



Influence of hormonal protocols on genomic prediction of sexual precocity in Nelore heifers

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ARTICLE INFO

Article history:

Received 11 September 2025

Revised 14 January 2026

Accepted 15 January 2026

Available online 22 January 2026

Keywords:

Bovine

Fixed-time artificial insemination

Genetic parameter

Genomic

Puberty

ABSTRACT

Reproductive efficiency is a key determinant of profitability in beef cattle systems, and hormonal protocols are widely used to improve reproductive performance in tropical breeds. The objective of this study was to assess the effect of hormonal stimulation on the estimation of variance components and genomic prediction ability of the probability of calving before 30 months of age (**PC30**) of Nelore heifers. The database contained information from 31 554 heifers of the National Association of Breeders and Researchers, Brazil. Among them, 22 105 heifers were not genotyped, and 9 449 were genotyped. These animals were categorised based on mating type (**MT**), with and without hormonal stimulation. For the estimation of genetic parameters and variance components in the complete database, two models were used: one with the inclusion of MT and one without. A single-step genomic BLUP animal threshold model was used. The Linear Regression (**LR**) validation method was employed to assess model performance. The dataset was divided into training subsets with 31 554 animals with phenotype records and validation subsets with 1 184 genotyped animals with phenotype records, but without progeny records. The subsets were further stratified by mating type. The heritability (**h²**) estimated for PC30 was of low magnitude and similar for both models (0.175 without MT and 0.18 with MT). Only the group of stimulated heifers with the inclusion of MT in the model exhibited a higher partial genomic breeding value (**GEBV**) than the complete GEBV. For LR estimators, Spearman correlation was not influenced by the inclusion of MT in the model. In animals with hormonal stimulation, a correlation of 0.95 was observed, whereas without hormonal stimulation, it was 0.96. Accuracy was similar across mating types (MT), and the inclusion of MT in the model did not alter the estimation (animals without hormonal stimulation: 0.36 without MT and 0.37 with MT; animals with hormonal stimulation: 0.38 with and without MT). The bias ($\pm$ SD) for stimulated animals (-0.09 ± 0.05 without MT and 0.04 ± 0.05 with MT) compared to non-stimulated animals (-0.01 ± 0.05 without MT and -0.02 ± 0.06 with MT). In conclusion, the estimation of variance components and **h²** for early pregnancy before 30 months is not influenced using hormonal stimulation and/or the inclusion of mating type in the evaluation model. However, there is a bias effect when considering hormonal stimulation in genomic prediction for PC30.

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Implications

Reproductive efficiency is a key factor affecting productivity in beef cattle systems, and hormonal protocols are widely used to improve reproductive performance in heifers. This study evaluated

whether hormonal stimulation influences genetic parameter estimation and the reliability of genomic predictions for early calving in Nelore heifers. The results showed that hormonal stimulation does not alter variance components, heritability, or prediction accuracy. However, genomic predictions for hormonally stimulated animals were more biased when this management practice was not accounted for in the model. These findings indicate that considering mating type in genetic evaluations can improve the

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interpretation of genomic predictions in herds where hormonal protocols are routinely applied.

Introduction

A strategy to improve the productive and economic indices of cattle herds in the tropics is by advancing the reproductive life of females, thereby reducing the age at puberty and, consequently, the age at first calving (Brunes et al., 2020). According to Moorey and Biase (2020), sustainable intensification of beef cattle production involves selection for sexual precocity in heifers, based on reducing age at first conception and calving. This strategy leads to increased productivity through a greater number of calves produced throughout the productive life of early-maturing females and a reduction in the generation interval.

An alternative approach for selecting earlier maturing animals involves using indicators of sexual precocity, such as age at first calving and early pregnancy in heifers. These indicators serve as markers for the onset of heifer reproductive life (Brunes et al., 2020), making them easily measurable traits. The trait probability of calving before 30 months of age (PC30) has been applied as a selection criterion in Zebu herds. This trait exhibits moderate h^2 (0.29) and is expected to respond to selection. Additionally, it is positively correlated with other traits such as male puberty and dam longevity in the herd (Silva Neto et al., 2020).

