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BIOLOGY

Genetic parameters and selection gain in tropical wheat populations via Bayesian inference.

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ABSTRACT: The development process of a new wheat cultivar requires time between obtaining the base population and selecting the most promising line. Estimating genetic parameters more accurately in early generations with a view to anticipating selection means important advances for wheat breeding programs. Thus, the present study estimated the genetic parameters of F_2 populations of tropical wheat and the genetic gain from selection via the Bayesian approach. To this end, the authors assessed the grain yield per plot of 34 F_2 populations of tropical wheat. The Bayesian approach provided an adequate fit to the model, estimating genetic parameters within the parametric space. Heritability (h^2) was 0.51. Among those selected, 11 F_2 populations performed better than the control cultivars, with genetic gain of 7.80%. The following populations were the most promising: Tbio Sossego/CD 1303, CD 1303/Tbio Ponteiro, BRS 254/CD 1303, Tbio Duque/Tbio Aton, and Tbio Aton/CD 1303. Bayesian inference can be used to significantly improve tropical wheat breeding programs.

Key words: deviance information criterion, early selection, *Triticum aestivum* L., wheat breeding.

Parâmetros genéticos e ganho de seleção em populações tropicais de trigo via inferência bayesiana.

RESUMO: O processo de desenvolvimento de uma nova cultivar de trigo requer tempo entre a obtenção da população base e a seleção da linhagem mais promissora. Estimar parâmetros genéticos com mais precisão nas primeiras gerações com vistas a antecipar a seleção significa avanços importantes para os programas de melhoramento de trigo. Assim, o presente estudo estima os parâmetros genéticos de populações F_2 de trigo tropical e o ganho genético da seleção via abordagem Bayesiana. Para tanto, os autores avaliaram a produtividade de grãos por parcela de 34 populações F_2 de trigo tropical. A abordagem Bayesiana proporcionou um ajuste adequado ao modelo, estimando parâmetros genéticos dentro do espaço paramétrico. A herdabilidade (h^2) foi de 0,51. Dentre as selecionadas, 11 populações F_2 obtiveram desempenho superior às cultivares controle, com ganho genético de seleção de 7,80%. As seguintes populações foram as mais promissoras: Tbio Sossego/CD 1303, CD 1303/Tbio Ponteiro, BRS 254/CD 1303, Tbio Duque/Tbio Aton e Tbio Aton/CD 1303. A inferência Bayesiana pode ser usada para melhorar significativamente programas de melhoramento de trigo tropical.

Palavras-chave: critério de informação de desvio, seleção precoce, *Triticum aestivum* L., melhoramento de trigo.

INTRODUCTION

Brazil consumes about 12 million tons of wheat annually; however, it produces only about 50% of this total, requiring imports to meet domestic demand (CONAB, 2021). The country is dependent on the production of exporting countries such as Argentina, the European Union, and the United States. Thus, the country is constantly affected by protectionist policies in these exporting countries and by occasional weather events that reduce yield in these agricultural areas. In this context, wheat breeding programs should focus on selecting genotypes with high grain yield, especially for areas in which wheat cultivation is secondary in importance despite its exploration potential, such as the Brazilian Cerrado (PASINATO et al., 2018).

The development of new cultivars starts with the identification of segregating populations with the potential to derive lines with superior genetic value, which depends on parents with a high concentration of trait-favorable alleles (FASAHAT et al., 2016). The definition of the best strategies both for identifying superior populations and for conducting them through breeding programs requires high accuracy prediction of breeding values, as well as the estimation of variance components and genetic parameters. Studies usually apply frequentist approaches such as the Restricted Maximum Likelihood/

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Best Linear Unbiased Prediction (REML/BLUP) to this end. This type of approach was used by PIMENTEL et al. (2014) in F_3 wheat populations, by THORWARTH et al. (2019) in wheat hybrids, and by MAHJOURIMAJD et al. (2016) in double haploid wheat. Although, the frequentist approach has several useful properties such as estimators with minimal and unbiased variance, it has limitations such as providing only approximate standard errors for heritability (RESENDE, 2002).

As an alternative to the frequentist approach, the Bayesian approach combines subjective information contained in *a priori* probability distributions with sample information, through *a posteriori* distribution of parameters. As a central feature in the Bayesian approach, probability distribution correlates with uncertainty regarding unknown parameters. In the frequentist approach, the parameters consist of fixed and constant values, not associated with any probability distribution (BOX & TIAO, 1992).

