Ciência Animal Brasileira
Brazilian Animal Science

DOI: 10.1590/1809-6891v25e-75632E

e-ISSN 1809-6891
Animal Science | Research article

Effect of age at first conception as a selection criterion on growth and carcass traits in Nellore cattle

Efeito da idade a primeira concepção como critério de seleção em características de crescimento e carcaça em bovinos Nelore

Ludmilla Costa Brunes[*1], Fernando Baldi[2], Marcos Fernando Oliveira e Costa[1], Raysildo Barbosa Lobo[3], Fernando Brito Lopes[3], Cláudio Ulhoa Magnabosco[1]

1 Empresa Brasileira de Pesquisa Agropecuária (Embrapa Cerrados), Brasília, Distrito Federal, Brasil
2 Universidade Estadual Paulista "Júlio Mesquita Filho" (UNESP), Jaboticabal, São Paulo, Brasil
3 Associação Nacional de Criadores e Pesquisadores, Ribeirão Preto, São Paulo, Brasil
4 Cobb-Vantress, Siloam Springs, Arkansas, USA
*corresponding author: ludmillabrunes@hotmail.com

Abstract: The aim was to identify predictive traits of relatively easy measurement and which can be recorded early in life (age at first conception - AFCo), besides estimating its genetic correlations with growth and carcass traits in Nellore cattle. Age at first conception was considered the age at which the female had the first positive diagnosis for pregnancy. The estimation of (co)variance components and genetic parameters was performed using a linear animal model in two-trait analysis. The estimates of heritability were moderate, enabling genetic selection for growth-, carcass-, and sexual precocity-related traits. The genetic correlation obtained between AFCo and age at first calving (AFCa) was high (0.88), indicating the feasibility of using AFCo as a selection criterion for early calving heifers. Genetic correlation estimates between AFCo and AFCa with weight at 120, 210, 365, and 450 days of age and carcass traits were moderate and negative (-0.33 to -0.62). Thus, genetic selection for animals with early AFCo and AFCa would enhance carcass yield, fat deposition, and growth performance, despite not affecting birth weight or daily weight gain. The results of this study encourage the use of AFCo in Nellore cattle since this trait displayed enough genetic variability in Nellore cattle, and can be used as selection criteria to improve sexual precocity. When the objective of genetic selection is to increase heifer sexual precocity, we could use the first trait as a criterion, as the measurement of this trait occurs at a lower AFCa.

Keywords: *Bos indicus*; carcass quality; genetic parameters; productive traits; sexual precocity

Resumo: Objetivou-se identificar características indicadoras de precocidade sexual de fácil mensuração e que podem ser registradas em menor idade (idade à primeira concepção - IPC), além de estimar as correlações genéticas dessa característica com aquelas de crescimento e carcaça em bovinos Nelore. A IPC foi considerada a idade em que a fêmea apresentou o primeiro diagnóstico positivo de prenhez. A estimativa dos componentes de (co)variância e dos parâmetros genéticos foi realizada usando modelo animal linear em análises bicaracterísticas. As estimativas de herdabilidade foram moderadas, indicando viabilidade de seleção genética para características de crescimento,

Received: March 18, 2023. Accepted: September 21, 2023. Published: December 13, 2023.

carcaça e precocidade sexual. As correlações genéticas obtidas entre o IPC e a idade ao primeiro parto (IPP) foram altas (0,88), indicando a viabilidade do uso de IPC como critério de seleção para parto em idade precoce de novilhas. As estimativas de correlações genéticas entre IPC e IPP com peso aos 120, 210, 365 e 450 dias de idade e características de carcaça foram moderadas e negativas (-0,33 a -0,62). Assim, a seleção genética para animais com IPC e IPP precoces aumentaria o rendimento de carcaça, a deposição de gordura e o peso corporal, embora não afete o peso ao nascer e o ganho de peso diário. Os resultados deste estudo encorajam o uso de IPC em bovinos Nelore, uma vez que esta característica apresentou variabilidade genética em bovinos Nelore, podendo ser utilizada como critério de seleção para melhorar a precocidade sexual. Quando o objetivo de seleção genética é aumentar a precocidade sexual das novilhas, indica-se o uso de IPC como critério, pois a mensuração desta característica ocorre em idade menor IPP.

