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Genetics/ Original Article

Informative prior distribution applied to linseed for the estimation of genetic parameters using a small sample size

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Abstract – The objective of this work was to evaluate a procedure for the elicitation of informative prior distribution, compared with non-informative prior distribution, in a small sample size, using 14 traits of three linseed (*Linum usitatissimum*) genotypes in seven sowing seasons. The values of the hyperparameters regulate the informativeness of the prior distribution; therefore, for each season, the hyperparameters to be used in the next season were calculated. The two prior distributions, non-informative and informative, were compared by the length of the credible interval and variance of the posterior distribution. In general, when the informative prior distribution is adopted, the genetic parameters present a shorter length of the credible interval and more precise estimates. The mechanism for informative prior elicitation using previous information from breeding programs is efficient for the estimation of genetic parameters, including heritability and genetic variance, even when the sample size is small. In genetic evaluation, the use of informative prior distribution is better than that of non-informative distribution for a small sample size. In general, the results of the informative prior distributions are indicative that the genetic values of the first sowing season are greater for the following traits: cycle length, plant height, and number of non-grained capsules and of productive branches.

Index term: *Linum usitatissimum*, flaxseed, plant breeding.

Distribuição a priori informativa aplicada à linhaça para estimação de parâmetros genéticos com uso de tamanho amostral reduzido

Resumo – O objetivo deste trabalho foi avaliar um procedimento para elicitação de distribuição a priori informativa, comparada à distribuição a priori não informativa, em tamanho amostral reduzido, com uso de 14 caracteres de três genótipos de linhaça (*Linum usitatissimum*), em sete épocas de semeadura. Os valores dos hiperparâmetros regulam a informatividade da distribuição a priori; portanto, para cada época, foram calculados os hiperparâmetros a serem utilizados na próxima época. As duas distribuições a priori, não informativa e informativa, foram comparadas pelo comprimento dos intervalos de credibilidade e pela variância da distribuição a posteriori. Em geral, quando a distribuição a priori informativa é adotada, os parâmetros genéticos apresentam menor comprimento do intervalo de credibilidade e estimativas mais precisas. O mecanismo de elicitação a priori informativa com uso de informações prévias de programas de melhoramento é eficiente para estimativa de parâmetros genéticos, incluindo herdabilidade e variância genética, mesmo quando o tamanho da amostra é pequeno. Na avaliação genética, o uso da distribuição a priori informativa é melhor do que o da distribuição não informativa para tamanho amostral pequeno. Em geral, os resultados das distribuições a priori informativas indicam que os valores genéticos da primeira época de semeadura são maiores para os seguintes caracteres: comprimento do ciclo, altura da planta, e número de cápsulas não granuladas e de ramos produtivos.

Termos para indexação: *Linum usitatissimum*, linhaça, melhoramento genético.

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Introduction

Linseed is a seed produced by flax (*Linum usitatissimum* L.), which belongs to the Linaceae family and the genus Linum (Yadeta Dabalo et al., 2020). Linseed is mainly known in Brazil for its use in preventive medicine due to its contents of omega 3 and omega 6 (*Linum usitatissimum* L., 2020). Among oilseeds, it is the most abundant source both of alpha-linolenic acid, a substance with an antioxidant function (Andruszczak et al., 2015), and of lignin (Kajla et al., 2015). Linseed can also be used as a raw material in the production of oil and bran because of its high content of oil, fibers, and proteins. In addition, it can be used in animal feed, cosmetics, or as a fiber mainly in textile industries and biofuel production (Rabetafika et al., 2011). In 2020, the world production of linseed was approximately 3.4 million tons in a cultivated area of 3.5 million hectares (FAO, 2020). In the same year, the production in Brazil was approximately 3.8 thousand tons in a cultivated area of 4.0 thousand hectares (IBGE, 2020). In the country, 100% of this production is located in the state of Rio Grande do Sul (IBGE, 2020), and there are only eight linseed genotypes registered and destined for oil.

In breeding programs, the estimation of genetic parameters is essential for designing and predicting outcomes. However, in the mixed model analysis, convergence problems and inadmissible estimates can occur when small samples are evaluated (Hox & McNeish, 2020). In this case, the Bayesian approach is advantageous due to the incorporation of prior knowledge about these parameters through prior distributions (Migon et al., 2014). Furthermore, although most studies assume a normal distribution for data, the Bayesian approach allows applying other distributions, such as the asymmetric one (Yousaf et al., 2019; Aslam et al., 2020), and the analysis of categorical data (Montesinos López et al., 2022). Since the impact of prior distribution in inferences increases as the sample size decreases (Tang, 2020), the elicitation of the prior distribution must be carried out with caution, and more informative prior distributions should be used instead of non-informative prior distributions (Van de Schoot et al., 2015, 2021).

The objective of this work was to evaluate a procedure for the elicitation of informative prior distribution, compared with non-informative prior distribution, in a small sample size, using 14 traits of three linseed genotypes in seven sowing seasons.