Although the genetic component of the animal can influence sexual precocity (Catussi et al., 2023), environmental aspects such as nutrition, environment and reproductive management also contribute to heifer reproductive performance (Araújo et al., 2019; Freitas et al., 2021). Management errors, such as late exposure of females to reproduction and failures in oestrus detection, are among these factors (Brunes et al., 2018; Oliveira Junior et al., 2021). However, in recent years, there has been a significant increase in the use of reproductive biotechnologies to enhance production efficiency and management conditions (Baruselli et al., 2017; Ferré et al., 2020; Mello et al., 2016). Among these biotechnologies, mention can be made of the use of hormonal protocols aimed at inducing puberty in heifers (Sá Filho et al., 2015; Magi et al., 2020). Another technology used is fixed-time artificial insemination (FTAI), which is a tool that allows for animal insemination without oestrus detection (Bó et al., 2003; Da Silva et al., 2021).

Several hormonal protocols using artificial insemination (AI) have been proposed to induce puberty in heifers, with prominence given to those using progesterone associated with estradiol (Sá Filho et al., 2015; Magi et al., 2020). The most widely used reproductive biotechnology in the world is AI, and its application brings significant benefits to herds compared to natural service (Baruselli et al., 2018). The use of AI, combined with synchronization protocols, offers numerous advantages related to increased productivity and economic return. The significant growth of AI in tropical regions coincided with the adoption of synchronization protocols for FTAI (Baruselli et al., 2022). According to Vilela et al. (2016), FTAI uses hormones to establish the ideal time for insemination in advance, regardless of oestrus observation. This biotechnology offers numerous advantages, such as better zootechnical control, maintenance of genetic variability, facilitation of selection and genetic improvement, choice of calving season, organization of management, and improved financial returns (Bó et al., 2007; Figueredo et al., 2019).

In practice, the advantages of hormonal protocols for FTAI are evident compared to reproductive management practices that do not utilise hormonal stimulation. However, there is still no consensus regarding the impact of this tool on the expression of the genetic component for female sexual precocity, as these protocols

may exert direct influence on heifer performance. Currently, there is a wide variety of FTAI protocols available on the market, which differ in duration, number of treatments, hormones used, among other factors (Baruselli et al., 2017). Thus, variation in reproductive management and differential treatment among animals and herds may mask phenotypes. FTAI protocols alter the reproductive physiology and endocrinology involved in oestrous cycles (Oliveira Junior et al., 2021). Females subjected to synchronization protocols for FTAI have a greater chance of becoming pregnant. In this sense, even genetically inferior heifers could have their performance altered due to hormonal protocols. Masked phenotypes or those with high environmental influence may introduce bias in genetic evaluation and modify genetic and residual variances (Oliveira Junior et al., 2021).

Currently, there are no published scientific studies evaluating how the use of hormonal protocol impacts the manifestation of female sexual precocity and how they could influence the genetic evaluation of early pregnancy occurrence or the probability of calving before 30 months of age. The interaction between genetic and environmental factors influencing reproduction is not yet well understood. A deeper understanding of this could significantly improve selection and genetic progress for sexual precocity in Zebu females. Thus, the aim was to assess the effect of hormonal stimulation on the estimation of variance components and genomic prediction ability of the probability of early calving before 30 months of age (PC30) in Nelore heifers.

Material and methods

Phenotypic data

The dataset used in this study consisted of Nelore cattle from a genetic improvement programme, the National Association of Breeders and Researchers (ANCP, Ribeirão Preto, Brazil). The database comprised 31 554 Nelore heifers with information on the probability of early calving at 30 months (PC30), of which 22 105 (36.96% of pregnant heifers) were not genotyped and 9 449 (85.86% of pregnant heifers) were genotyped. These heifers were divided by mating type (MT), with hormonal stimulation in FTAI protocols and without hormonal stimulation (AI or natural mating in pasture) (Table 1).

Heifers were exposed to reproduction between 10 and 14 months of age, with a reproductive season lasting three months. Females that did not become pregnant were re-exposed around 24 months of age. All heifers under evaluation for PC30 were exposed to reproduction in their weaning year to determine sexual precocity. The trait PC30 was modelled as a binary variable under a threshold approach. Heifers that calved before 30 months of age were coded as successes (2), and those calving after 30 months as failures (1). Heifers that did not have reproductive records or did not calve within the observation window were considered missing data (not censored) and excluded from the analysis.

Table 1
Number of records and pregnancy percentage for Nelore heifers by mating type and genotyped animals.

Category	Mating type		
	With stimulation	No stimulation	Total
Non-genotyped	4 994 (49.20%)	13 879 (78.02%)	22 105 (36.96%)
Genotyped	5 110 (50.80%)	3 910 (21.98%)	9 449 (85.86%)
Total	10 059 (64.06%)	17 789 (48.38%)	31 554

Percentages in parentheses for “With stimulation” and “Without stimulation” refer to the proportion of genotyped and non-genotyped animals within each mating type. Percentages in the “Total” column correspond to the proportion of animals within the complete dataset.