Palavras-chave: *Bos indicus;* características produtivas; parâmetros genéticos; qualidade de carcaça; precocidade sexual

1. Introduction

Beef cattle breeding programs have placed greater emphasis on growth traits in relation to those related to carcass, fertility, and sexual precocity. However, selection for enhanced growth-related traits can result in a negative impact on carcass and sexual precocity-indicator traits since heavier animals at the same age are later-maturing, or large frame, with learner carcasses and delayed occurrence of puberty[1–3]. In addition, including genetic selection for carcass quality can increase the profitability of systems[4] since meat and carcass attributes affect consumer acceptance and purchase intention[5].

Female sexual precocity-indicator traits have a great impact on the productivity of cow–calf systems[6]. Beef cattle profitability is associated with reduced onset of females' maturity since it allows for a greater number of calves to be produced per cow and increased productive longevity[6–9]. Heifers that calve earlier during the calving season have heavier calves and a longer post-partum recovery time, resulting in increased chances of displaying early pregnancies in subsequent breeding seasons[10,11]. Thus, the genetic improvement of heifers' sexual precocity allows optimizing the productive cycle, and, in a beef cattle production system, economic sustainability is related to growth, reproductive efficiency, carcass, and production[12].

Genetic selection for sexual precocity is carried out indirectly considering scrotal circumference (SC), which is easily obtained in males and shows high heritability; however, it is a sex-limited trait[6,13]. The target of sexual precocity selection is to reduce the age at puberty, but the identification of the onset of puberty in heifers is complex, requiring management for the detection of the first ovulation, i.e. the use of hormone measurement, which entails additional production costs[8].

A way to optimize genetic selection for sexual precocity through traits measured directly in heifers that display a high and favorable correlation with age at puberty and increasing genetic gain, such as age at first conception (AFCo) and age at first calving (AFCa)[6,13,14]. Age at first conception, measured considering the difference between the birth date and the date at the first positive pregnancy diagnosis heifer, is easy to asses for all heifers, dispensing with the use of penalties for heifers that did not calve. Age at first conception does not depend on gestation length, unlike AFCa. Performing pregnancy diagnosis is a common practice in beef cattle selection herds. Heifer pregnancy displays moderate-to-high additive genetic variability, warranting the use of this trait as a selection criterion in Nellore cattle breeding programs(6). This trait is evaluated commonly as a binary trait and is known as "early calving at 30 months" (EC30) (6). It often relies on Bayesian inference based on preliminary knowledge (*a priori* distribution) (15), which is associated with the highest computational demands(16). Difficulty in achieving the convergence criteria has also been reported when evaluating the genetic correlation between EC30 and other traits(17). Therefore, evaluating heifer pregnancy using AFCo can be an alternative to facilitate genetic evaluation and expand genetic selection for sexual precocity. This is a quantitative and easy-to-measure trait in the herd since it is part of routine data collection. Additionally, AFCo has an advantage over AFCa since AFCo is evaluated before the first calving.

Several studies have shown that SC has a high correlation with EC30 and productive traits, such as weight at 120 (W120) and 450 days of age (W450) (0.30 to 0.66), in beef cattle(6,17–19). However, SC has a low correlation with carcass traits, such as rib-eye area (REA), backfat thickness (BF), and rump fat thickness (RF) in beef cattle(6,17–19). Low genetic correlations were also reported between AFCa and productive traits, although the genetic correlation estimates between AFCa and carcass traits show a broad variation in beef cattle(6,17–20).

To the present date, the relationships between easy-to-measure traits of female sexual precocity, such as AFCo, and productive and carcass traits using Zebu cattle in grazing systems have not been fully explored. For AFCo, an evaluation is necessary to expose heifers to mate at the same age and perform pregnancy diagnosis, which may imply a higher evaluation cost than the AFCa. However, the early identification of precocious females can reduce production costs, through the culling of late heifers.