Materials and Methods

The field experiment was carried out in an experimental area located in the municipality of Augusto Pestana, in the state of Rio Grande do Sul, Brazil (28°26'30"S, 54°00'58"W, at an altitude of 280 m). The soil is classified as a Latossolo Vermelho distroférrico típico (Santos et al., 2018), corresponding to a Rhodic Hapludox, and the climate of the region is of the Cfa type according to Köppen-Geiger's climatic classification. The experimental design was a randomized complete block, in a 37 factorial arrangement – three linseed genotypes (IJUI001, IJUI002, and IJUI003) seven sowing seasons in 2020 (April 15, April 30, May 15, May 30, June 15, June 30, and July 15) –, with six replicates per treatment. The harvest dates for each sowing season were, respectively: October 05, October 15, October 22, October 28, October 27, December 9, and December 9. The plots consisted of 17 sowing rows spaced at 0.18 m, totaling 15 m^2; a useful area formed by the two central sowing rows was used to minimize border effects and evaluate plant traits. Sowing was performed at a density of 50 kg ha^{-1} or 150 seeds per linear meter, and a base fertilization using 200 kg ha^{-1} N-P_2O_5-K_2O (05-20-20) in the sowing line furrow, and 60 kg ha^{-1} urea (45% N) was applied at 30 days after sowing. Crop treatments were carried out preventively to minimize abiotic effects on the results of the experiment. The following traits were analyzed: cycle length, in days; capsule mass, in grams; grained capsules, in units; grain mass per plant, in grams; grain yield, in kilogram per hectare; non-grained capsules, in units; number of grains per plant, in units; productive branches, in units; plant height, in centimeters; rod diameter, in millimeters; reproductive insertion height, in centimeters; stem branch, in units; mass of a thousand grains, in grams; and total number of capsules, in units.

In order to understand the genotype × season interaction, the present study included climatic covariates obtained from the database of the Prediction of Worldwide Energy Resource project of National Aeronautics and Space Administration (Nasa, 2021) for the coordinates of the environment. The climatic covariates determined were: rainfall, in millimeter per day; minimum temperature, in degrees Celsius;

average temperature, in degrees Celsius; maximum temperature, in degrees Celsius; temperature range, in degrees Celsius; solar radiation, in watts per square meter per day; relative humidity, in percentage; and wind speed, in meter per second.

A statistical model containing all phenotypic observations in all seasons was evaluated; therefore, the used model included a systematic effect of season and an interaction effect of genotype × season, given by: $y = 1\mu + Xb + Z_1u_1 + Z_2u_2 + Z_3u_3 + e$, where y is the vector of phenotypic values; 1 is a vector with the same dimension of y and μ is the population mean; X and b are, respectively, the incidence matrix and the correspondent vector of season effects; Z_1, Z_2, and Z_3 are the incidence matrices of the random effects; u_1 is the vector of block effects; u_2 is the vector of the additive genetic values; u_3 is the vector of the effects of the genotype × season interaction; and e is the residual vector. Assuming that $e \sim N(0, I\sigma_e^2)$, the distribution of the observed data is given by:

$$y \mid \mu, b, u_1, u_2, u_3, \sigma_{u1}^2, \sigma_{u2}^2, \sigma_{u3}^2, \sigma_e^2 \sim N\begin{pmatrix} 1\mu + Xb + Z_1u_1 + \\ Z_2u_2 + Z_3u_3, I\sigma_e^2 \end{pmatrix}$$

where σ_{u1}^2 is the block variance, σ_{u2}^2 is the additive genetic variance, σ_{u3}^2 is the genetic variance for the interaction effect, and σ_e^2 is the residual variance.

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

$$\mu \sim N(0, I10^8), b \sim N(0, I10^8); u_1 \sim N(0, I_{u1}\sigma_{u1}^2),$$
$$u_2 \sim N(0, I_{u2}\sigma_{u2}^2); u_3 \sim N(0, I_{u3}\sigma_{u3}^2)$$

For the variance components, the prior distributions were given by:

$$\sigma_{u1}^2 \sim IG\left(\frac{\alpha_1}{2}, \frac{\alpha_1\beta_1}{2}\right); \sigma_{u2}^2 \sim IG\left(\frac{\alpha_2}{2}, \frac{\alpha_2\beta_2}{2}\right);$$
$$\sigma_{u3}^2 \sim IG\left(\frac{\alpha_3}{2}, \frac{\alpha_3\beta_3}{2}\right) \sigma_{e2}^2 \sim IG\left(\frac{\alpha_e}{2}, \frac{\alpha_e\beta_e}{2}\right)$$

where IG is the inverse-gamma distribution; and α_1, β_1, α_2, β_2, α_3, β_3, α_e, and β_e are the known constants called hyperparameters.

The statistical inference on the assessed parameters (b, u_1, u_2, u_3, σ_{u1}^2, σ_{u2}^2, σ_{u3}^2, and σ_e^2) is based on the posterior marginal distributions obtained through the Markov Chain Monte Carlo (MCMC) algorithms. Therefore, the j-th value of the chain of additive genetic heritability is given by:

$$h^{2(j)} = \frac{\sigma_{u2}^{2(j)}}{\sigma_{u1}^{2(j)} + \sigma_{u2}^{2(j)} + \sigma_{u3}^{2(j)} + \sigma_e^{2(j)}},$$

where $\sigma_{u1}^{2(j)}$, $\sigma_{u2}^{2(j)}$, $\sigma_{u3}^{2(j)}$ and $\sigma_e^{2(j)}$ are the values of the components of variance in the j-th iteration. In the present study, broad-sense heritability was also calculated, since the data are related to genotypes, and these are pure lines.