The Bayesian approach provides more complete results, allowing the selection of the best segregating populations to continue breeding programs. In this process, the selection of progenies occurs from a performance evaluation according to the breeder's criteria (SILVA et al., 2019). The literature reports different successful cases involving Bayesian inference, such as the selection of guava (*Psidium guajava* L.) (SILVA et al., 2020), kale (*Brassica oleracea* L. var *acephala* DC) (AZEVEDO et al., 2017), and eucalyptus populations (*Eucalyptus globulus*) (MORA et al., 2019).

The definition of selection strategies in a breeding program requires information on the populations under study, the estimation of variance components and breeding values, as well as the achievement of heritability (SEARLE et al., 1992; GONÇALVES-VIDIGAL et al., 2008). Bayesian inference can be used with advantages in these cases, since it allows to obtain *posterior* densities of the marginal distributions and credibility intervals for the variance components, breeding values, and genetic parameters such as heritability (WALDMANN & ERICSSON, 2006).

Bayesian approaches have many practical applications in breeding programs, including the study of adaptability and stability in genotypes of *Gossypium* L. (NASCIMENTO et al., 2020) and *Zea mays* (OLIVEIRA et al., 2018), repeatability analysis in *Jatropha curcas* (PEIXOTO et al., 2021), and parameter estimates and population selection in *Brassica oleracea* L. (AZEVEDO et al., 2017). Moreover, the Bayesian approach produces information regarding distributions and credibility intervals; however, wheat breeding programs do not often report its use. There is a lack of information on wheat improvement regarding the obtaining of population parameters, the selection of F_2 populations, and the estimates of genetic gain from selection. In this sense, the present study analyzes 34 F_2 populations for grain yield using a Bayesian approach, assessing heritability, breeding values, and genetic gain from selection.

MATERIALS AND METHODS

Genetic material and experimental design

This study included 34 F_2 segregating populations belonging to the Wheat Breeding Program of the Federal University of Viçosa (UFV), Brazil, and eight commercial cultivars used as parents (Table 1). The F_2 populations come from crosses conducted in 2019 (winter) in a greenhouse, involving eight parents selected for presenting genetic variability for cycle, health, and agronomic performance. The F_1 seeds harvested from the crosses were sown under greenhouse conditions in the summer season of 2020 for generation advancement. Then, physiologically mature ears were harvested and threshed manually, and F_2 seeds and parents were separated and arranged according to the experimental design.

The experiment was conducted in the winter season of 2020, in a randomized block design with two replications. The plots consisted of two 1.5 m rows, spaced 0.2 m apart. Sowing density was 350 seeds m^{-2}. Cultural treatments followed technical indications for wheat cultivation in central Brazil (EMBRAPA, 2020). The plot was harvested manually, with manual cutting of plants, followed by mechanical threshing and cleaning and drying of grains up to 13% to determine yield per plot, in grams (g).

Statistical analysis

The Bayesian approach was used to analyze plot production data. Parameter estimates via Bayesian inference were obtained using Monte Carlo Markov Chain (MCMC) algorithms. The analysis was performed using the MCMCglmm package (HADFIELD, 2010) in the R software (R CORE TEAM, 2020). A total of 1,000,000 iterations (nitt) were determined, discarding the first 50,000 (burn-in). After each set of five iterations (thin)

Table 1 - Description of the cultivars used in the crossings as maternal (♀) and paternal (♂) parents regarding the breeding institution, commercial class, cycle and weight of 1000 seeds (W1000S, g) and F_2 populations obtained by artificial crossings.

Parent		Description				
♀	♂	Cultivar	Breeder[1]	Class	Cycle	W1000S
A	1	Tbio Aton	Biotrigo	Bread	Medium	34
B	2	BRS 254	Embrapa	Breeder	Early	40
C	3	BRS 264	Embrapa	Bread	Early	40
D	4	BRS 394	Embrapa	Breeder	Early	40
E	5	CD 1303	Coodetec	Bread/Breeder	Early	35
F	6	Tbio Duque	Biotrigo	Bread/ Breeder	Early	33
G	7	Tbio Ponteiro	Biotrigo	Bread	Medium/Late	33
H	8	Tbio Sossego	Biotrigo	Bread	Medium	33

	1	2	3	4	5	6	7	8
A		×			×	×	×	
B	×			×	×	×	×	
C	×	×		×	×			×
D	×	×			×	×		×
E	×					×	×	×
F	×	×	×		×	×		
G			×		×	×		
H				×	×		×	

[1] Embrapa: Empresa Brasileira de Pesquisa Agropecuária, Coodetec: Cooperativa Central de Pesquisa Agrícola de Cascavel, Biotrigo Genética.

were performed, a sample was retained, totaling a chain with 190,000 iterations, from which *posterior* estimates were obtained. Convergence analysis was performed according to Geweke's criteria (GEWEKE, 1991), and graphical analysis was performed using the BOA package (SMITH, 2007) of the R software (R CORE TEAM, 2020).

