

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

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51 **Abstract**

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

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

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73

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78

79 **Conflicts of interest/Competing interests**

80 The authors have no conflicts of interest to declare that are relevant to the content of this article.

81 **Availability of data and material**

82 Not applicable.

83 **Code availability**

84 Not applicable.

85 **Authors' contributions**

86 Not applicable.

87 **Ethics approval**

88 Not applicable.

89 **Consent to participate**

90 Not applicable.

91 **Consent for publication**

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93

94 **Introduction**

95 Rice is one of the most important sources of the global population's daily caloric and nutritional
96 requirement (FAO, 2020). The global population is increasing, but the available area of suitable wetland is
97 decreasing (Ray et al., 2013). Therefore, the need to increase crop productivity rather than expand
98 agricultural land has grown over the years (Lobell et al., 2011; Phalan et al., 2011; Ray et al., 2013). It is
99 estimated that by 2050 the agricultural production of rice should be between 60 and 110% (Hunter et al.,
100 2017; Juliana et al., 2019). Thus, in rice cultivation, the evaluation of multiple traits aims to maximize grain
101 yield potential (Liang et al., 2021).

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

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

119 frequentist when it uses informative prior distributions (van de Schoot et al., 2021). Thus, informative prior
120 distributions should be preferable for breeding purposes to improve the accuracy of the selection process.

121 Silva et al. (2013) and Azevedo et al. (2022) presented a system, respectively, for updating
122 knowledge about the hyperparameters from the prior distributions of the variance components in the
123 univariate analysis in maize and white oat breeding, using the phenotypic data collected in different years.
124 However, these procedures for eliciting informative prior distributions have not been presented yet for
125 multi-trait analysis. Furthermore, although multi-traits and multi-environment studies in rice have already
126 been reported in the literature (Bhandari et al., 2019, Yu et al., 2019, Ahmadi et al., 2021, Sharma et al.,
127 2021), the combination of multi-trait models under a multi-environment under a Bayesian framework with
128 informative prior, so far, has not been investigated.

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

132

133 **Materials and methods**

134 *Experimental data*

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

143 The useful area consisted of 4 m of three internal rows (4×0.9 m, 3.60 m²). The experiments were
144 conducted on floodplain soils with continuous flood irrigation. The cultural treatments were carried out
145 according to the recommendations for irrigated rice cultivation in the evaluated regions (Soares et al., 2005).

146

147 *Model and Bayesian inference*

148 The fitted multi-trait statistical model was given by:

$$149 \quad y = Xb + Z_1r + Z_2u + e$$

150 Which can be rewritten as:

$$\begin{matrix}
151 \\
152 \\
153 \\
154 \\
155 \\
156 \\
157 \\
158 \\
159 \\
160 \\
161
\end{matrix}
\begin{pmatrix}
y_{11} \\
y_{12} \\
y_{13} \\
\cdots \\
y_{21} \\
y_{22} \\
y_{23} \\
\cdots \\
y_{31} \\
y_{32} \\
y_{33}
\end{pmatrix}
= X
\begin{pmatrix}
b_{11} \\
b_{12} \\
b_{13} \\
\cdots \\
b_{21} \\
b_{22} \\
b_{23} \\
\cdots \\
b_{31} \\
b_{32} \\
b_{33}
\end{pmatrix}
+ Z_1
\begin{pmatrix}
r_{11} \\
r_{12} \\
r_{13} \\
\cdots \\
r_{21} \\
r_{22} \\
r_{23} \\
\cdots \\
r_{31} \\
r_{32} \\
r_{33}
\end{pmatrix}
+ Z_2
\begin{pmatrix}
u_{11} \\
u_{12} \\
u_{13} \\
\cdots \\
u_{21} \\
u_{22} \\
u_{23} \\
\cdots \\
u_{31} \\
u_{32} \\
u_{33}
\end{pmatrix}
+
\begin{pmatrix}
e_{11} \\
e_{12} \\
e_{13} \\
\cdots \\
e_{21} \\
e_{22} \\
e_{23} \\
\cdots \\
e_{31} \\
e_{32} \\
e_{33}
\end{pmatrix}$$

152 where y_{ij} is the vector of phenotypic values of the i th trait ($i = 1,2,3$) in the j th environment ($j = 1,2,3$);
153 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
154 trait in the j th environment and e_{ij} is the residual vector of the i -th trait in the j -th environment. \mathbf{X} is the
155 incidence matrix of systematic effects, Z_1 is the incidence matrix of block effects and Z_2 is the incidence
156 matrix of genotype effects.

