

Communication

Effect of X Chromosome on the Estimated Genetic Parameters for Growth Traits in Nellore Cattle

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Simple Summary

Genomic information has become essential for improving the accuracy of genetic evaluations in beef cattle. However, most genomic analyses focus exclusively on autosomal chromosomes, leaving aside the X chromosome, which is the second-largest chromosome in the bovine genome. Many economically important traits, such as body weight and weight gain, show differences between males and females, raising the question of whether the X chromosome could contribute relevant genetic information for these traits. In this study, we evaluated whether including X-chromosome markers alongside autosomal markers improved the estimation of genetic parameters for yearling weight and postweaning gain in Nellore cattle, one of the most economically significant zebu breeds in Brazil. We found no differences in heritability estimates regardless of whether we used only pedigree information, added autosomal markers, or further added X-chromosome markers. These results suggest that, at least for these growth traits and with the marker densities currently available on commercial genotyping panels, the X chromosome does not provide additional information. Future studies with higher X-chromosome marker coverage may be necessary to clarify the role of this chromosome in bovine genomic evaluations.

Abstract

Most studies involving genomic data in animal breeding use only the effects of autosomal chromosome markers, excluding the sex chromosomes. However, the X chromosome is the second-largest chromosome in the bovine genome, and several economically important traits are sexually dimorphic, such as those related to growth. Therefore, the objective of this study was to evaluate whether there are predictive advantages for genetic parameters when including genomic markers from the X chromosome for yearling weight (YW) and postweaning gain (PWG) in Nellore cattle. Genetic parameter estimates were obtained under three scenarios: (1) only pedigree and phenotypic information; (2) pedigree, phenotypes, and autosomal chromosome markers; and (3) pedigree, phenotypes, autosomal chromosome markers, and X chromosome markers. Analyses were carried out using Bayesian inference with BLUPF90 family software version 2025. The heritability estimates obtained and their respective standard errors were 0.41 ± 0.004 for YW and 0.21 ± 0.004 for PWG. No differences were observed among the three scenarios tested for either trait. Therefore, the inclusion of the X chromosome did not influence the estimates of genetic parameters for these growth traits in Nellore cattle. Nevertheless, further molecular and genomic studies on the bovine X chromosome are still needed to explain the genetic



Academic Editor: Juan Vicente Delgado Bermejo

Received: 15 June 2026

Revised: 13 July 2026

Accepted: 20 July 2026

Published: 21 July 2026

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effects and biological functions associated with this chromosome and with different traits of economic interest, as well as to justify whether to include the X chromosome in genomic prediction analyses.

Keywords: beef cattle; heritability; yearling weight; weight gain; X chromosome

1. Introduction

Brazil is the world's largest beef exporter and the second-largest producer [1]. Brazilian beef cattle production spans the entire country, with approximately 80% of the national herd composed of zebu breeds—primarily Nellore—due to their strong adaptation to tropical environments [2]. Genetic improvement has been a key investment to strengthen productivity and maintain global competitiveness.

Genetic improvement seeks to select genetically superior animals for economically relevant traits, using them as parents of the next generation to enhance herd performance. For productivity gains, breeding programs traditionally emphasize body weights and weight gains because these traits are easy to measure, genetically correlated with other important traits, and have moderate to high heritability [3–7].

However, most breeding programs use molecular information only from autosomal markers, often excluding sex chromosomes. This omission is commonly attributed to X-chromosome dosage compensation in females, male hemizyosity, and the pseudoautosomal region shared by X and Y chromosomes [5,8].

The X chromosome, however, is the second largest in the bovine genome [5] and may contain genes that influence performance. Additionally, many livestock traits exhibit sexual dimorphism, including body weights and gains, suggesting distinct sex-specific genetic architectures [9]. Consequently, disregarding X-linked genomic information may omit biologically relevant variation and reduce the accuracy of genomic evaluations [10].

This study therefore evaluated whether incorporating X-chromosome genomic markers improves genetic parameter estimation for growth traits in Nellore cattle.

2. Materials and Methods

2.1. Phenotypic Data

Phenotypic records for yearling weight (YW), measured at approximately 550 d of age, from Nellore males and females born between 1987 and 2022 were obtained from herds in the southeastern and northeastern regions of Brazil participating in the GenSys® (Jaboticabal, Brazil) breeding program. Postweaning gain (PWG) was calculated as the difference between YW and weaning weight (measured at approximately 210 d of age).