The *posterior* means and medians, credibility intervals, and standard deviation of estimates were obtained according to the linear model presented below:

$$y = Xb + Zg + e \quad (1)$$

Where y is the vector of phenotypic values (with dimension $nm \times 1$, where $n = 42$, which is the number of populations, and $m = 2$, which is the number of blocks), g is the vector of breeding values of populations, and e is the vector of random errors, with Equação A, where σ_e^2 is the residual variance, and I is an identity matrix. X and Z are incidence matrices, respectively, of effects b and g.

Joint data distribution is normal, with mean and variance given by:

$$y|b, g, \sigma_e^2, \sigma_g^2 \sim N(Xb + Zg, I\sigma_e^2) \quad (2)$$

where σ_g^2 is the genetic variance.

The *a priori* distributions of the parameters are:

$$b \sim N(0, I10^8) \quad (3)$$

$$g \sim N(0, I\sigma_e^2) \quad (4)$$

$$\sigma_e^2 \sim GI\left(\frac{\eta_e}{2}, \frac{\eta_e V_e}{2}\right) \quad (5)$$

$$\sigma_g^2 \sim GI\left(\frac{\eta_g}{2}, \frac{\eta_g V_g}{2}\right) \quad (6)$$

Where b assumes a non-informative distribution (the normal distribution with a large variance value), *G1* represents the inverse gamma distribution with hyperparameters given by $\eta_e = 0.002$, $\eta_g = 1$, and $V_e = V_g = 1$

$$p(y) \propto p(b, g, \sigma_e^2, \sigma_g^2)p(b)p(g)p(\sigma_g^2)p(\sigma_e^2) \quad (7)$$

Statistical inference about the parameters $b, g, \sigma_e^2, \sigma_g^2$ relies on the *posterior* marginal distributions. In summary, random samples of the *posterior* marginal distributions are indirectly generated from the full conditional *posterior* distributions (f.c.p.d) (likelihood function × prior distribution of each parameter) by means of the MCMC algorithms. Thus, after a sufficiently large number of iterations, the values generated from the f.c.p.d. are samples of the *posterior* marginal distributions.

Two models were defined, the first with the presence of genetic effects (complete model) and the second without them (reduced models). The goodness of fit of these models was compared using the deviance information criteria (DIC) proposed by SPIEGELHALTER et al. (2002). The DIC is given by:

$$DIC = D(\bar{\theta}) + 2p_D \tag{8}$$

where $D(\bar{\theta})$ is the deviance estimate applied to the *posterior* mean of the parameters of the evaluated model, and p_D is the effective number of parameters in the model.

The density of the components of genetic and environmental variance was calculated to obtain the density and the heritability estimate (h^2), as follows:

$$h^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2}$$

where σ_g^2 is the genetic variance; σ_e^2 is the residual variance.

The selection differential (SD) was obtained as follows:

$SD = \bar{x}_s - \bar{x}_0$

where $\bar{x}_s$ is the *posterior* mean of the selected populations (with the standardized value of 30% of selection intensity of the populations, corresponding to 12 populations), and $\bar{x}_0$ is the *posterior* mean of all populations and parents in the experiment. With the information on heritability and selection differential, the expected genetic gain from selection was estimated, according to Falconer and Mackay (1996); ST MARTIN & FUTI (2000), by the expression:

$GS = (\bar{x}_s - \bar{x}_0) \times h^2$

and the expected genetic gain in percentage was calculated according to the expression:

$$GS\ (\%) = \left(\frac{(\bar{x}_s - \bar{x}_0) \times h^2}{\bar{x}_0}\right) \times 100$$