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

$$bN(\mu, I \otimes \Sigma_b)$$

$$rN(0, I \otimes \Sigma_r)$$

$$uN(0, I \otimes \Sigma_u)$$

$$eN(0, I \otimes \Sigma_e)$$

162 where I is the identity matrix, Σ_b , Σ_r , Σ_u and Σ_e are the (co)variance matrix estimates with prior
163 distributions given by:

$$\Sigma_b IW(I, 0.002)$$

$$\Sigma_r IW(V_r, \eta_r)$$

$$\Sigma_u IW(V_u, \eta_u)$$

$$\Sigma_e IW(V_e, \eta_e)$$

168 where IW is the inverted Wishart distribution, V_r , V_u and V_e are matrices with known values and η_r , η_u
169 and η_e are known constants called hyperparameters. The j -th value of the chain of additive genetic
170 heritability associated with i -th trait, $h_i^{2(j)}$, is given by:

$$171 \quad h_i^{2(j)} = \frac{\sigma_{u2(i)}^{2(j)}}{\sigma_{r(i)}^{2(j)} + \sigma_{u(i)}^{2(j)} + \sigma_{e(i)}^{2(j)}}$$

172 where $\sigma_{r(i)}^{2(j)}$, $\sigma_{u(i)}^{2(j)}$ and $\sigma_{e(i)}^{2(j)}$ are, respectively, block, genetic and residual variances of j -th interaction and
173 i -th trait. The j -th value of the chain of genetic correlation between traits i and k , $r_{ik}^{(j)}$, is given by:

174
$$r_{ik}^{(j)} = \frac{\sigma_{u(ik)}^{(j)}}{\sqrt{\sigma_{u(i)}^{2(j)} \sigma_{u(k)}^{2(j)}}$$

175 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
 176 $\sigma_{u(k)}^{2(j)}$ is the genetic variance of k -th trait. The j -th value of the chain of genetic correlation between
 177 environments l and h , $r_{lh}^{(j)}$, is given by:

178
$$r_{lh}^{(j)} = \frac{\sigma_{u(lh)}^{(j)}}{\sqrt{\sigma_{u(l)}^{2(j)} \sigma_{u(h)}^{2(j)}}$$

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

181 The relative variation index is the ratio of the coefficient of genotypic variation to the coefficient
 182 of residual variation, this is $\frac{CV_g}{CV_e}$.

183 The informativeness of prior distribution is associated with the values of the hyperparameters and,
 184 consequently, in this study, with the (co)variance matrices of the normal distribution (van de Schoot et al.,
 185 2021). Thus, we consider $V_r = V_u = V_e = I$ and $\eta_r = \eta_u = \eta_e = 2$ (Hadfield, 2010) for analyses using
 186 non-informative prior distributions. Furthermore, we know that, if $\Sigma \sim IW(V, \eta)$ (the dimension of Σ is
 187 3×3), then the expected value of Σ is given by $\frac{V\eta}{\eta-10}$ where $\eta \geq 10$ and the mode of Σ is given by $\frac{V\eta}{\eta+10}$.

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

191 $V = \underline{\Sigma} \frac{(\eta-10)}{\eta}$. A similar procedure was used by Silva et al. (2013) to select hyperparameters for inverse
 192 gamma prior distributions (mean and variance) in univariate Bayesian inference of mixed models in
 193 quantitative genetics of crop species, while Azevedo et al. (2022) used it to select hyperparameters for
 194 inverse gamma prior distributions (mean and mode) in univariate Bayesian inference in white oat.