Heifers were classified according to mating type (MT) as either subjected to hormonal stimulation (FTAI protocols) or not (AI or natural mating in pasture). The distribution of genotyped and non-genotyped animals by mating type is shown in Table 1. Percentages in parentheses for “With stimulation” and “Without stimulation” refer to the proportion of genotyped and non-genotyped animals within each mating type. Percentages in the “Total” column correspond to the proportion of animals within the entire dataset.

Genotypic data

A total of 9 449 animals were genotyped using a low-density panel (Zoetis CLARIFIDE® Nelore version 3.1) containing 26 915 single-nucleotide polymorphism (SNP) markers. Samples with a call rate below 90%, markers with minor allele frequency below 0.05, call rate for SNPs below 90%, and Hardy-Weinberg equilibrium failure exceeding a threshold of > 0.01 were not considered in subsequent analyses. Markers with redundant positions and those located on non-autosomal chromosomes were also excluded, resulting in a final genotype file with 16 922 SNPs and 9 449 animals.

Estimation of genetic parameters and genomic prediction

For the estimation of genetic parameters and variance components for the complete database, two threshold models were used, one without the inclusion of mating type (no MT) and one with the inclusion of mating type (with MT). Both models considered the effect of contemporary group (year and farm of birth, management group at weaning and at year), and cow age class (early heifer progeny, traditional primiparous, or multiparous). Contemporary groups with fewer than five animals and without phenotypic variability were excluded, resulting in the removal of approximately 15% of the original records. Gibbs chains were generated with 500 000 iterations, with an initial burn-in period of 100 000 and a sampling interval of 100. Heritability (h^2) for PC30 was calculated with samples generated at each Gibbs sampling iteration, and subsequently, the mean of the samples was estimated. Convergence was tested using the R Bayesian Output Analysis package (Smith, 2007).

The mating types used in the models were with hormonal stimulation and without hormonal stimulation. The animal model was used to estimate the variance components for the categorical trait (as described by Henderson, 1984), utilizing the threshold model approach (Gianola and Foulley, 1983) as follows:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \mathbf{e}$$

where $\mathbf{y}$ is a vector of dependent variables; $\boldsymbol{\beta}$ is a vector of fixed effects, including contemporary group and dam category of the heifer (early heifer, traditional heifer, multiparous cow); $\mathbf{X}$ is the incidence matrix associating $\boldsymbol{\beta}$ with $\mathbf{y}$; $\mathbf{u}$ is a vector of random effects of direct additive genetic effects; $\mathbf{Z}$ is the incidence matrix associating $\mathbf{u}$ with $\mathbf{y}$; and $\mathbf{e}$ is the residual effects.

In the threshold model, it was assumed that the underlying scale follows a normal distribution:

$$\mathbf{U}|\boldsymbol{\theta} \sim N(\boldsymbol{\theta}, \mathbf{I}\sigma_e^2)$$

where $\mathbf{U}$ is the vector of the base scale of order r (with r : number of animals); $\boldsymbol{\theta} = (\boldsymbol{\beta}, \mathbf{u})$ is the parameter vector of order s (with s : number of classes); $\boldsymbol{\beta}$ is a vector of fixed effects of order s ; $\mathbf{u}$ is the additive genetic effect; $\mathbf{I}$ is the identity matrix of order $r \times r$; and σ_e^2 is the residual variance.

The method used to predict genomic values was the single-step genomic BLUP (ssGBLUP), which is a modified version of the

animal model (BLUP) and assumes $\mathbf{u} \sim N(0, \mathbf{H}\sigma_u^2)$, where $\mathbf{H}$ integrates the additive relationship matrix ($\mathbf{A}$) and the genomic relationship matrix ($\mathbf{G}$) into a single matrix (Christensen and Lund, 2010; Aguilar et al., 2010). The inverse of the $\mathbf{H}$ matrix ($\mathbf{H}^{-1}$) was calculated as follows:

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix}$$

where $\mathbf{G}^{-1}$ is the inverse of the genomic relationship matrix and $\mathbf{A}_{22}^{-1}$ is the inverse of the $\mathbf{A}$ matrix for the genotyped animals. In order to minimise issues during matrix inversion, the genomic relationship matrix was blended with the pedigree-based relationship matrix for genotyped animals using weights of 0.95 and 0.05 for $\mathbf{G}$ and $\mathbf{A}_{22}$, respectively.