In the analysis, 300,000 iterations were used for the MCMC algorithms, and the first 20,000 iterations were discarded as burn-in. Following the performance of every set of 5 iterations (thin), a sample was retained to calculate posterior statistics. The convergence of the Markov chains was verified through Geweke's diagnostic. The posterior means and highest posterior density (HPD) region of genetic variance and heritability were obtained for the inferences. The interaction term was evaluated by the deviance information criterion (DIC), by comparing the model with and without the genotype x season interaction. The model with the lower DIC was selected. When the interaction term was not relevant, the phenotype information was analyzed within each season. Therefore, as the sample size becomes much smaller, it is necessary to use a mechanism to elicit informative prior distributions. For analyses using non-informative prior distributions, hyperparameters equal to $\alpha_1 = \alpha_2 = \alpha_e = 0.001$ and $\beta_1 = \beta_2 = \beta_e = 10^8$ were considered.

For the analyses using informative prior distributions, assuming

$$\sigma^2 \sim IG\left(\frac{\alpha_1}{2}, \frac{\alpha_1\beta_1}{2}\right),$$

the expected value and mode of σ^2 are given by, respectively,

$$\frac{\alpha_1\beta_1}{\alpha_1 - 2}(\alpha_1 \geq 2) \text{ and } \frac{\alpha_1\beta_1}{\alpha_1 + 2}.$$

Therefore, by equating the posterior mode (M_o) and the posterior mean ($\hat{\sigma}^2$) to these expressions,

$$\alpha_1 = \frac{2(M_0 + \hat{\sigma}^2)}{(\hat{\sigma}^2 - M_0)} \text{ and } \beta_1 = \hat{\sigma}^2\left(\frac{\alpha_1 - 2}{\alpha_1}\right)$$

(Azevedo et al., 2022). Non-informative prior distributions were used in the first season and in the i-th season (i = 1, ..., 7), and the hyperparameters were obtained by

$$\alpha_1 = \frac{2(M_0 + \hat{\sigma}^2)}{(\hat{\sigma}^2 - M_0)} \text{ and } \beta_1 = \hat{\sigma}^2\left(\frac{\alpha_1 - 2}{\alpha_1}\right)$$

and used in the (i + 1) – th season.

All computational implementations of the analysis were performed using the R software (R Core Team, 2020). The model was fitted in the MCMCglmm package (Hadfield, 2010) through the MCMCglmm function. The computational routine is available at Licae (2022).

Results and Discussion

For all parameters, the p-values of Geweke's Z statistics were higher than 0.01, which indicates that convergence was achieved and inferences can be made.

According to the DIC, there was a positive evidence of interactions between genotypes and seasons for nine traits – cycle length, grain mass per plant, non-grained capsules, number of grains per plant, productive branches, plant height, rod diameter, reproductive insertion height, and total number of capsules (Table 1). However, no interaction was observed for capsule mass, grained capsules, grain yield, stem branch, and mass of a thousand grains. Since, for grain yield, both DICs were similar, the most parsimonious model (without the interaction term) was chosen.

Table 1. Deviance information criteria (DIC) for the full (considering the genotype × season interaction) and null (not considering the interaction) models using the phenotypic data of 14 traits associated with three linseed (*Linum usitatissimum*) genotypes evaluated in seven sowing seasons in 2020 (April 15, April 30, May 15, May 30, June 15, June 30, and July 15), in the municipality of Augusto Pestana, in the state of Rio Grande do Sul, Brazil.

Trait	DIC[2]	
	Full model	Null model
Cycle length (days)	**1,123.88**	1,201.70
Capsule mass (g)	1,229.38	**1,201.60**
Grained capsules (units)	1,208.13	**1,202.64**
Grain mass per plant	**1,132.07**	1,201.51
Grain yield (kg ha^{-1})	1,967.38	**1,967.46**
Non-grained capsules (units)	**1,120.87**	1,202.03
Number of grains per plant	**1,218.28**	1,249.29
Productive branches (units)	**1,176.20**	1,203.16
Plant height (cm)	**1,182.16**	1,204.86
Rod diameter (mm)	**1,069.41**	1,201.46
Reproductive insertion height (mm)	**1,170.23**	1,203.97
Stem branch (units)	1,210.68	**1,201.54**
Mass of a thousand grains (g)	1,232.93	**1,202.23**
Total number of capsules (units)	**1,096.31**	1,203.09

[1] The DIC values in bold represent the model (full or null) chosen for the interpretations.

Given the detection of interaction for nine traits, it is important to understand the climatic factors that could influence the genotype × season interaction. The genetic values of the traits in each season are presented in Figure 1, and the climatic covariates for the sowing and harvesting seasons in April, May, June, July, August, September, October, November, and December 2020 are shown in Figure 2.