Before recommending producers to include genetic selection for AFCo and AFCa in their breeding programs, it is vital to understand the genetic relationship of these two efficiency traits with other traits of economic importance, such as growth and carcass quality traits. This study hypothesizes that genetic selection to obtain earlier heifers can be carried out using AFCo as a selection criterion without unfavorable effects on other profitability traits. Thus, this study aimed to identify predictive traits of relatively easy measurement recorded early in life (AFCo), besides estimating their genetic correlations with growth and carcass traits in Nellore cattle.

2. Material and methods

2.1 Phenotypic data and evaluated traits

The collection of phenotypic information is not categorized as an experiment as the interventions are related to farming practices according to law No. 11.794 (October 8th, 2008; subsection VII of § 1o of clause 225 of the Brazilian Federal Constitution), which lays down procedures for the scientific use of animals. Hence, this study was not submitted to an ethics committee, considering that a data set from a commercial production system was used.

The data used in this study were provided by Vera Cruz Farm, which is based on the semi-extensive production and grazing system and is located in the state of Mato Grosso, Brazil, and by the Nellore Brazil Genetic Improvement Program, coordinated by the National Association of Breeders and Researchers (ANCP). Since 2009, the evaluated herd has been subjected to selection for sexual precocity using AFCo as a selection criterion. The dataset included 4,081 field records from animals born between 2009 and 2015. Additionally, the ANCP provided a pedigree data set with 11,198 animals, which was used to compose the relationship matrix. The pedigree data included 1,606 sires and 6,129 dams with progeny. On average, each dam and sire had 2.10 and 6.13 progeny, respectively. The animals that composed the dataset had an average inbreeding coefficient of 0.041%.

The animals were weighed every 90 days, from birth to 18 months of age. The mating season was from November to February, using fixed-time artificial insemination for all heifers and one natural mating after the second artificial insemination. The heifers were exposed to service at 11 months of age and when their minimum weight was at least 250 kg, so all heifers in the evaluated herd were challenged for sexual precocity. All heifers were subjected to the same reproductive management without evaluating the manifestation of the first estrus. All heifers were subjected to the same synchronization protocol. Heifers which became pregnant at 20 months were classified as precocious; otherwise, they were classified as conventional. All records for early and conventional heifers were analyzed. The births occurred annually between August and November, with calves being weaned at 240±30 days of age, on average.

Despite affecting reproductive performance, the traits that specifically indicate the onset of a female's reproductive activity were considered sexual precocity indicators, which were AFCo and AFCa. Age at first conception was considered the age, in months, at which the female had the first positive diagnosis for pregnancy. Pregnancy diagnosis was performed by the same veterinarian using ultrasound examinations performed on the 28th day post-artificial insemination, using a 7.5MHz linear array transducer. The observation of allantoic fluid or a visible embryo yielded a positive gestation diagnosis[21]. Age at first calving was calculated, in months, as the difference in days between the date of the first calving and the date of the dam's birth. The differences between AFCo and AFCa, that is, heifers that had an early pregnancy but did not calve can be attributed to different factors, such as embryonic loss, and voluntary abortion, among other factors intrinsic to females.

Seven productive traits were included in these analyses: birth weight (BW), weight at 120 days of age (W120), weight at 210 days of age (W210), weight at 365 days of age (W365), and weight at 450 days of age (W450), and pre (PREWWG) and post-weaning (POSTWWG) daily weight gain. The standardized weight and daily weight gain were calculated according to the method proposed by Garnero et al.[22]. Six carcass traits were included in the analyses: REA, BF, RF, marbling (MAR), hot carcass weight (HCW), and edible weight (EW). Rib-eye area, BF, RF, and MAR were obtained by ultrasound evaluation (Aloka 500 SSD with transducer 3.5 MHz) as described by BIF[23]. Rib-eye area (evaluated in cm^2), BF (measured in millimeters, mm), and MAR (%) were measured between the 12^{th} and 13^{th} ribs on the *Longissimus dorsi* muscle. Rump fat thickness (obtained in millimeters, mm) was measured at the intersection of the *Gluteus medius* and *Biceps femoris* muscles, located between the ileum and ischium bones. Hot carcass weight and EW were estimated using equations based on the phenotypic measurements of REA, BF, RF, and weight measured on ultrasound day[24].