Validation

The Linear Regression (LR) validation method (Legarra and Reverter, 2018) was used to assess the genomic predictive ability of the model and the effect of the influence of FTAI on the prediction of young animals. Initially, the LR validation method requires evaluations with a partial (p) dataset where the phenotypic records of target validation or validation subset animals are removed; thus, the partial GEBV (GEBV_p) is calculated from relatives and genomic information. Then, the phenotypes of validation animals are included for further evaluation, and the whole (w) genomic breeding value (GEBV_w) is achieved ($N = 31\,554$ animals). Heifers born in 2020 were selected as target validation subset for being the young selection candidates. The validation subset ($N = 1\,184$) is composed of genotyped young animals with phenotype records but without progeny records. Animals from validation subset were divided by mating type, with 537 not subjected to hormonal stimulation and 609 subjected to hormonal stimulation.

The genomic predictions of the validation subset were obtained using genotype and phenotype (GEBV_w, total evaluation) or using only genotype when the phenotype of the validation subset is omitted (GEBV_p, partial evaluation). This validation strategy simulates the practical situation of genomic selection, where the genomic prediction of younger animals (i.e., selection candidates) is based on the phenotypic and genotypic information of proven or older animals in the entire population.

Under the LR method, prediction accuracy was calculated as a direct estimate of the population reliability (or accuracy squared, acc_p^2) of the estimated genetic value based on partial data. In this methodology, the covariance $\text{cov}(\hat{\mathbf{u}}_w, \hat{\mathbf{u}}_p)$ of the estimated genetic value based on partial and complete data is a function of the reliability of the estimated genetic value:

$$\text{acc}_p^2 = \frac{\text{cov}(\hat{\mathbf{u}}_w, \hat{\mathbf{u}}_p)}{(1 - F)\sigma_u^2}$$

where $\mathbf{u}$ is the vector of genomic breeding value (GEBV) and $\bar{F}$ is the average coefficient of inbreeding for validation subset animals; σ_u^2 is the additive genetic variance. Bias was calculated as the difference between the mean of the partial ($\hat{\mathbf{u}}_p$) and total ($\hat{\mathbf{u}}_w$) GEBV, that is, $\hat{\mathbf{u}}_{w,p} = \hat{\mathbf{u}}_p - \hat{\mathbf{u}}_w$, with an expected estimator of 0 if unbiased. The dispersion of GEBV was evaluated as the deviation of the regression coefficient (b_1) from 1, where b_1 was obtained from the regression of $\hat{\mathbf{u}}_w$ on $\hat{\mathbf{u}}_p$: $\hat{\mathbf{u}}_w = b_0 + b_1\hat{\mathbf{u}}_p$. Under neither over- nor under-dispersion conditions, the expectation of this estimator would be 1. Accuracy, bias, and dispersion are the main performance indicators for predicting genomic values (Jang et al., 2022). These three indicators can reflect the predictability of selection response, model correctness, improper use of variance components, and various

Table 2

Posterior mean and high probability density interval (HPD) of heritability for probability of early calving before 30 months of age (PC30) with and without mating type (MT) in Nelore cattle.

Model	Mean	SD	HPD ^a 5% 95%		Geweke (Z-score)	r-Lag50
without MT	0.175	0.020	0.125	0.242	0.06	0.047
with MT	0.180	0.025	0.106	0.246	0.14	0.017

Abbreviations: HPD = high probability density interval; PC30 = probability of early calving before 30 months of age; r-Lag50 = autocorrelation at lag 50.

^a 95% highest posterior density interval.

unaccounted effects in the models (Macedo et al., 2020). The data were transformed from the underlying scale to the probability scale using the LOGNORM function in SAS 9.4 (SAS Institute Inc., Cary, NC, USA).

Results

Convergence of the Markov Chain Monte Carlo (MCMC) chains was assessed using Geweke's diagnostic and the autocorrelation (Lag-50) between samples (Table 2) and was further confirmed by visual inspection of the trace plots of the samples (Supplementary Figures S1 and S2). The h^2 estimate for PC30 was moderate to low magnitude and similar for both models analyzed (Table 2). The inclusion of MT in the model did not affect the h^2 estimate or the genetic variance for PC30, indicating that MT did not alter the genetic determinism of the trait. Despite the trait being analyzed under a threshold model, the relatively narrow high probability density interval obtained for h^2 is consistent with the large number of phenotypic records and the stability of the posterior distribution after convergence. Thus, the reproductive management adopted did not influence the estimated variance components, although a significant variation in PC30 is attributed to the environment offered to the heifers. In this sense, it is inferred that environmental and physiological factors may have a greater impact on the manifestation of sexual precocity than the mating type chosen.