Rainfall was high in June and July (6.95 mm per day), and low in April and October (1.39 and 1.74 mm per day, respectively). The lowest minimum temperatures were recorded in July and August (-0.70 and -2.39°C, respectively). Considering these covariates, most traits presented a lower genetic value in the sixth season – with sowing on June 30 and harvesting on December 9 –, when the vegetative and reproductive phases of the crop occurred from June to August. According to Bosco et al. (2021), these phases are the most affected by air temperature, as noted in the present study for the genetic values of productive branches, total number of capsules, and reproductive insertion height. High temperatures, for example, can lower significantly grain yield (Čeh et al., 2020), which explains the lowest values for grain mass per plant and number of grains per plant. Casa et al. (1999) concluded that air temperatures from -4 to -7°C during the germination period could inhibit emergence due to seed freezing, and that the formation of light frosts at -1°C can cause severe damage to the flower and immature capsules. Bosco et al. (2021) highlighted that, for a better plant development, thermal limits should be established. However, in the case of linseed, these limits are not clearly defined in the literature, varying according to the assessed genotypes.

Concerning rainfall, high amounts during maturation can lead to new shoots, uneven maturation, and reduced yield (Kohn et al., 2016). The lack of rain also affects negatively linseed yield. In the initial phase, water deficit inhibits plant development, especially of the root part (Guo et al., 2012), and, in the reproductive phase, it causes flower abortion and number reduction, which limits the number of capsules per plant and of seeds per capsule (Bosco et al., 2021). Čeh et al. (2020) also found that water shortages affect linseed yield, shortening the plant growth cycle, and

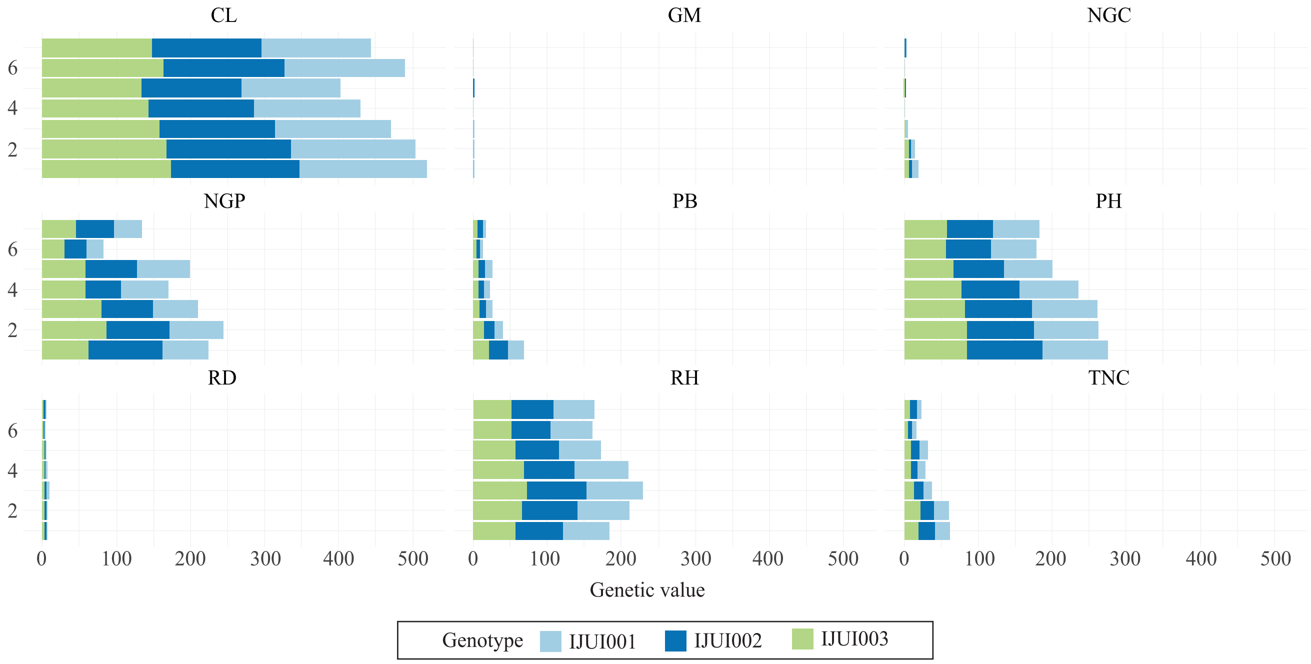

Figure 1. Genetic values of nine traits associated with three linseed (*Linum usitatissimum*) genotypes evaluated in seven sowing seasons in 2020 (April 15, April 30, May 15, May 30, June 15, June 30, and July 15), in the municipality of Augusto Pestana, in the state of Rio Grande do Sul, Brazil. Traits: CL, cycle length, in days; GM, grain mass per plant, in grams; NGC, non-grained capsules, in units; NGP, number of grains per plant, in units; PB, productive branches, in units; PH, plant height, in centimeters; RD, rod diameter, in millimeters; RH, reproductive insertion height, in centimeters; and TNC, total number of capsules, in units.