195 Based on phenotypic databases containing several years of collection, it is possible to update the
 196 hyperparameters and, consequently, our knowledge regarding the (co)variance matrices. Azevedo et al.
 197 (2022) demonstrated in univariate analyses with ten years of data that the procedure for updating knowledge
 198 for the year k -th should be carried out only with information from the $(k-1)$ -th year. Thus, the
 199 hyperparameters were calculated by analyzing the $(k-1)$ -th year with the expression above. Therefore,
 200 in this work, two approaches were performed aiming to evaluate different strategies for eliciting informative
 201 prior distribution: i) five analyses considering year by year separately and non-informative prior
 202 distributions; ii) five analyses considering year by year separately for the construction of informative prior
 203 distributions.

204 The following parameters were calculated to assess the impact of prior knowledge insertion : i)
205 the posterior coefficient of variation (CV) of the estimates of the components of variance, heritability,
206 genetic correlation and additive genetic values; ii) length of the Highest Posterior Density intervals (HPD)
207 of the parameter estimates; iii) the deviance information criterion (DIC), when possible, since the quality
208 of the fit can only be compared using the DIC when the model uses the same data; iv) agreement between
209 genetic estimates by non-informative and informative prior distribution, considering 30% of the selection
210 differential (total of 6 genotypes).

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

217

218 **Results and discussion**

219 *Model selection and convergence of parameters*

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

224

225 *Insert Table 1*

226

227 For all parameters, the p-values of Geweke's Z statistics were greater than 1% significance (Tables
228 2 and 3), which indicates that the convergence was achieved, and the inferences can be performed.

229

230 *Insert Table 2*

231 *Insert Table 3*

232

233 *Comparison between informative and non-informative prior distributions*

234 The smaller posterior coefficient of variation (CV) values of the genetic variance and heritability
235 (Table 2) and genetic correlation (Table 3) were observed considering the informative prior to the
236 estimation process. In this approach, the hyperparameters from the prior distributions were obtained by
237 analyzing the previous year. Therefore, the length of the HPD interval is also smaller due to the higher
238 precision provided by this informative prior (Tables 2 and 3). The same results were found by Azevedo et
239 al. (2022) considering univariate analyses in white oat (*Avena sativa L.*). However, the same was not
240 observed for genetic values. In most analyses, the CV of genetic value presented increased amplitude in the
241 informative priors. Despite these amplitude values, considering a selection differential of 30%, the
242 agreement between the selected genotypes in both prior distributions is above 50% (Table 4).

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Insert Table 4

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246 *Heritability of traits*

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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).

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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.

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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.

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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.

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Genetic correlation between environments

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The genetic correlations between environments for all traits were significant and ranged from 0.14 to 0.47 for GY; 0.14 to 0.36 for FLOR; and 0.34 to 0.47 for PH, which indicates the existence of interaction

282 between environments (Table 5). The genetic correlations between environments were positive for all traits.
283 Leopoldina was the environment that presented the highest correlations with other locations. Considering
284 the genetic correlations below 0.30 as low and above 0.60, (Oliveira et al., 2020) suggest, respectively, the
285 occurrence of high (0.14-0.22) and moderate (0.34-0.47) $G \times E$, i.e., the performance of genotypes changed
286 across environments.

287

288 *Insert Table 5*

289

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

296

297 *Genetic correlation between the traits*

298 In Figures 1, 2, and 3, it is possible to verify that the HPD lengths of genetic correlation, using the
299 informative prior distribution, have decreased over the years. In addition, for four pairs of the traits and
300 environment ($GY \times FLOR$ in the Lambari and Leopoldina locality and $GY \times PH$), they are not significant
301 in the first years. With the accumulation of information over the years, these correlations have presented
302 significance. In contrast, all the correlations obtained using the non-informative model were not significant.

303 The correlations obtained, using the informative model, for GY and PH traits, were significant for
304 all locations. For the localities of Lambari and Leopoldina, the correlations were 0.14 [0.09, 0.20] and 0.15
305 [0.10, 0.21], respectively, while for Janaúba, the correlation was -0.50 [-0.54, -0.46]. Similar results were
306 observed by Lakshmi et al. (2014) and Oladosu et al. (2018), in their study on rice genotypes under tropical
307 conditions, who found correlations of 0.18 and -0.34, respectively. This divergence can be explained by the
308 effect of the environment on the expression of these traits, as observed in the results of Table 5. The
309 estimated correlation values for GY and FLOR were 0.11 [0.05, 0.16] for Lambari and 0.13 [0.07, 0.18]
310 for Leopoldina, which corroborates the correlation of 0.11 estimated by Lakshmi et al. (2014).