RESULTS

The chains reached convergence by the Geweke criterion after 1,000,000 iterations at 5% significance level (Table 2). The DIC value was 895.48 for the complete model, and 933.73 for the reduced model (without the presence of genetic effects). Consequently, the best-fit model contained the population genetic effects, and the *a posteriori* inference will be based on it. Thus, *a posteriori* estimates and densities for the sources of variation, populations (pop) and error (units) were obtained. The Bayesian density distribution for heritability estimation is given in figure 1. This allows a clear graphical representation of the degree of uncertainty around the average heritability estimates; and are therefore, intuitive ways to present the results. The evaluation of the best model fit was performed using DIC, in which the model with the lowest DIC value has the best fit. In the present study, the complete model showed the best fit, with DIC equal to 895.48, to the detriment of the reduced model. This value indicated the significance of the breeding effects of the populations under study. The deviance information criterion (DIC) is widely applied to assess the goodness of fit of models in Bayesian inference (RESENDE et al., 2014). Bayesian inference has advantages over the commonly used frequentist inference, including the incorporation of *a priori* knowledge and more accurate credibility intervals (0.025 and 0.975 quantile), increasing the reliability of components and estimated effects (PEIXOTO et al., 2021).

When using noninformative *a priori* information, the estimates of genetic parameters obtained by Bayesian inference present values similar to those obtained by frequentist inference by restricted maximum likelihood (REML) (BEAUMONT & RANNALA, 2004). Nonetheless, SILVA et al. (2020) obtained different results when testing three approaches in segregating populations of *Psidum guajava*. Two of these approaches were Bayesian approaches (one with informative and the other with noninformative *a priori* distribution) and the other was a mixed model. The authors reported greater accuracy through Bayesian analysis with informative *a priori* information, followed by Bayesian analysis with noninformative *a priori* information and, finally, REML/BLUP analysis.

The *a posteriori* mean of broad-sense heritability (h^2) for grain production in the plot was 0.51, the credibility intervals were HPD (0.025) 0.01 and HPD (0.975) 0.73, and the *a posteriori* standard deviation was 0.15 (Table 2). Figure 2 shows the results for the estimates of heritability density. According to RESENDE (2002), the heritability of the present study (0.51) is high ($h^2 > 0.50$). This estimate is within the expected range for grain yield, considering that this characteristic is controlled by a large number of genes and is highly influenced by the environment. Previous studies on segregating wheat populations estimate heritability using frequentist approaches.

Table 2 - Mean, standard deviation (STD), credibility (0.025, 0.500 and 0.975), Geweke test (Z) and probability for the Geweke test (prob.) of 34 F_2 populations and eight tropical wheat cultivars obtained by Bayesian approach for the yield per plot trait. Viçosa, MG, 2020.