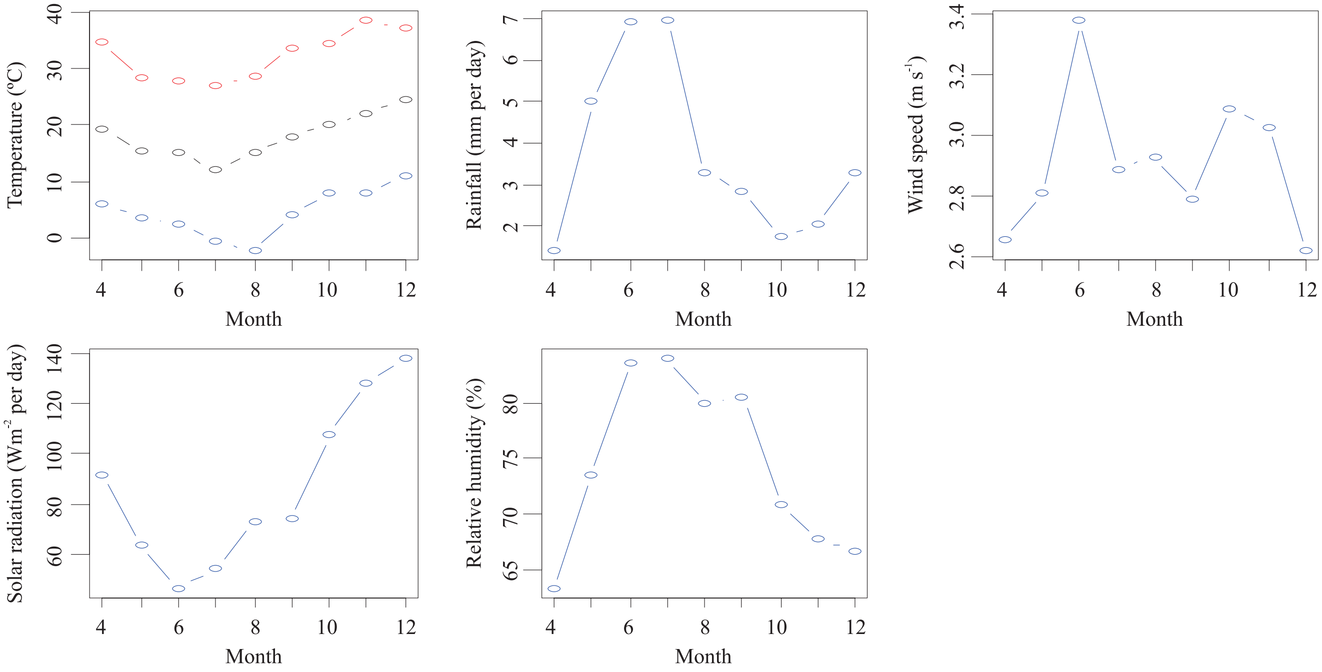

Figure 2. Climate covariates of the sowing months in 2020 (April, May, June, July, August, September, October, September, and December), in the municipality of Augusto Pestana, in the state of Rio Grande do Sul, Brazil. For temperature, the red, blue, and black lines represent, respectively, the maximum, minimum, and average temperatures.

that weather conditions could greatly impact the length of the crop growing season. Bosco et al. (2021) added that the productive performance of the crop can also be impaired by strong winds that can cause plant lodging; in the present study, wind speed was higher in June, October, and November. Therefore, extreme event conditions – such as hail, frost, rain excess or deficit, and wind speed – can significantly alter seeds, oil, and fiber yield and quality.

For the traits for which no interaction between genotypes and seasons was detected, each season was studied separately. Specifically, the information from previous seasons was used to update the prior distribution used to estimate the genetic parameters under a Bayesian framework. In the literature, other hyperparameter estimation methods are proposed, such as that of Silva et al. (2013), who used a similar procedure to this one in corn (*Zea mays* L.) data but with the scaled inverted chi-square distribution and the JAGS software that requires a greater computational effort than the one used in the present study (Azevedo et al., 2022). In another work, Migon et al. (2014) adopted the procedure called empirical Bayes method that uses current data for the estimation of the hyperparameter.

The heritability estimates were equal to 0.64 in all seasons for four of the five evaluated traits: capsule mass, grained capsules, stem branch, and mass of a thousand grains; the exception was grain yield (Figure 3). For the small sample size assessed, there was no influence of the data only from the prior distribution. Therefore, when using the non-informative prior distribution, the heritability values were identical for all five traits, a behavior that has also been observed by Tang (2020). Moreover, with the non-informative prior distribution, the HPD lengths of the heritabilities were around 0.80 for all traits, a value almost equal to the range of possible heritability values.

The heritability estimates varied throughout the seasons when the informative prior distribution was used, which is plausible due to the influence of the environment, shown by weather conditions even when