311 The Bayesian estimation of parameters such as genetic correlation is advantageous, compared to
312 the classical estimation using the maximum likelihood method (Nustad et al., 2018). In classical statistics,
313 confidence intervals are only possible through Bootstrap and delta method procedures (Manichaikul et al.,
314 2006). These intervals generally have great amplitudes (Beyene and Moineddin, 2005). In the Bayesian
315 approach, it is possible to estimate credibility intervals (in general, they are smaller than the confidence
316 intervals). Thus, with a shorter length of intervals, it is easier to detect correlations between traits and even
317 between environments.

318

319 **Conclusion**

320 We demonstrated the feasibility of the proposed multi-trait multi-environment Bayesian model for
321 plant breeding involving a low number of genotypes that are evaluated for multiple traits across a range of
322 environments. In addition, we presented a knowledge-updating mechanism for eliciting an informative prior
323 distribution. The use of more informative prior distributions makes it possible to detect genetic correlations
324 between traits, which was not feasible with the use of non-informative prior distributions.
325

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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
Non-informative	2010-2011	4257.48	4482.73
	2011-2012	4770.29	4862.28
	2012-2013	4790.47	4788.56
	2013-2014	4553.67	4653.66
	2014-2015	4610.33	4676.94
Informative	2010-2011	4257.48	4482.73
	2011-2012	4953.24	4972.15
	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
GY	Janaúba	Non-informative	σ_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^\dagger	-157.90, 146.26	-4289.26, 3217.16		0.02, 0.73	
		Informative	σ_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^\dagger	-633.45, 554.98	-1558.94, 7797.58		0.05, 0.97	
	Lambari	Non-informative	σ_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^\dagger	-84.49, 67.25	-4798.25, 1335.09		0.04, 0.70	
	Informative	σ_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^\dagger	-672.79, 676.69	-531.31, 660.67		0.13, 0.99		
Leopoldina	Non-informative	σ_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^\dagger	-13.13, 13.68	-16649.59, 4632.50		0.05, 0.98		

		σ_u^2	151921.97	4.06	[140198.12, 164347.37]	24149.25	0.68	
	Informative	h^2	0.14	3.84	[0.13, 0.15]	0.02	0.66	
		u^\dagger	-247.54, 368.66	-744.00, 6979.67			0.02, 1.00	
		σ_u^2	25.36	66.46	[3.84, 56.74]	52.89	0.25	
	Non-informative	h^2	0.47	29.61	[0.21, 0.74]	0.54	0.09	
		u^\dagger	-4.50, 5.32	-1364.57, 408.16			0.02, 0.92	
	Janaúba	σ_u^2	18.89	4.04	[17.42, 20.40]	2.99	0.24	
	Informative	h^2	0.47	2.48	[0.44, 0.49]	0.05	0.11	
		u^\dagger	-4.53, 4.99	-13476.08, 4827.68			0.02, 0.85	
		σ_u^2	13.43	74.10	[1.30, 31.83]	30.53	0.67	
FLOR	Non-informative	h^2	0.33	41.81	[0.08, 0.59]	0.51	0.78	
		u^\dagger	-2.69, 4.46	-7116.56, 346.96			0.11, 0.90	
	Lambari	σ_u^2	35.20	4.04	[32.45, 38.01]	5.56	0.03	
	Informative	h^2	0.62	1.77	[0.60, 0.64]	0.04	0.01	
		u^\dagger	-4.26, 3.94	-4207.17, 409.63			0.02, 0.82	
		σ_u^2	63.88	58.72	[15.85, 133.92]	118.07	0.43	
	Leopoldina	Non-informative	h^2	0.69	15.49	[0.48, 0.89]	0.41	0.64
		u^\dagger	-8.58, 8.35	-453.60, 242.41			0.02, 0.95	