Table 3 shows the genomic breeding value (GEBV) for pregnancy probability on the underlying scale for the PC30 trait of

Table 3

Genomic breeding value (GEBV) for probability of early calving before 30 months of age (PC30), expressed as pregnancy probability on the underlying scale, for Nelore heifers in the validation subset, by mating type (MT) and model for the validation subset animals.

Mating Type	Model	Complete GEBV ¹	Partial GEBV ²
No stimulation (N = 575)	without MT	0.463	0.458
	with MT	0.429	0.423
With stimulation (N = 609)	without MT	0.481	0.444
	with MT	0.446	0.461

Abbreviations: GEBV = genomic breeding value; PC30 = probability of early calving before 30 months of age; MT = mating type.

¹ genomic breeding value estimated using genotyped animals with phenotypic records.

² genomic breeding value estimated using genotyped animals without phenotypic records.

Table 4

Prediction accuracy and dispersion (mean $\pm$ SD) estimated using the linear regression (LR) method and the single-step genomic BLUP (ssGBLUP) for the Genomic Breeding Value (GEBV) for probability of early calving before 30 months of age (PC30) in Nelore heifers from the validation subset animals.

Mating Type	Model	Rank correlation	Prediction accuracy	Dispersion (SD)	Inbreeding Coefficient
No stimulation (N = 575)	without MT	0.96 ($p < 0.01$)	0.36	1.013 (0.012)	0.029
	With MT	0.96 ($p < 0.01$)	0.37	1.023 (0.013)	0.028
With stimulation (N = 609)	without MT	0.95 ($p < 0.01$)	0.38	0.947 (0.012)	0.033
	With MT	0.96 ($p < 0.01$)	0.38	1.003 (0.011)	0.033

Abbreviations: MT = Mating Type.

the validation subset. Females that did not undergo hormonal stimulation showed higher complete GEBV with and without mating type (MT) in the model compared to the GEBV obtained in the partial population. Females that received hormonal stimulation, when including MT in the model, showed higher GEBV than the complete GEBV. This indicates that not including the effect of MT in the model for the group of stimulated animals could impair the assessment of pregnancy probability. A slight change in the relative magnitude between partial and complete GEBV values was observed for hormonally stimulated heifers when the mating type (MT) effect was included in the model, with partial GEBV being marginally higher than complete GEBV.

Table 4 presents the estimators calculated using the LR method. It also includes the rank correlations of the validation subset evaluated through the partial and complete GEBV of the validation subset animals assessed under different models. The rank correlations of partial and total predictions for PC30 were not influenced by the inclusion or exclusion of mating type (MT) in the model. In stimulated animals, the inclusion of MT in the model did not alter the rank correlation (0.95–0.96). The inbreeding coefficient (Table 4) was similar across mating types, with average genomic F values ranging from 0.028 to 0.033.

The highest prediction accuracy observed was in animals that underwent hormonal stimulation (0.38 without and with MT; Table 4). However, upon comparing the models, it is noticeable that there were no significant changes in accuracy; in other words, prediction accuracy was not influenced by the addition of MT to the model. Thus, we can conclude that the biological effect of hormonal interference did not affect the predictive ability of genomic breeding value (GEBV), whether MT was included in the model or not. Prediction accuracies were similar between mating types, and the biases observed were generally small. Stimulated animals showed slightly higher bias values (-0.09 ± 0.05 without MT and 0.04 ± 0.05 with MT) compared to non-stimulated animals (-0.01 ± 0.05 without MT and -0.02 ± 0.06 with MT), but all values remained close to the expected bias of 0.

Discussion

The h^2 estimate for PC30 reveals that the puberty-indicating trait of heifers candidates for selection when phenotypic information is available in the female candidates for selection. Other authors have reported higher h^2 estimates for indicators of sexual

precocity traits. Kluska et al. (2018) reported h^2 estimates of 0.37 for the same trait (Probability of early calving) in Nelore cattle. Bonamy et al. (2019) found an h^2 estimate of 0.26 for PC30 in Nelore. These differences are likely due to Kluska et al. (2018) and Bonamy et al. (2019) working with the same population but having a larger number of phenotypic data. In the current study, we also considered the mating type (natural service, AI, or FTAI) as a criterion in animal sampling, leading to a reduction in the sample size.