Contemporary groups (CG) were defined using the GLM procedure from the stats package in R 4.2.2 [11]. The CG with the highest coefficient of determination was constructed by combining sex, birth season, farms of birth, weaning and yearling locations, and management groups from birth to weaning and from weaning to yearling. Cow age at calving (days) was included as a covariate for all traits, as well as the animal age at weighing (days) for YW and the interval between weighings (days) for PWG. All the covariates were tested using the GLM procedure from the stats package in R 4.2.2 [11].

CGs with fewer than five observations and records outside the CG mean $\pm$ 3.5 standard deviations were excluded. The pedigree file included 3,684,030 animals, with approximately 600,000 having growth trait records. All known relationships up to 10 generations were used. Descriptive statistics of the phenotypic data, after consistency filtering, are shown in Table 1.

Table 1. Number of observations (N), mean ($\bar{x}$), standard deviation (SD), minimum (MIN) and maximum (MAX) values, and number of contemporary groups (CG) of the yearling weight (YW) and postweaning gain (PWG).

Traits	N	$\bar{x}$	SD	MIN	MAX	CG
YW	604,636	297.09 kg	52.35 kg	151 kg	449 kg	31,550
PWG	589,276	105.89 kg	37.53 kg	21 kg	219 kg	31,087

2.2. Genotypic Data

A total of 5469 genotypes from animals born between 1993 and 2022 were used, of which 2552 had YW and 2511 had PWG records. Genotyping was performed using the Illumina BovineHD panel (Illumina, San Diego, CA, USA) (777,962 SNPs). SNPs with minor allele frequency <0.05 or call rate <0.90 were removed. The bovine reference genome ARS-UCD1.2 was used in the analysis.

For X-chromosome annotation, female genotypes were coded as 0 (AA), 1 (AB), and 2 (BB). Male hemizygotes were coded as 0 (A) and 2 (B). After quality control, analyses including autosomes and the X chromosome comprised 473,345 SNPs and 5469 animals; analyses excluding the X chromosome contained 453,342 SNPs. The differentiation and attempt to account for dose compensation were performed according to Diaz et al. (2021) [8].

2.3. Genomic Prediction

Genomic prediction for growth traits considered three scenarios: (1) pedigree + phenotypic information; (2) pedigree + phenotypes + autosomal markers; and (3) pedigree + phenotypes + autosomal + X-chromosome markers. The full model can be written in matrix notation as

$$y = X\beta + Zu + e;$$

where y is the vector of observations for animals with or without a specific genotype; X and Z are incidence matrices that associate β and u with the observations, respectively; β is the vector of contemporary group effects; u is the vector of direct additive genetic effects; and e is the vector of residual effects.

A single-trait ssGBLUP animal model was used to estimate (co)variance components and genetic parameters. Additive genetic and residual effects were fitted as random effects; CG as a fixed effect; and linear and quadratic effects of cow age at calving as covariates. Linear effects of animal age at weighing were included as a covariate for YW and the weighing interval for PWG. Analyses were conducted via Bayesian inference using BLUPF90 software [12].

Gibbs chains of 1,000,000 iterations were run with 100,000 burn-in cycles and a sampling interval of 50 for both traits. Convergence and autocorrelation were assessed with POSTGIBBSF90 [12]. Genetic parameter standard deviations were computed following Meyer and Houle [13]. The data reported in this manuscript originate from the first author's Master's thesis [14].

3. Results

Table 2 presents the genetic parameters estimated for YW and PWG across three scenarios: using phenotypes and pedigree only (Pedigree), including autosomal markers (Pedigree + Autosomal), and including X-chromosome markers (Pedigree + Autosomal + X Chromosome). No differences were observed among the three scenarios for either trait. Heritability estimates were 0.41 ± 0.004 for YW and 0.21 ± 0.004 for PWG.

Table 2. Genetic parameters and their respective standard deviations for yearling weight (YW) and postweaning weight gain (PWG) in Nellore cattle without the inclusion of genomic data, with the inclusion of autosomal marker effects, and with the inclusion of X-chromosome marker effects.