2.2 Statistical analysis and genetic parameter estimates

Fixed effects were tested for significance ($P < 0.05$) using the *lm* function with R software[25]. The effects tested for each evaluated trait were year and season of birth, sex, management lot, bull, animal age, and dam age. Hence, the contemporaneous groups (CG) were composed of animals of the same sex, born in the same year-season, and receiving the same feed management. Preliminary analyses were conducted with R statistical software[25]. In data editing, the following were eliminated: data lower and higher than 3.5 standard deviations of the mean of their CG; CG with less than four animals; and sires with less than five progeny.

We also tested the connectedness between CGs based on the total number of genetic ties. The existence of at least 10 ties was considered a restriction using the AMC program[26]. After the AMC analysis, final report, data, and relationship files were prepared, including only connected CGs. Genetic analyses involved a record file with 4,081 observations and a relationship file with 11,198 animals, considering six generations in the relationship matrix. Table 1 shows the trait-by-trait distributions.

Table 1. **Number of records (N), mean, standard deviation (SD), coefficient of variation (CV), minimum and maximum, number of contemporary groups (CG), and number of animals per CG for growth, carcass, and sexual precocity-indicator traits in Nellore cattle**

Trait	N	Mean	Minimum	Maximum	SD	CV (%)	N CG	N animals/CG
BW (kg)	4081	34.10	23.00	45.00	2.92	8.56	186	22
W120 (kg)	3158	134.03	68.00	193.21	18.43	13.75	203	16
W210 (kg)	3222	203.67	102.00	308.00	28.59	14.04	217	15
W365 (kg)	2846	283.85	132.00	433.00	48.63	17.13	216	13
W450 (kg)	2157	324.15	172.00	481.00	55.51	17.12	157	14
PREWWG (kg)	3070	0.79	0.07	1.71	0.20	25.32	200	15
POSTWWG (kg)	2051	0.54	0.04	1.36	0.21	38.92	113	18
REA (cm^2)	1906	55.87	24.46	96.07	9.85	17.63	61	31
BF (mm)	1844	2.63	0.27	8.83	1.35	51.55	61	30
RF (mm)	1299	3.41	1.02	12.74	1.77	52.05	61	21
MAR (%)	1137	2.24	1.00	4.94	0.83	37.05	61	19
HCW (kg)	1952	207.83	93.95	358.65	42.31	20.36	58	34
EW (kg)	1952	82.15	34.06	143.75	17.23	20.97	58	34
AFCo (months)	1695	22.03	11.33	40.95	5.95	27.01	101	17
AFCa (months)	1490	33.14	21.13	48.33	5.62	16.97	101	15

BW: birth weight; W120: weight at 120 days of age; W210: weight at 210 days of age; W365: weight at 365 days of age; W450: weight at 450 days of age; PREWWG: pre-weaning daily weight gain; POSTWWG: post-weaning daily weight gain; REA: rib-eye area; BF: backfat thickness; RF: rump fat thickness; MAR: marbling; HCW: hot carcass weight; EW: edible weight; AFCo: age at first conception; AFCa: age at first calving.

Traits were analyzed using single- and two-trait animal models. The two-trait analyses were performed to estimate covariance and genetic and phenotypic correlations between the evaluated traits. The animal model was based on the restricted maximum likelihood method, which uses a derivative-free algorithm, available in the REML (restricted maximum likelihood) and AIREML (average-information – restricted maximum likelihood) of the BLUPF90 program[27]. The convergence criteria were set to 10^{-12} to ensure convergence in the global maximum of the likelihood function.

