (GY × FLOR), using the non-informative and informative prior distribution along the five years. Grain yield (GY), in kg.ha⁻¹; Flowering (FLOR) in days and Plant Height (PH), in cm.

Figure 2. (a) Mean posterior (in bars) and Highest posterior density (in arrows) of genetic correlation (GY × PH), (b) absolute value of Coefficient of variation (CV) of genetic correlation (GY × PH) using the non-informative and informative prior distribution along the five years. Grain yield (GY), in kg.ha⁻¹; Flowering (FLOR) in days and Plant Height (PH), in cm.

Figure 3. (a) Mean posterior (in bars) and Highest posterior density (in arrows) of genetic correlation (FLOR × PH), (b) absolute value of Coefficient of variation (CV) of genetic correlation (FLOR × PH) using the non-informative and informative prior distribution along the five years. Flowering (FLOR) in days and Plant Height (PH), in cm.
Figures

Figure 1

(a) Mean posterior (in bars) and Highest posterior density (in arrows) of genetic correlation (GY × FLOR),
(b) absolute value of Coefficient of variation (CV) of genetic correlation (GY × FLOR), using the non-
informative and informative prior distribution along the five years. Grain yield (GY), in kg ha⁻¹; Flowering
(FLOR) in days and Plant Height (PH), in cm.
Figure 2

(a) Mean posterior (in bars) and Highest posterior density (in arrows) of genetic correlation (GY × PH), (b) absolute value of Coefficient of variation (CV) of genetic correlation (GY × PH) using the non-informative and informative prior distribution along the five years. Grain yield (GY), in kg.ha⁻¹; Flowering (FLOR) in days and Plant Height (PH), in cm.

Figure 3

(a) Mean posterior (in bars) and Highest posterior density (in arrows) of genetic correlation (FLOR × PH), (b) absolute value of Coefficient of variation (CV) of genetic correlation (FLOR × PH) using the non-informative and informative prior distribution along the five years. Flowering (FLOR) in days and Plant Height (PH), in cm.