Genetic Parameters	Trait	Pedigree	Pedigree + Autosomal	Pedigree + Autosomal + X Chr.
	YW			
σ^2_a		274.35 $\pm$ 3.03	275.73 $\pm$ 3.04	275.48 $\pm$ 3.04
σ^2_e		388.27 $\pm$ 2.17	387.41 $\pm$ 2.18	387.54 $\pm$ 2.18
h^2		0.414 $\pm$ 0.004	0.416 $\pm$ 0.004	0.415 $\pm$ 0.004
	PWG			
σ^2_a		70.42 $\pm$ 1.40	70.87 $\pm$ 1.39	70.73 $\pm$ 1.39
σ^2_e		266.58 $\pm$ 1.14	266.30 $\pm$ 1.13	266.38 $\pm$ 1.13
h^2		0.209 $\pm$ 0.004	0.210 $\pm$ 0.004	0.210 $\pm$ 0.004

σ^2_a : additive genetic variance (kg²); σ^2_e : residual variance (kg²); h^2 : heritability. YW: yearling weight (kg); PWG: postweaning gain (kg).

4. Discussion

The heritability estimate obtained for YW without genomic data (Table 2) was consistent with those reported in other Nellore studies using only pedigree and phenotypic information [2,15,16]. However, it exceeded values reported by Araujo et al. [15], Ferriani et al. [16], and Lacerda et al. [17], who found heritabilities of 0.26, 0.19, and 0.34, respectively. For PWG, our estimate was consistent with previously published values for the breed [18,19].

No differences were observed among the three scenarios for either trait (Table 2). One possible explanation for the absence of differences, even with genomic data, is the disproportion between the number of genotyped animals (5469) and the total number with phenotypic records (more than 589,000). Together with pedigree information, over 910,000 animals were evaluated (animals with and without phenotype). This large dataset may have already provided highly accurate parameter estimates, requiring a higher proportion of genotyped animals to detect differences between genomic and non-genomic analyses.

The lack of an effect from X-chromosome inclusion is also noteworthy given the observed sexual dimorphism: males showed means of 317.81 $\pm$ 50.08 kg for YW and 116.66 $\pm$ 37.38 kg for PWG, while females averaged 278.29 $\pm$ 47.02 kg and 96.06 $\pm$ 34.89 kg, respectively. A possible explanation is that sex chromosomes may contain genes that act directly or regulate the expression of autosomal genes (epistatic effects). The absence of differences between analyses with and without the X chromosome may have occurred because, during quality control, 20,007 SNPs from this chromosome were discarded, leaving only 20,003 SNPs for analysis; many SNPs were already fixed in the evaluated population. According to Su et al. [20], lower marker density on the X chromosome compared to autosomes in current SNP chips may reduce the efficiency of X-chromosome markers for genomic prediction. Genomic selection requires a large number of well-chosen genetic markers representative of the entire genome [21]; when this requirement is not met, the efficiency of molecular markers is reduced.

5. Conclusions

The inclusion of X-chromosome markers did not influence the estimates of genetic parameters for yearling weight and postweaning weight gain in Nellore cattle. No differences were observed across the three scenarios tested: phenotypes and pedigree only, with autosomal markers, and with additional X-chromosome markers. Nevertheless, further molecular and genomic studies on the X chromosome in cattle are needed to clarify its

genetic effects and biological functions for economically important traits and to determine whether its inclusion is warranted in genomic prediction analyses.

Author Contributions: N.M.C.: Formal analysis, investigation, writing—original draft; F.L.B.F., L.M.A. and L.S.M.d.O.: Data curation; R.B.C., L.G.d.A. and G.M.F.d.C.: Conceptualization, resources, supervision, project administration, funding acquisition. All authors have read and agreed to the published version of the manuscript.

Funding: This research was financially supported by Fundação de Amparo à Pesquisa do Estado da Bahia (FAPESB) (Process #2021/121986), and by Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP) (Process #2017/10630-2).

Institutional Review Board Statement: The animal procedures and data sampling presented in this study were approved and performed following the Animal Care and Ethical Committee recommendations of the São Paulo State University (UNESP), School of Agricultural and Veterinary Science (protocol number 18.340/16). All the data sampling was performed following the CEUA/FCAV-UNESP guidelines and regulations in agreement with the Regulations for the Administration of Affairs Concerning Experimental Animals (Ministry of Science and Technology, Brazil). In addition, we confirmed the statement that the study was conducted following the ARRIVE guidelines.

Informed Consent Statement: Not applicable.

Data Availability Statement: The data presented in this study are available on request from the corresponding author due to commercial restrictions.

Acknowledgments: The data reported in this manuscript originate from the first author's Master's thesis.

Conflicts of Interest: The authors declare no conflicts of interest.

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