Code	Cross	Mean	STD	0.025	0.500	0.975	Z	prob.*
-	Tbio Aton	-34.28	25.90	-85.54	-34.28	14.34	0.41	0.68
-	BRS 254	-56.44	28.22	-109.96	-57.36	0.43	0.20	0.84
-	BRS 264	6.32	24.43	-41.95	5.57	54.82	-0.85	0.39
-	BRS 394	-27.00	25.35	-77.16	-26.80	21.17	-0.08	0.93
-	CD 1303	-41.18	26.53	-92.71	-41.48	7.98	0.22	0.82
-	Tbio Duque	11.31	24.53	-36.65	10.62	60.26	-0.22	0.82
-	Tbio Ponteiro	-42.89	26.63	-94.49	-42.88	6.66	0.48	0.63
-	Tbio Sossego	24.34	25.21	-23.65	24.04	74.74	-0.69	0.49
F2_A2	Tbio Aton/BRS 254	6.74	24.51	-41.71	6.04	55.49	0.59	0.55
F2_A5	Tbio Aton/CD 1303	63.66	29.12	0.14	64.94	118.01	-0.24	0.81
F2_A6	Tbio Aton/Tbio Duque	3.80	24.46	-44.42	3.01	52.52	1.36	0.17
F2_A7	Tbio Aton/Tbio Ponteiro	-12.77	24.70	-62.14	-12.06	35.32	-0.40	0.69
F2_B1	BRS 254/Tbio Aton	-19.00	24.90	-68.64	-18.53	29.12	-0.34	0.74
F2_B4	BRS 254/BRS 394	8.94	24.48	-38.93	8.17	58.01	-1.80	0.07
F2_B5	BRS 254/CD 1303	76.61	31.03	0.81	78.45	132.86	-0.41	0.68
F2_B6	BRS 254/Tbio Duque	0.11	24.47	-48.57	0.10	48.44	-0.56	0.58
F2_B7	BRS 254/Tbio Ponteiro	8.09	24.53	-40.10	7.38	57.06	-0.56	0.56
F2_C1	BRS 264/Tbio Aton	7.78	24.50	-40.49	7.05	56.60	1.00	0.32
F2_C2	BRS 264/BRS 254	1.74	24.51	-46.62	1.18	50.40	0.27	0.79
F2_C4	BRS 264/BRS 394	-0.19	24.41	-48.71	-0.11	48.07	-1.31	0.19
F2_C5	BRS 264/CD 1303	14.92	24.69	-33.13	14.34	64.05	-1.17	0.24
F2_C8	BRS 264/Tbio Sossego	-74.91	24.69	-131.07	-76.69	-0.76	-1.17	0.24
F2_D1	BRS 394/Tbio Aton	15.00	24.78	-33.44	14.41	64.40	-1.41	0.16
F2_D2	BRS 394/BRS 254	-33.66	25.85	-85.85	-33.67	14.76	0.77	0.44
F2_D5	BRS 394/CD 1303	-19.62	25.83	-69.36	-19.17	28.34	0.19	0.85
F2_D6	BRS 394/Tbio Duque	11.84	24.59	-36.19	11.17	60.96	1.29	0.20
F2_D8	BRS 394/Tbio Sossego	14.98	24.73	-33.13	14.37	64.50	0.40	0.69
F2_E1	CD 1303/Tbio Aton	3.45	24.50	-44.95	2.68	52.45	-0.07	0.95
F2_E6	CD 1303/Tbio Duque	9.36	24.50	-38.70	8.66	58.32	-1.08	0.28
F2_E7	CD 1303/Tbio Ponteiro	77.72	31.18	0.87	79.60	134.01	-0.29	0.77
F2_E8	CD 1303/Tbio Sossego	-3.67	24.38	-52.22	-2.95	44.43	1.82	0.07
F2_F1	Tbio Duque/Tbio Aton	68.80	29.86	0.47	70.21	124.01	-0.30	0.77
F2_F2	Tbio Duque/BRS 254	-27.46	25.34	-77.91	-27.15	20.47	1.03	0.30
F2_F3	Tbio Duque/BRS 264	-10.50	24.61	-59.53	-9.80	37.64	0.37	0.71
F2_F5	Tbio Duque/CD 1303	-16.91	24.80	-66.37	-16.33	31.07	0.42	0.67
F2_F6	Tbio Duque/Tbio Ponteiro	4.03	24.41	-44.21	3.27	52.41	-0.46	0.65
F2_G3	Tbio Ponteiro/BRS 264	-18.43	24.89	-68.20	-18.01	29.74	0.58	0.56
F2_G5	Tbio Ponteiro/CD 1303	-37.23	26.17	-88.57	-37.37	11.42	0.65	0.52
F2_G6	Tbio Ponteiro/Tbio Duque	-23.27	25.12	-73.35	-22.82	24.66	-0.21	0.83
F2_H4	Tbio Sossego/BRS 394	-39.17	26.29	-90.67	-39.41	9.55	0.58	0.56
F2_H5	Tbio Sossego/CD 1303	92.23	33.47	1.24	94.98	150.57	-0.10	0.92
F2_H7	Tbio Sossego/Tbio Ponteiro	6.67	24.52	-41.60	5.96	55.57	0.78	0.44
Intercept	-	244.61	9.50	225.92	244.61	263.30	0.61	0.55
h^{2+}	-	0.51	0.15	0.01	0.53	0.73	-0.27	0.79

*prob: p-value > 0.01 – not significant; +h^2: heritability.

For instance, AKEL et al. (2018) analyzed separately F_1 hybrids of *Triticum durum* and reported an h^2 of 0.67 for grain yield (t ha^{-1}) and 0.40 analyzing the parents. In turn, PIMENTEL et al. (2014) observed heritability at an average level for grain yield equal to 39.15% in F3 populations of *Triticum aestivum*.