		σ_u^2	73.38	4.03	[67.70, 79.28]	11.57	0.92	
	Informative	h^2	0.77	1.06	[0.76, 0.79]	0.03	0.48	
		u^\dagger	-9.46, 8.67	-98.02, 640.33			0.12, 1.00	
		σ_u^2	3.79	80.67	[0.38, 9.33]	8.95	0.36	
	Non-informative	h^2	0.19	54.91	[0.03, 0.39]	0.36	0.29	
		u^\dagger	-1.32, 0.90	-3587.57, 1197.57			0.07, 0.97	
	Janaúba	σ_u^2	37.07	7.24	[31.87, 42.38]	10.52	0.53	
	Informative	h^2	0.79	0.95	[0.77, 0.80]	0.03	0.71	
		u^\dagger	-4.10, 2.84	-1774.26, 10040.04			0.05, 0.96	
		σ_u^2	19.58	65.94	[3.28, 43.58]	40.30	0.95	
PH	Non-informative	h^2	0.52	26.40	[0.26, 0.79]	0.53	0.96	
		u^\dagger	-4.44, 3.60	-1125.65, 152.34			0.15, 1.00	
	Lambari	σ_u^2	18.29	6.64	[15.93, 20.68]	4.75	0.79	
	Informative	h^2	0.43	2.58	[0.40, 0.45]	0.05	0.50	
		u^\dagger	-3.66, 3.84	-160.88, 5894.24			0.02, 0.91	
		σ_u^2	17.01	66.49	[2.58, 38.05]	35.48	0.78	
	Leopoldina	Non-informative	h^2	0.49	28.65	[0.22, 0.76]	0.54	0.82
		u^\dagger	-5.74, 3.58	-422.70, 666.13			0.06, 0.95	

	σ_u^2	52.72	4.04	[48.63, 56.96]	8.33	0.57
Informative	h^2	0.58	1.88	[0.56, 0.60]	0.04	0.29
	u^{\dagger}	-7.00, 3.42	-5999.53, 2215.48			0.13, 1.00

σ_u^2 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.

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
	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	-0.03	-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
	Lambari	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	0.15	18.17	[0.10, 0.21]	0.11	0.03
FLOR, PH	0.03	87.38	[-0.02, 0.09]	0.11	0.15

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	Rank agreement (%)		
		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	Correlation genetic		
		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 ($GY \times FLOR$), (b) absolute value of Coefficient of variation (CV) of genetic correlation ($GY \times FLOR$), 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 ($GY \times PH$), (b) absolute value of Coefficient of variation (CV) of genetic correlation ($GY \times PH$) 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 ($FLOR \times PH$), (b) absolute value of Coefficient of variation (CV) of genetic correlation ($FLOR \times PH$) using the non-informative and informative prior distribution along the five years. Flowering (FLOR) in days and Plant Height (PH), in cm.