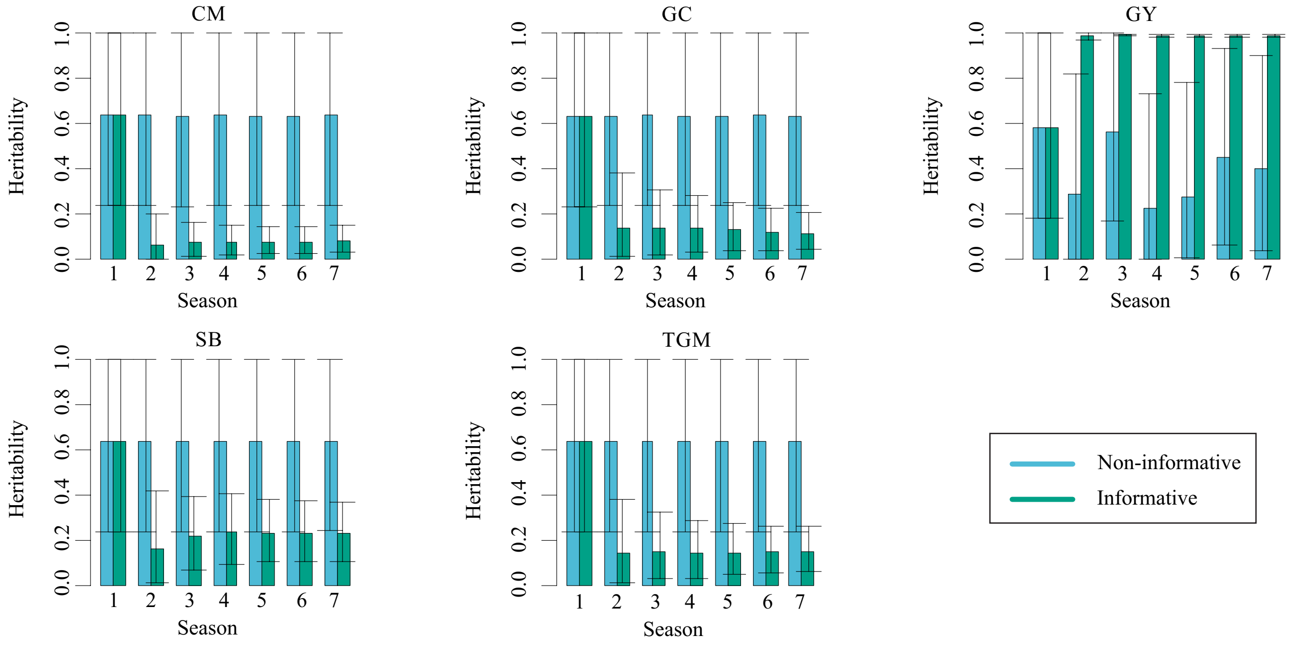

Figure 3. Posterior mean and highest posterior density of the heritabilities of five traits associated with three linseed (*Linum usitatissimum*) genotypes evaluated in seven sowing seasons in 2020 (April 15, April 30, May 15, May 30, June 15, June 30, and July 15), in the municipality of Augusto Pestana, in the state of Rio Grande do Sul, Brazil. Traits: CM, capsule mass, in grams; GC, grained capsules, in units; GY, grain yield, in kilogram per hectare; SB, stem branch, in units; and TGM, mass of a thousand grains (TGM), in grams.

this interaction had not been previously detected. In this scenario, the value and lengths of the HPD of the heritabilities after a specific season remain unchanged. Conversely, Azevedo et al. (2022) and Silva et al. (2013) reported a decrease in HPD lengths over the years; however, these authors evaluated a larger sample size. In the present study, the HPD lengths were longer in the non-informative prior distribution, which must be pointed out since, when the sample size is small, the prior specification might have a strong effect on posterior results (Van de Schoot et al., 2021).

The prior and posterior densities in the analysis with non-informative and informative prior distributions, respectively, were obtained for mass of a thousand grains and grain yield, whose behavior was similar that of the other traits (Figures 4 and 5). According to Azevedo et al. (2015), plots between prior and posterior densities, that is, the distance between them, also show the extent of Bayesian learning (learning with data). When there is little or no knowledge (non-informative prior distributions), a greater distance between prior and posterior densities suggests a high Bayesian learning. Therefore, using non-informative distribution, some learning was obtained from the data, as indicated by the difference between the distributions. However, when there is a high knowledge about the parameters (informative prior distributions), a smaller distance between prior and posterior densities can also indicate a high Bayesian learning, mainly in a knowledge update mechanism using previous data, since a highly informative prior distribution is built. Despite this, when the posterior distributions in both analyses were compared, the variance of distribution in the informative analysis was much smaller than that in the non-informative analysis, indicating a greater precision of the estimates and a greater cumulative knowledge about heritability. Similar results were obtained for the posterior mean of the additive genetic