For BW, W120, W210, and PREWWG, the model included the direct additive genetic, maternal additive genetic, maternal permanent environment, and residual effect as random effects and the fixed effects of CG and cow age at calving as covariates (linear and quadratic effect). For W365, W450, POSTWWG, AFCo, and AFCa, the model included the direct additive genetic and residual effects as random and the CG effect as fixed. For carcass traits, the model included the direct additive genetic and residual effects as random and the fixed effects of CG and animal age as covariates (linear effect). The animal model equation used was:

$$y = X\beta + Z_1 a + Z_2 m + Z_3 mpe + e$$

where y is the vector of the phenotypes; X is the incidence matrix associating β with y; β is the vector of fixed effects, including CG, dam age at calving (BW, W120, and W210), and animal age (carcass traits); Z_1 is the incidence matrix associating a with y; a is the vector of random direct additive genetic effects; Z_2 is the incidence matrix associating m with y, only for BW, W120, and W210; m is a vector of maternal additive genetic effects; Z_3 is the incidence matrix associating mpe with y, only for BW, W120, and W210; mpe is a vector of maternal permanent environmental effects; and e is the vector of random residual effects. It was assumed that E(y) = $X\beta$; with the direct additive genetic, additive maternal, maternal permanent environmental, and residual effects assumed to be normally distributed, with a mean of zero and Var(a) = $H \otimes S_a$, Var(m) = $H \otimes S_m$, Var(mpe) = $H \otimes S_{mpe}$ and Var(e) = $H \otimes S_e$, in which S_a, S_m, S_{mpe}, and S_e is the additive genetic, additive maternal, maternal permanent environmental, and residual covariance matrix respectively, and I is an identity matrix of appropriate order.

The variance and (co)variance estimates obtained by the AIREMLF90 were used as initial values for REMLF90[27], and analyses for parameter estimation were repeated until the results remained constant. The standard deviations were obtained for the coefficients of heritability and genetic correlations, using the normal multivariate asymptotic distribution, proposed by Meyer and Houle[28]. Then, the standard error values were divided by the square root of the number of observations, yielding the standard deviations. Estimates of heritability as well as genetic and phenotypic correlations were computed using the variance components from REMLF90[27].

3. Results

Table 2 shows the variance component estimates, heritabilities, and their respective standard errors for growth, carcass, and sexual precocity-indicator traits. Direct heritability estimates for growth, carcass, and sexual precocity-indicator traits were moderate. Maternal heritability estimates for BW, W120, and W210 were low.

Table 2. Estimation components for additive genetic (σ^2a), maternal (σ^2m), permanent (σ^2pe), environmental (σ^2e), and phenotypic (σ^2p) variances and direct (h^2d) and maternal (h^2m) heritabilities with their respective standard errors (SE) for growth, carcass, and sexual precocity-indicator traits in Nellore cattle.

Trait	Genetic parameter						
	σ^2a	σ^2m	σ^2pe	σ^2r	σ^2p	h^2d±SE	h^2m±SE
BW (kg)	1.35	0.22	0.07	1.81	3.45	0.39±0.06	0.06±0.03
W120 (kg)	102.00	24.28	42.09	146.57	314.94	0.32±0.03	0.08±0.02
W210 (kg)	199.05	46.23	64.54	331.64	641.46	0.31±0.04	0.07±0.03
W365 (kg)	214.58	-	-	354.35	568.93	0.33±0.03	-
W450 (kg)	316.90	-	-	505.49	822.39	0.34±0.07	-
PREWWG (kg)	0.10	0.05	0.05	0.22	0.42	0.23±0.02	0.06±0.03
POSTWWG (kg)	0.08	-	-	0.18	0.26	0.27±0.02	-
REA (cm^2)	20.07	-	-	33.03	53.10	0.39±0.04	-
BF (mm)	0.59	-	-	1.16	1.74	0.34±0.03	-
RF (mm)	0.67	-	-	1.32	1.99	0.34±0.05	-
MAR (%)	0.23	-	-	0.38	0.62	0.38±0.16	-
HCW (kg)	165.63	-	-	261.59	427.21	0.39±0.08	-
EW (kg)	60.91	-	-	95.55	156.46	0.39±0.08	-
AFCo (months)	3.61	-	-	13.34	16.95	0.21±0.08	-
AFCa (months)	4.27	-	-	13.40	17.67	0.24±0.08	-