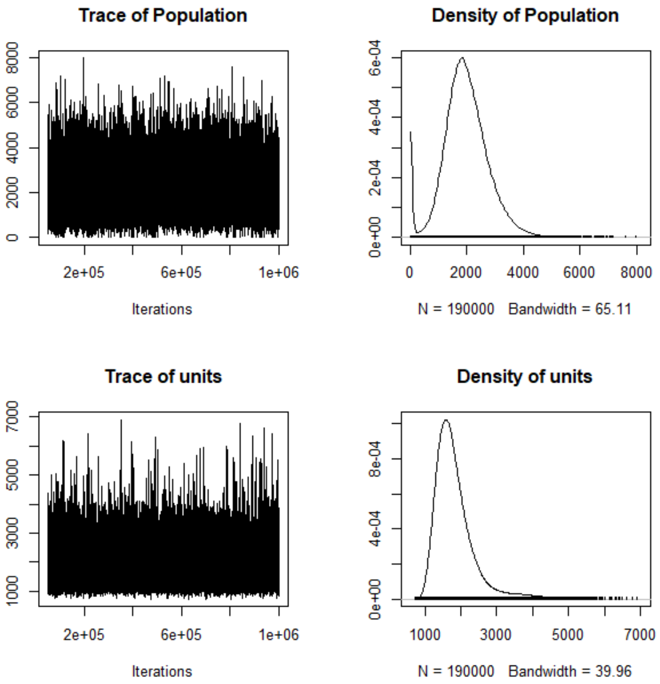

Figure 1 - Distribution chain of mean estimates of 190,000 estimates for the sources of variation population (pop) and error (units) of the model using noninformative prior, on the left. On the right, the distribution density function corresponding to the chain.

The heritability value of the present study is in an intermediate position in relation to previous literature. However, it is noteworthy that estimates of genetic parameters from Bayesian analyses tend to be more accurate (SILVA et al., 2020).

The grain yield intercept of the 34 populations and eight parents was 244.61 grams, with credibility intervals HPD (0.025) 225.92 g and HPD (0.975) 263.3 g, and with *a posteriori* standard deviation of 9.50 g. Significant breeding values (with credibility intervals that do not pass through zero) occurred for the populations: Tbio Aton/CD 1303, BRS 254/CD 1303, CD 1303/Tbio Ponteiro, Tbio Duque/Tbio Aton, and Tbio Sossego/Tbio Aton, being of 63.66, 76.61, 77.72, 68.8, and 92.23, respectively. All presented credibility intervals of 5% with values above zero, except for BRS 264/Tbio Sossego, which presented negative values (Table 2).

Bayesian models are more robust, generating more accurate estimates (JUNQUEIRA et al., 2016). This fact collaborates with the perspective of selection of superior populations with improved accuracy. In this context, the best F_2 populations were selected for generation advancement and for deriving promising lines for the breeding program, capable of meeting the demand of agricultural producers in the Brazilian Cerrado. Since the objective is to increase average grain yield, 13 populations were selected among those with estimates higher than the overall average of the experiment.

Regarding the *a posteriori* standard deviation, the populations with the highest values were Tbio Sossego/CD 1303 (33.47 g), CD 1303/Tbio Ponteiro (31.18 g), and BRS 254/CD 1303 (31.03 g). Conversely, the populations with the lowest values for the *a posteriori* standard deviation were: BRS 264/BRS 394 (24.41 g), Tbio Duque/Tbio Ponteiro (24.41 g), and CD 1303/Tbio Sossego (24.38 g). The range between the population with the highest (Tbio Sossego/CD 1303) and lowest (CD 1303/Tbio Sossego) *a posteriori* standard deviation was 9.09 grams (Table 2).

Figure 3A shows that among parents and F_2 populations, 23 crosses and genotypes had positive breeding value, ranging from 0.11 to 92.23. Figure 3B