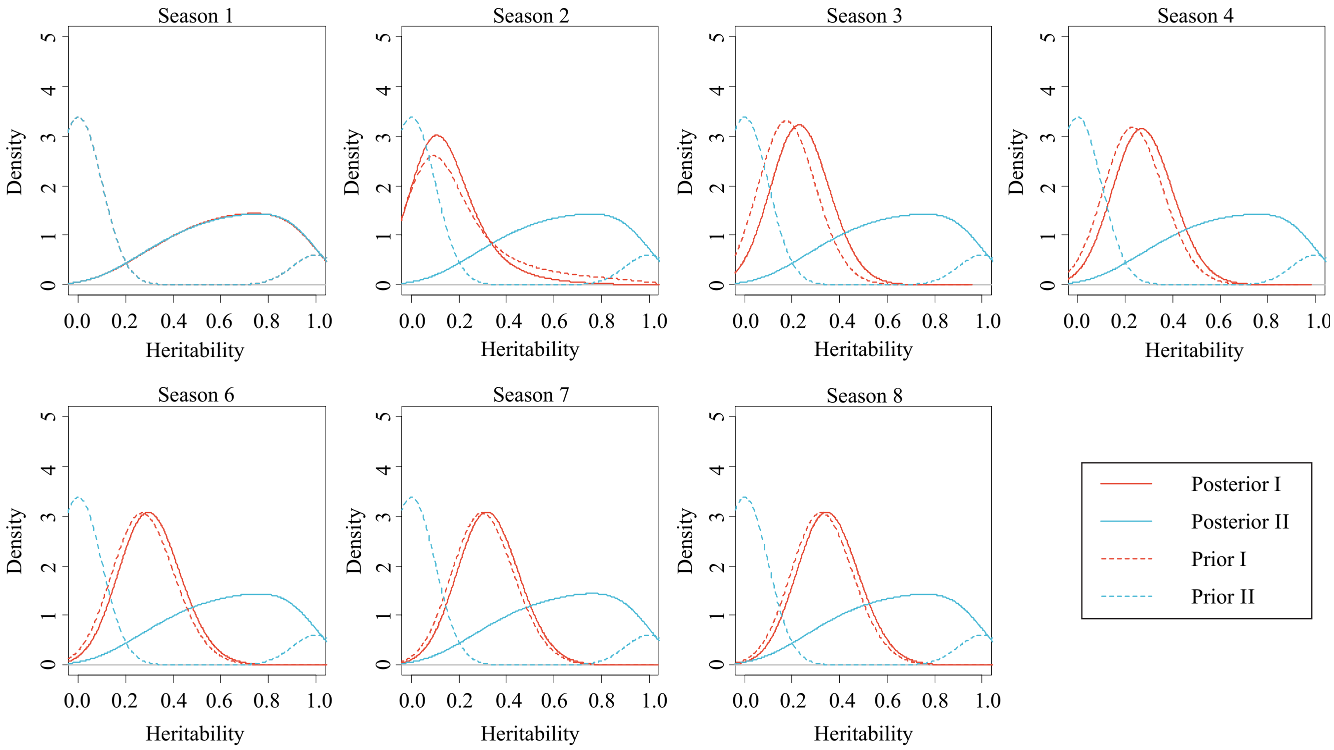

Figure 4. Marginal posterior densities and prior densities of the heritability of mass of a thousand grains (grams), considering informative prior distributions (Posterior I and Prior I) and non-informative prior distributions (Posterior II and Prior II), for three linseed (*Linum usitatissimum*) genotypes evaluated in seven sowing seasons in 2020 (April 15, April 30, May 15, May 30, June 15, June 30, and July 15), in the municipality of Augusto Pestana, in the state of Rio Grande do Sul, Brazil.

variances and their respective HPDs. This shows that the lengths of the HPDs are smaller in the informative prior distribution, except for the grain yield trait.

Considering the results of the informative prior distribution in the seventh season, the estimates of heritability were low to high (Figure 3), being of: 0.08 [0.03, 0.15] for capsule mass, 0.12 [0.05, 0.21] for grained capsules, 0.98 [0.98, 1.00] for grain yield, 0.22 [0.11, 0.37] for stem branch, and 0.15 [0.06, 0.26] for mass of a thousand grains. In the literature, few studies have included a range for linseed traits. For mass of a thousand grains, for example, Tadesse et al. (2010) and Adugna & Labuschagne (2004) reported a heritability, respectively, equal to 0.34 and 0.40, values slightly higher than those found in the present study, except for grain yield, with a high estimate close to 1. This result could have been overestimated because, according to Silva et al. (2013), a data-based informative prior distribution can lead to biased estimates of the mean and variance of scale parameters. However, although high, the value obtained in the present study is in line with those found in other works. Mirza et al. (2011) reported values ranging from 0.74 to 0.97 throughout several years of evaluation, whereas Bibi et al. (2013) observed a heritability equal to 0.67. Considering the results of the conjoint analysis, the estimates of heritability were low (Figure 6), being of: 0.17 [0.07, 0.28] for cycle length, 0.12 [0.05, 0.20] for grain mass per plant, 0.06 [0.02, 0.12] for non-grained capsules, 0.04 [0.01, 0.07] for number of grains per plant, 0.12 [0.04, 0.21] for productive branches, 0.06 [0.02, 0.10] for plant height, 0.04 [0.01, 0.07] for rod diameter, 0.07 [0.02, 0.14] for reproductive insertion height, and 0.04 [0.01, 0.07] for total number of capsules. For plant height, Tadesse et al. (2010) and Terfa & Gurmu (2020) found a heritability, respectively, equal to 0.30 and 0.36, which are values higher than that of 0.06 found here. For total number of capsules, Terfa & Gurmu (2020) observed a heritability equal to 0.12, a value close to that of the present study, while Dhirhi & Mehta (2019) reported a higher value of 0.35. For grain mass per plant, Adugna & Labuschagne (2004) and Dhirhi & Mehta (2019) found a heritability, respectively, equal to 0.16 and 0.14. Heritability values can, therefore, vary, since the heritability of traits greatly depends on the materials under study, as well as on the variability among environments and the used statistical estimation method.