h^2d: direct heritability; h^2m: maternal heritability; BW: birth weight; W120: weight at 120 days of age; W210: weight at 210 days of age; W365: weight at 365 days of age; W450: weight at 450 days of age; PREWWG: pre-weaning daily weight gain; POSTWWG: post-weaning daily weight gain; REA: rib-eye area; BF: backfat thickness; RF: rump fat thickness; MAR: marbling; HCW: hot carcass weight; EW: weight of edible portion; AFCo: age at first conception; AFCa: age at first calving.

The genetic and phenotypic correlation estimates obtained between AFCo and AFCa were positive and high (0.88±0.13 and 0.96±0.13, respectively) (Table 3), representing a favorable relationship. Table 3 describes the genetic and phenotypic correlation estimates between AFCo and AFCa. Favorable genetic correlations were obtained between sexual precocity-indicator and live weight traits, which were moderate and negative (-0.51 to 0.40), except for BW, whose correlation was low. Similarly, daily weight gain displayed low genetic correlations with sexual precocity traits, except between AFCa and POSTWWG, which is favorable (-0.33). Favorable phenotypic correlation estimates were obtained between AFCo and AFCa with BW, W210, W365, and W450, with moderate negative values.

Table 3. Genetic and phenotypic correlation estimates with their respective standard errors (SE) between age at first conception (AFCo) and at first calving (AFCa) with growth traits in Nellore cattle.

Trait	Genetic correlation		Phenotypic correlation	
	AFCo	AFCa	AFCo	AFCa
BW	-0.17±0.04	-0.15±0.19	-0.63±0.04	-0.52±0.14
W120	-0.41±0.15	-0.48±0.07	-0.25±0.02	-0.21±0.01
W210	-0.40±0.04	-0.45±0.06	-0.52±0.11	-0.51±0.12
W365	-0.43±0.03	-0.49±0.01	-0.56±0.06	-0.42±0.05
W450	-0.51±0.03	-0.43±0.04	-0.50±0.04	-0.47±0.04
PREWWG	-0.25±0.02	-0.28±0.02	-0.30±0.04	-0.22±0.12
POSTWWG	-0.29±0.03	-0.33±0.01	-0.21±0.03	-0.15±0.12
AFCa	0.88±0.13	-	0.96±0.13	-

BW: birth weight; W120: weight at 120 days of age; W240: weight at 240 days of age; W365: weight at 365 days of age; W450: weight at 450 days of age; PREWWG: pre-weaning daily weight gain; POSTWWG: post-weaning daily weight gain.

Overall, favorable genetic and phenotypic correlations between sexual precocity-indicator and carcass traits were obtained, ranging from -0.62 to -0.33, except for the phenotypic correlations for MAR with AFCo and AFCa (-0.22 and -0.17, respectively), which were low (Table 4).

Table 4. Genetic and phenotypic correlation estimates with their respective standard errors (SE) between age at first conception (AFCo) and at first calving (AFCa) and carcass traits in Nellore cattle.

Trait	Genetic correlation		Phenotypic correlation	
	AFCo	AFCa	AFCo	AFCa
Rib-eye area	-0.62±0.19	-0.60±0.11	-0.52±0.11	-0.33±0.01
Backfat thickness	-0.45±0.15	-0.48±0.14	-0.49±0.06	-0.47±0.02
Rump fat thickness	-0.39±0.15	-0.43±0.14	-0.53±0.06	-0.41±0.03
Marbling	-0.33±0.12	-0.37±0.06	-0.22±0.16	-0.17±0.03
Hot carcass weight	-0.45±0.17	-0.42±0.09	-0.41±0.11	-0.35±0.01
Edible weight	-0.40±0.14	-0.41±0.15	-0.36±0.05	-0.35±0.11