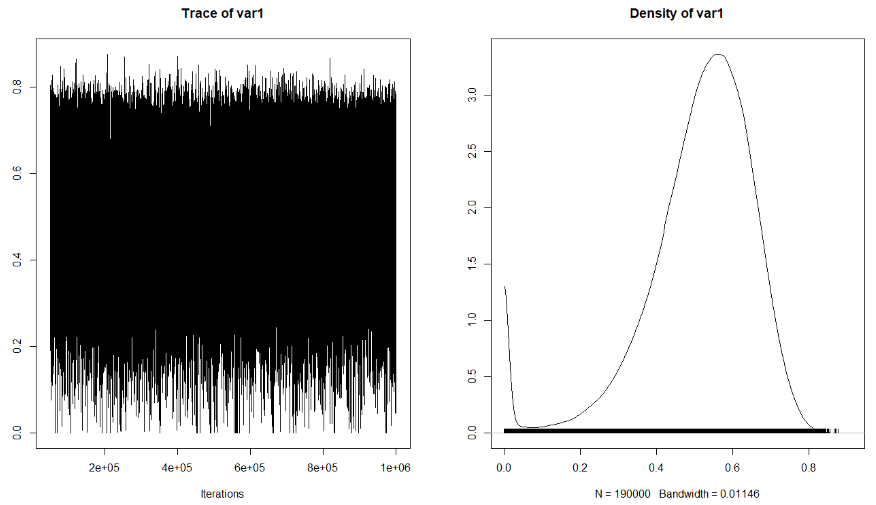

Figure 2 - Distribution chain of heritability estimates of 190,000 estimates of the model using noninformative priori, on the left. On the right, the distribution density function corresponding to the chain.

shows the populations selected based on the positive breeding value intercept. When considering the group with the 13 selected populations, its mean was 282.28 g plot^{-1}, with a selection differential of 37.67 g plot^{-1} in relation to the intercept of all populations and parents, of 244.61 g plot^{-1}. The expected genetic gain from selection was 19.2 g plot^{-1}, equivalent to 7.8%, for a selection intensity of 30%. The smallest positive breeding value intercept within the selected group belongs to population F2_B4 (BRS 254/BRS 394), with 253.55 g plot^{-1}. The population with the highest average was F2_H5 (Tbio Sossego/CD 1303), with average plot production of 336.84 g plot^{-1}.

The populations F2_H5 (Tbio Sossego/CD 1303), F2_E7 (CD 1303/Tbio Ponteiro), F2_B5 (BRS 254/CD 1303), F2_F1 (Tbio Duque/Tbio Aton), and F2_A5 (Tbio Aton/CD 1303) showed average grain yield per plot superior to all parents used in the crosses and in the experiment as controls. This shows the potential for selection of superior transgressive individuals within the wheat populations developed by the UFV Wheat Breeding Program, with a view to meeting the demand of the agricultural market in the Brazilian Cerrado. Another six F_2 populations of tropical wheat were selected together with two commercial control cultivars, Tbio Duque and Tbio Sossego.

The five populations that showed significant genetic effects, mentioned in the previous paragraph, presented an average estimate of 320.41 g plot^{-1}. The intercept of all hybrid and parent combinations was 244.61 g plot^{-1}. For the selection differential (SD) between populations with significant genetic effects and all combinations, SD was 75.80 g plot^{-1}. Considering only the parents used, the differences are even greater, since the average of the parents was of 234.29 g plot^{-1}, then the SD was 86.12 g plot^{-1}.

Of the five F_2 populations with significant effects, the three populations with the highest breeding values were Tbio Sossego/ CD 1303 (F2_H5), CD 1303/Tbio Ponteiro (F2_E7), and BRS 254/CD 1303 (F2_B5). For the three most promising populations among all 34 combinations, crosses involving wheat parents from different breeders (Biotrigo Genética, Coodetec, and Embrapa Trigo) resulted in F_2 populations with high average grain yield plot^{-1}, and with greater probability of extracting wheat progenies with satisfactory agronomic performance.

Strategies aimed launching cultivars with high yield potential are desirable, as they allow the intensification of wheat agricultural areas and enable satisfactory gains in production per unit of area. However, the intensification of annual gain in wheat yield is limited, with indications of stagnation. BECHE et al. (2014) reported gains of 0.92% year^{-1} when evaluating wheat cultivars released in the last 60 years in Brazil. In turn, WOYANN et al. (2019) observed gains of up to 1.28% year^{-1} in cultivars released between 1985 and 2014. Therefore, the