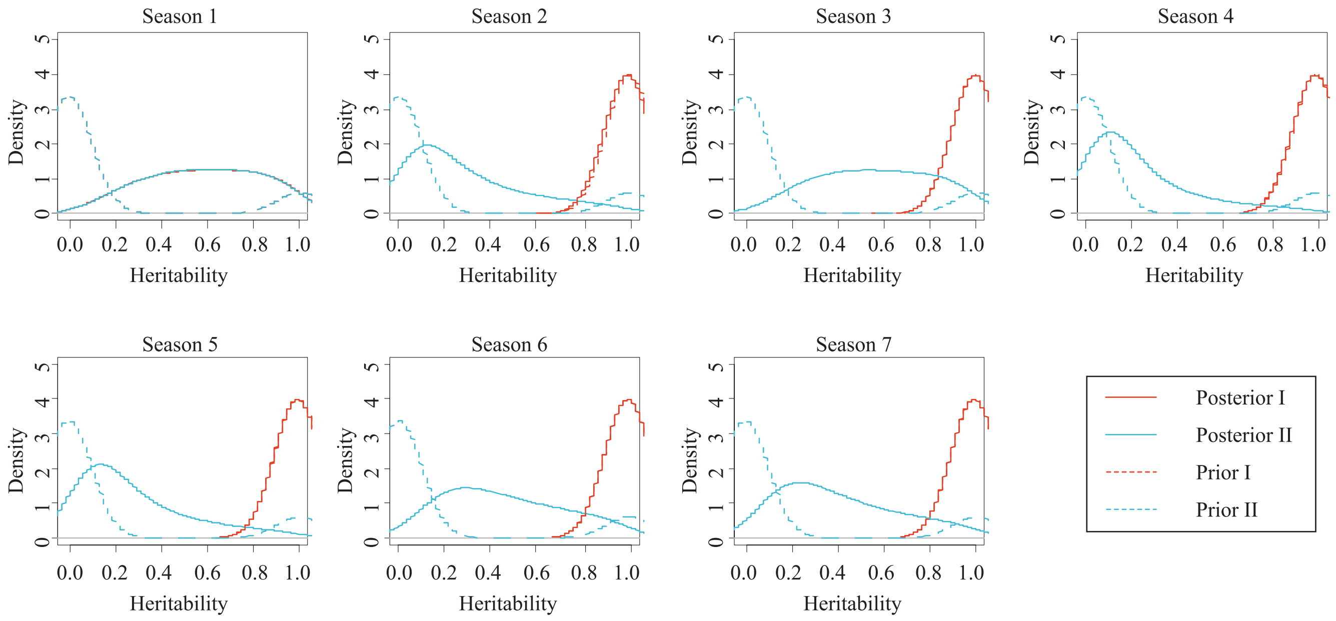

Figure 5. Marginal posterior densities and prior densities of the heritability of grain yield (kilogram per hectare), considering informative prior distributions (Posterior I and Prior I) and non-informative prior distributions (Posterior II and Prior II), for three linseed (*Linum usitatissimum*) genotypes evaluated in seven sowing seasons in 2020 (April 15, April 30, May 15, May 30, June 15, June 30, and July 15), in the municipality of Augusto Pestana, in the state of Rio Grande do Sul, Brazil.

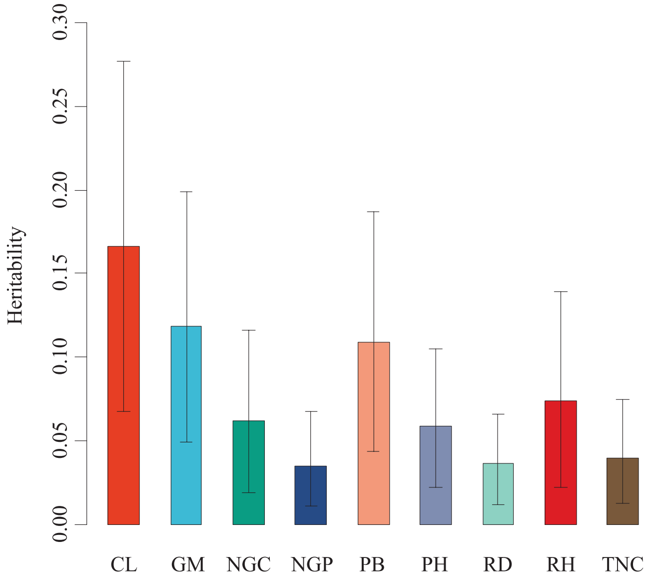

Figure 6. Posterior mean and highest posterior density of the heritabilities of nine traits associated with three linseed (*Linum usitatissimum*) genotypes evaluated in seven sowing seasons in 2020 (April 15, April 30, May 15, May 30, June 15, June 30, and July 15), in the municipality of Augusto Pestana, in the state of Rio Grande do Sul, Brazil. Traits: CL, cycle length, in days; GM, grain mass per plant, in grams; NGC, non-grained capsules, in units; NGP, number of grains per plant, in units; PB, productive branches, in units; PH, plant height, in centimeters; RD, rod diameter, in millimeters; RH, reproductive insertion height, in centimeters; and TNC, total number of capsules, in units.

Conclusions

1. In general, when informative prior distribution is used, the genetic parameters evaluated present a shorter length of the credible interval and more precise estimates.
2. The mechanism for informative prior elicitation using previous information from breeding programs is efficient for the estimation of genetic parameters, including heritability and genetic variance, even when the sample size is small.
3. The use of informative prior distribution is better than that of non-informative distribution when using a small sample size in genetic evaluation.
4. In general, the results of the informative prior distributions are indicative that the genetic values of the first sowing season, on April 15, are greater for the traits cycle length, non-grained capsules, productive branches, and plant height, whereas genotype IJUI002 has more genetic values for number of grains per plant and plant height in all sowing seasons.

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