4. Discussion

Regarding BW, a direct heritability estimate of 0.39 (Table 2) was observed, which was similar to that reported by Araujo et al.[29] and higher than that reported by Kamei et al.[30] in Nellore cattle. Moderate direct heritability estimates were also obtained for weights at 120, 210, 365, and 450 days of age, which were higher than values reported for Nellore cattle by Kamei et al.[30], but similar to those presented by Araujo et al.[29], Bonamy et al.[6], and Kluskaa et al.[17]. The higher magnitude observed compared to other studies can be attributed to the larger proportion of additive variance in relation to environmental variance, considering that the evaluated animals were subjected to uniform management, leading to less environmental influence. The evaluated data originate from only one herd, which may result in lower environmental variance for birth weight and other live weight traits evaluated. Another factor that may have contributed to the higher heritability estimates for growth traits is the genetic selection the herd underwent, which considers maternal ability and weight traits as selection criteria.

The use of BW in breeding programs is a crucial factor for calving ease and is directly associated with dystocia and perinatal mortality. Therefore, determining the heritability estimates of BW might boost economic productivity by improving growth traits and limiting associated birth weight problems(4,31). It is even more important considering that heifers subjected to selection for sexual precocity are still completing the body development in the occurrence of the first calving.

Moderate heritability estimates for pre- and post-weaning weight gains were similar to those reported in previous studies with indicine cattle (0.15 to 0.22)(20,32), indicating the further scope of genetic improvement through selection in these traits. However, they were lower than heritability for live weight, which could be attributed to the greater environmental influence on weight gains, considering that these traits are directly influenced by the diet offered.

Maternal heritability estimates observed for BW, W120, W210, and PREWWG are within the range from 0.03 to 0.11 described in the literature for Nellore cattle(17,20,29,30). Despite the importance of the inclusion of maternal effects in the genetic analysis and the influence of the genetic potential of the dam on pre-weaning performance, as evidenced by the proportion of maternal variance in relation to phenotypic variance, the low maternal heritability values found may be associated with the higher influence of additive variance on live weight(33). These results suggest that BW and weight traits in Nellore would respond sluggishly to selection for maternal ability. Nonetheless, the additive genetic and maternal effects must be considered when constructing genetic selection indices(4).

Moderate heritability estimates for REA, BF, and RF were consistent with those reported in the literature for Nellore cattle, ranging between 0.17 to 0.34(6,17,19,20). Moderate heritability estimates for MAR and HCW were also reported by Gordo et al.(34), Tonussi et al.(35), and Weik et al.(36) in Nellore cattle. The obtained results indicate that part of the variation in these traits is attributed to additive effects, and carcass traits would respond to genetic selection, modifying body composition over a short time if selection pressure is intense(20).

Heritability estimates for AFCo are within the range reported in previous studies with Nellore cattle where it was evaluated as a binary trait, specifically as the probability of early calving (0.21 to 0.37)(6,17,19). For AFCa, the value obtained in this study was higher than values (0.08 to 0.16) reported in Nellore cattle(17,20,37,38). On the other hand, it was close to the estimate of 0.25 described by Buzanskas et al.(19). Although genetic group differences and large unexplainable residual variances bring discrepancies to heritability estimates, the superiority obtained for AFCa heritability resulted from the genetic selection imposed on the evaluated herd for sexual precocity, as well as the management practice of sexually challenging the heifers since 11 months of age. Thus, if heifers are exposed to reproductive activity at early ages, higher heritability estimates would be obtained, as confirmed by Pereira et al.[39], Boligon et al.[40], and Heise et al.[41]. Moderate estimates of heritability for AFCo and AFCa indicated that these traits would respond to genetic selection. Thus, due to the economic importance of sexual precocity-indicator traits for the beef production system and the genetic differences between individuals, genetic selection can be an effective tool to obtain genetic changes in the herd, thus reducing AFCo and AFCa[37].