The difference observed between partial and complete GEBV for hormonally stimulated heifers can be explained by both statistical and biological factors. From a statistical perspective, adding phenotypic information in the complete evaluation increases the magnitude of GEBV, as genomic predictions based only on genotypes (partial) tend to be more regressed towards the mean. Biologically, hormonally stimulated heifers are often genetically less precocious than non-stimulated ones and usually belong to commercial herds that rely on fixed-time artificial insemination (FTAI) protocols to improve fertility. Therefore, the correction associated with including MT in the model is greater for hormonally stimulated females, resulting in a slightly higher adjustment between partial and complete GEBV.

The rank correlations of partial and total predictions for PC30, from a practical standpoint, indicate that there was no significant difference in the rank of these young animals when phenotype was added, regardless of whether they received hormonal stimulation or not. In contrast, Oliveira Junior et al. (2021) observed a reduction in correlations between estimated and actual genetic values when using simulated data from dairy cattle. The correlations ranged from 0.67 to 0.38, with a decrease as the number of synchronised females increased.

Regarding the result found for bias, similarly, Oliveira Junior et al. (2021), using simulated data from dairy cattle, reported that predictions of genetic values including information from cows subjected to FTAI are biased, with this bias being proportional to the number of synchronised animals. This behaviour may be associated with possible masking of the phenotype using hormonal stimulation, biasing the estimation of marker effects in genomic prediction. Additionally, the greater bias observed for animals without hormonal stimulation and without MT added to the model may have been caused by unaccounted environmental effects affecting the estimation of genomic value. The inclusion of MT in the model for animals subjected to hormonal stimulation led to a reduction in the bias effect for these predictions, demonstrating that considering this factor in the model reduces bias but does not improve prediction accuracy (Bis, 2023). This bias could mainly affect young animals or selection candidates whose genomic values are predicted based on parental and genomic information. However, this bias could also lead to misclassification and selection errors of animals whose genetic evaluation is influenced by masked phenotype.

According to Jang et al. (2022), the dispersion estimator can indicate genomic prediction overdispersion if the dispersion coefficient is less than 1 or underdispersion if it is greater than 1. For animals that did not undergo hormonal stimulation, the observed dispersion was close to 1 with and without the inclusion of MT. For animals that received hormonal stimulation, the dispersion indicated an overestimation of model predictions without MT. By including MT in the model, the dispersion for the animals approached 1. Overdispersion of genomic value is a common phenomenon in this type of prediction (Legarra and Reverter, 2018).

The inbreeding coefficient (Table 4) was similar across mating types. Most of the bulls used in production nowadays are from commercial herds and, therefore, are less related. According to Bessa et al. (2021), the effects of inbreeding have consequences

on the productive efficiency and reproductive ability of Zebu cattle, mainly affecting age at first calving and BW. Overall, our findings indicate that the estimation of variance components and h^2 for PC30 was not affected by hormonal stimulation or by including mating type in the model. Heritability was low, indicating a strong environmental influence but potential response to selection. Animals subjected to hormonal stimulation showed similar prediction accuracy and dispersion to non-stimulated ones, although their predictions were slightly more biased. Including mating type in the model reduced this bias, leading to less overestimated genomic predictions. Despite this, the reproductive benefits of hormonal protocols outweigh the small bias observed in these animals.

Supplementary material

Supplementary Material for this article (<https://doi.org/10.1016/j.animal.2026.101769>) can be found at the foot of the online page, in the Appendix section.

Ethics approval

This study was exempt from evaluation by the Animal Ethics Committee (CEUA), as established by Law No. 11 794 of 08/10/2008 and Normative Resolution No. 51 of 05/19/2021 from the National Council for Animal Experimentation Control (CON-CEA) because the data were obtained from an existing database.

Data and model availability statement

None of the data were deposited in an official repository. The data that support the findings of this study are available from the corresponding author upon reasonable request. The data are not publicly available due to privacy or legal restrictions because they belong to a commercial breeding programme.

Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this work the author(s) did not use any AI and AI-assisted technologies.

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Declaration of interest

None.

Acknowledgements

The authors express their gratitude to the National Association of Breeders and Researchers (ANCP) for providing the data during this project. Additionally, the authors appreciate financial support from Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) - Finance Code 001. This manuscript is part of the MSc thesis of Flávia Cristina Bis, defended at the University of São Paulo, Brazil.

Financial support statement

This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) - Finance Code 001.

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