Figures

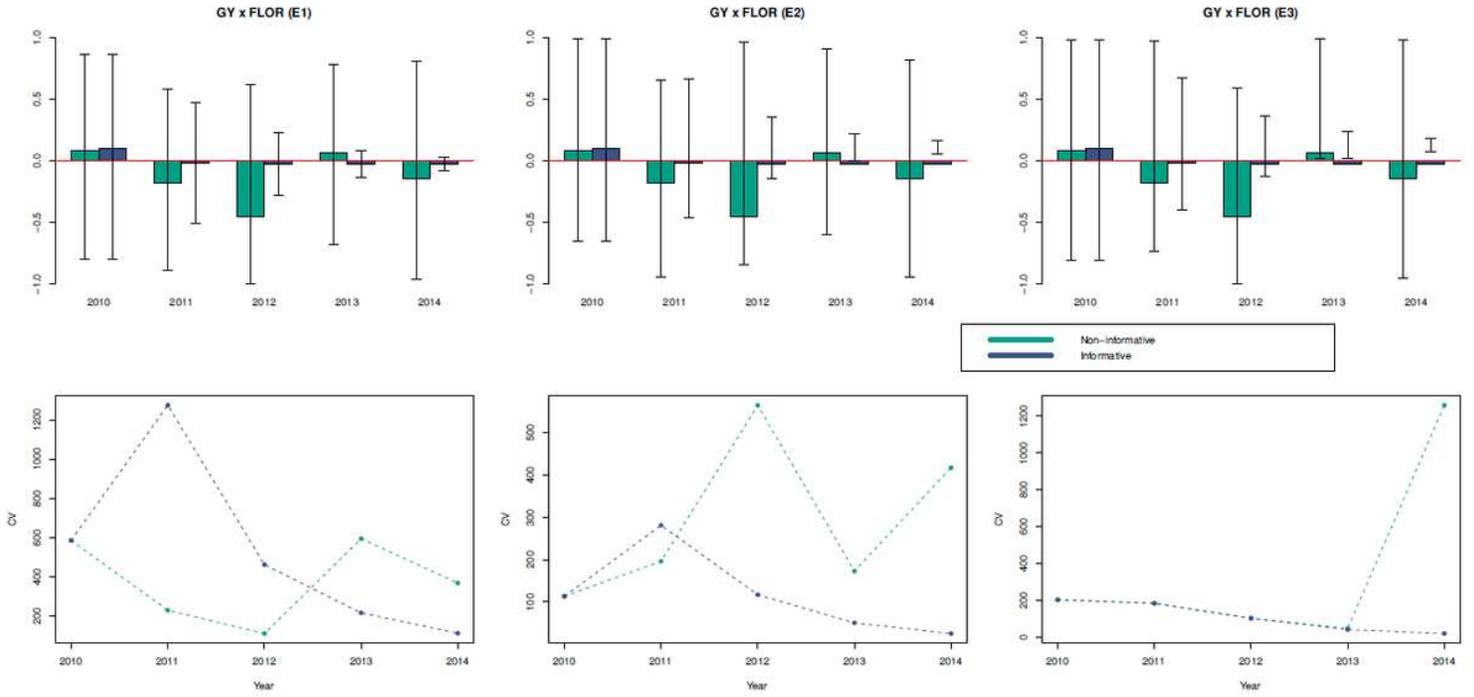


Figure 1

(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.