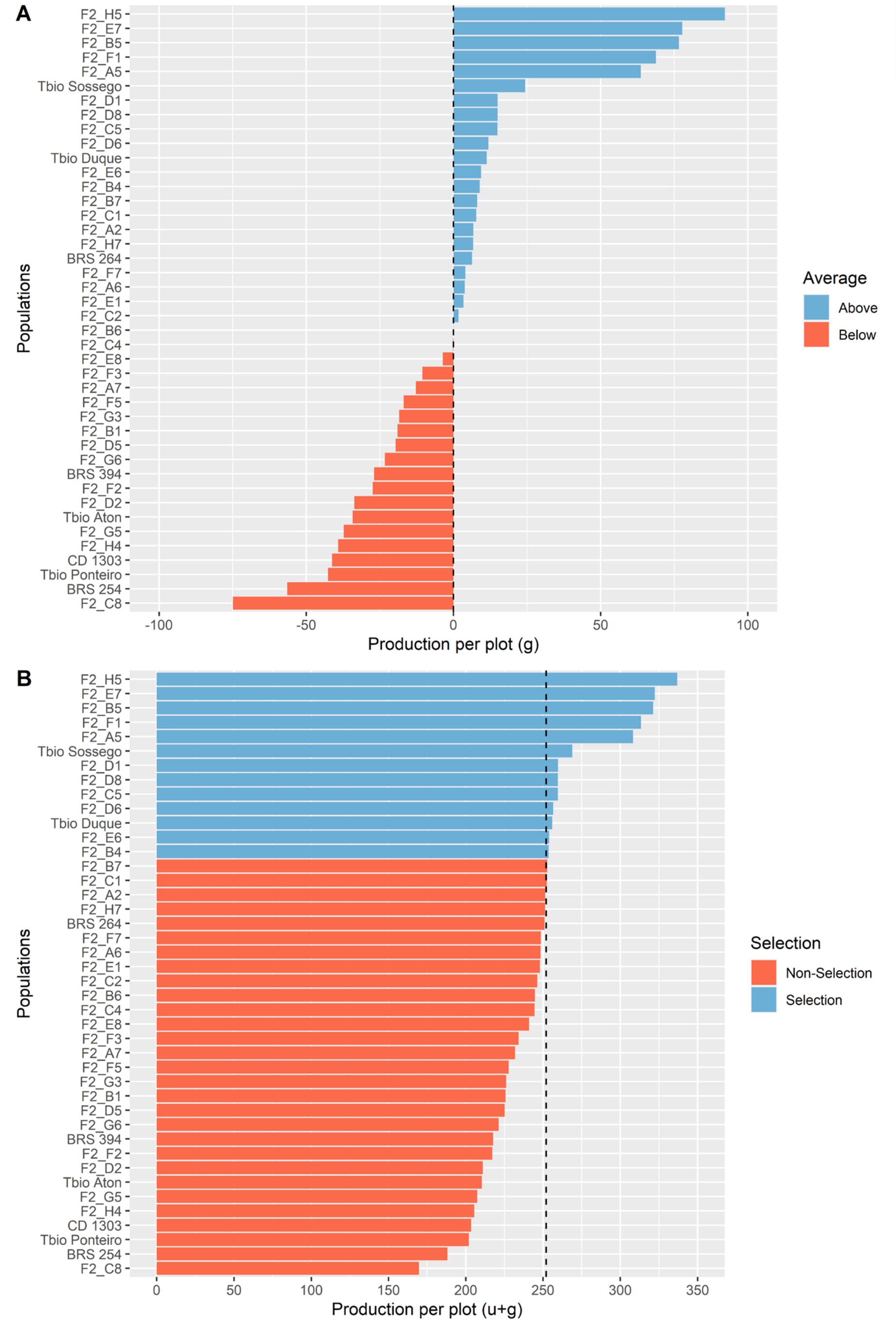

Figure 3 - Estimates of genetic value (A) and genetic value plus intercept (B) of 34 F2 populations and eight tropical wheat cultivars obtained by Bayesian approach for the yield per plot trait (g). Viçosa, MG, 2020.

significant selection gains obtained are noteworthy, especially when considering the gain of selected F_2 populations in relation to the parents, which are commercial cultivars.

The results of the gains are expressive and point to the possibility of extracting lines with high yield. It is noteworthy that the F_2 populations come from crosses involving parents from different breeders. This is because the maintenance of existing variability in groups of segregating populations allows for the improvement of selection, with a consequent increase in gains. The alleles fixed for a certain variable of a germplasm are usually different from those fixed for the same variable of another germplasm, thus leading to gene complementarity, which increases the possibility of identifying superior transgressive individuals.

CONCLUSION

Considering F_2 populations of tropical wheat, Bayesian inference provided an adequate model fit for the dataset. This approach can be used in tropical wheat breeding programs in early generation populations. Finally, 11 F_2 populations showed superior performance and were selected for generation advancement.

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DECLARATION OF CONFLICT OF INTEREST

The authors declare no conflict of interest. The founding sponsors had no role in the design of the study; in the collection, analysis, or interpretation of the data; in the writing of the manuscript, and in the decision to publish the results.

AUTHORS' CONTRIBUTION

All the authors contributed equally for the conception and writing of the manuscript. All authors revised the manuscript and approved the final version.

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Erratum

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