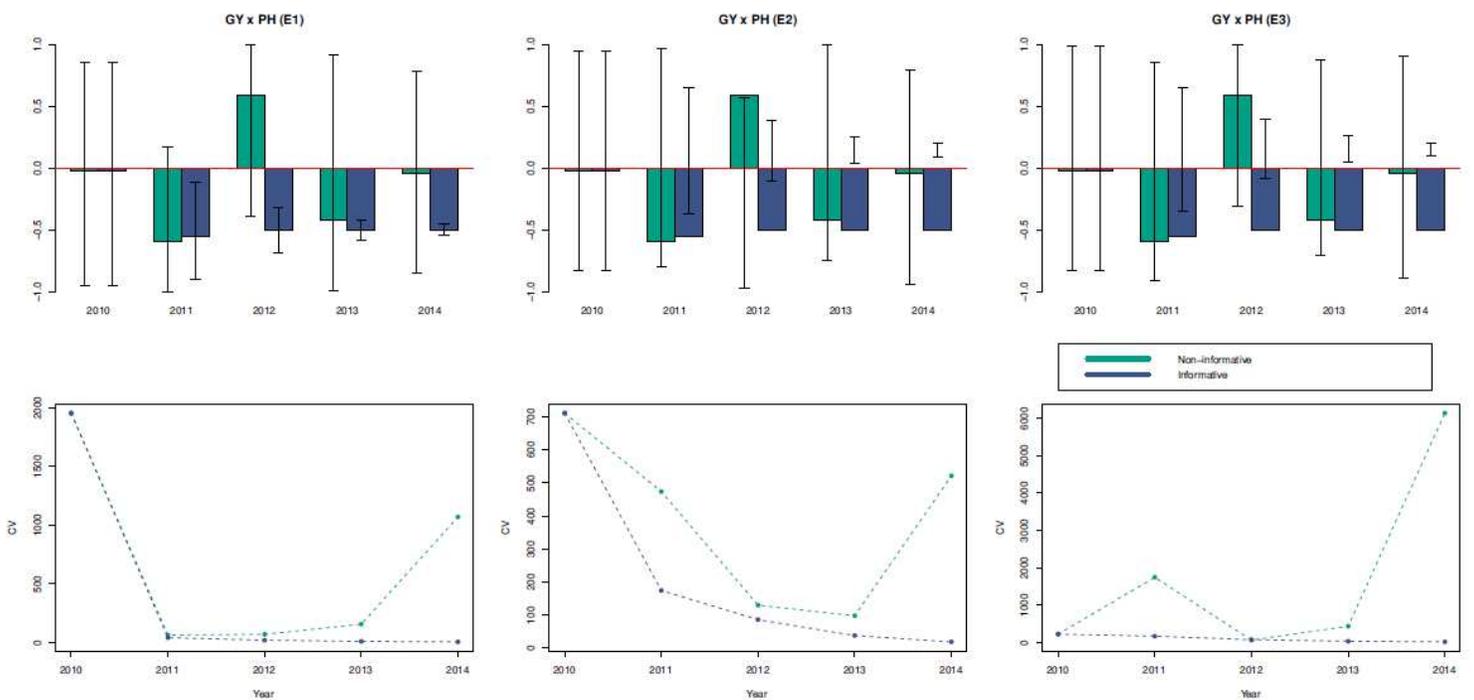


Figure 2

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

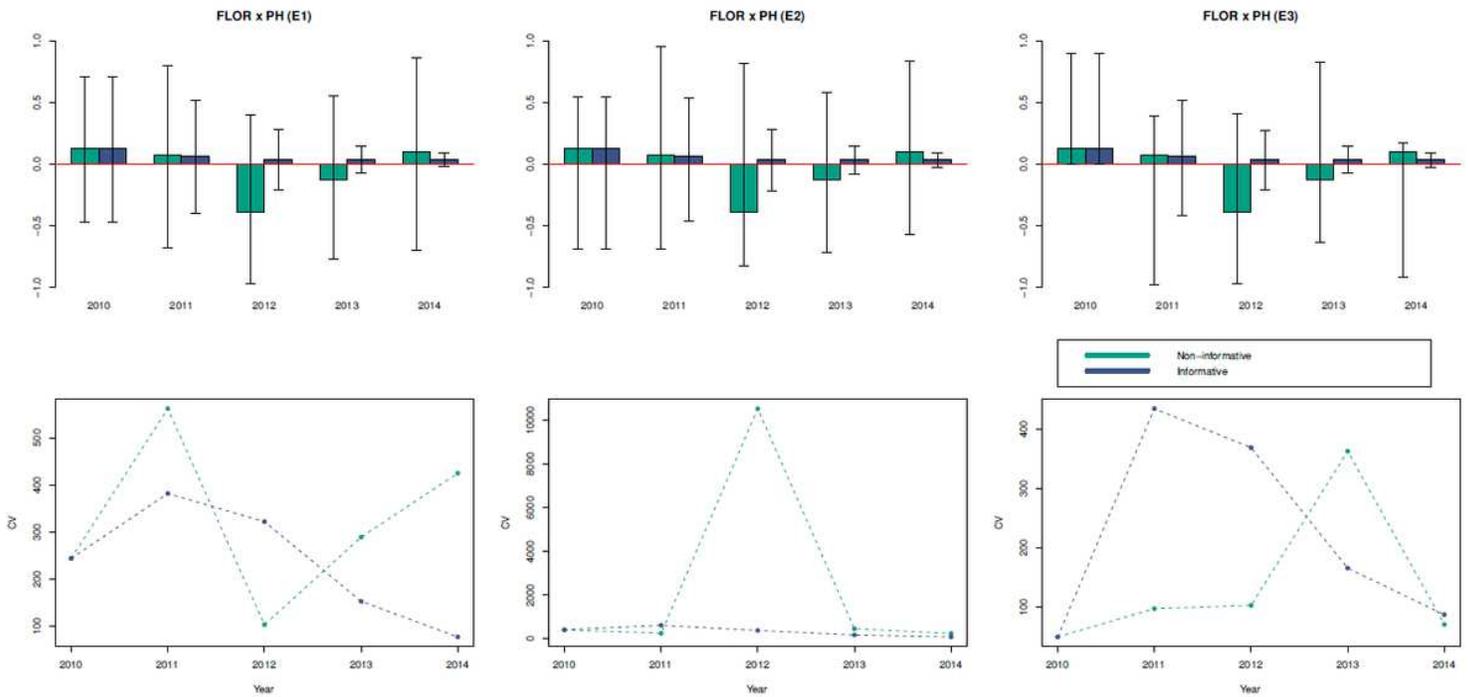


Figure 3

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