The differences between AFCo and AFCa, that is, heifers that displayed early pregnancy but did not calve, can be attributed to different factors, such as embryonic loss, and voluntary abortion, among other factors intrinsic to females. Nevertheless, favorable estimates of high genetic and phenotypic correlations between AFCo with AFCa demonstrate that most of the genes affect these traits, and genetic selection to reduce age at first conception would also reduce age at first calving since the only difference between them is the gestation period. These results also demonstrated that AFCo may be a phenotypic indicator of ACFa or vice versa, being indicators of heifers that showed the highest sexual precocity. Favorable genetic correlations between AFCo, evaluated as the probability of early calving and as a binary trait, with AFCa were also reported by Kluskaa et al.[17] and Shiotsuki et al.[42] with Nellore cattle. However, the estimates observed in this study show a greater magnitude, resulting from the genetic selection imposed on the evaluated herd for sexual precocity. In fact, Boligon and Albuquerque[43] stated that genetic correlations are influenced by genetic selection criteria adopted in the herd. In addition, when the productive goal is to increase sexual precocity, AFCo could be indicated as a genetic selection criterion since this trait is obtained at a younger age than AFCa, reducing the time used to identify the earliest heifers.

Although the genetic correlation between BW and sexual precocity-indicator traits was low, the phenotypic estimates were favorable, moderate, and negative, i.e. higher birth weights are associated with younger AFCo and AFCa. These estimates pointed out that environmental and non-additive factors are acting simultaneously on these traits and that a variation in fetal development can influence the occurrence of early pregnancy. The relationship between these traits may be attributed to the influence that fetal development, reflected in birth weight, has on reproductive performance and age at first calving[44]. An extensive discussion about that can be found in Brunes et al.[45].

The low phenotypic correlations between AFCo and AFCa with W120 may be attributed to a greater influence of maternal ability in this growth phase than the environment offered to the calf. Hence, milk production influences the growth of calves, and this live weight is assessed at the age that coincides with the peak lactation of Nellore cattle[46]. The favorable and moderate phenotypic and genetic correlations between W210, W365, and W450 with sexual precocity-indicator traits indicated that heifers that show higher live weight would also be those with a lower age at first conception and calving and that environmental conditions that lead to increased live weight can also increase sexual precocity in Nellore heifers. Thus, maintaining appropriate live weights in heifers is essential to facilitate successful pregnancy and complete it [47]. Given that, for the initial ovulation, weight holds more significance than age due to its role in accelerating growth and development, leading to earlier puberty[48], this association between genetic and phenotypic traits is well-founded.

In fact, Funston et al.[49] stated that live weight can influence the onset of puberty in females, which is dependent on the action of genetic selection. Thus, the moderate genetic correlation observed in this study may have resulted from the genetic selection imposed on the evaluated herd for sexual precocity, which aims to reduce the age at sexual maturity of heifers. However, massive selection for live weight may result in animals with a higher adult live weight, larger body size[50,51], and sexually delayed[1]. Thus, genetic selection for growth and sexual precocity-indicator traits may be recommended. For Nellore cattle, negative genetic correlations, but of smaller magnitude between growth traits and AFCo, evaluated as a binary trait (EC30), have been reported[6]. Negative genetic correlations between AFCa and growth traits have also been reported for beef cattle (-0.50 to -0.13)[18,20,43,50].

The favorable and moderate correlation estimate between AFCa with POSTWWG was also reported by Boligon et al.[50] with Nellore cattle, and indicates that additive genes for post-weaning weight gain could be connected somehow to those responsible for the sexual precocity of the animal. The results obtained indicated that heifers with the highest potential for post-weaning daily weight gain are also the most sexually precocious, and this effect is more pronounced in the post-weaning phase, which corroborates the descriptions of Caetano et al.[20]. This pattern may be related to the fact that heifers under selection for sexual precocity have not completed their body development and those with a higher post-weaning weight gain may have better body condition and higher chances of first calving at a younger age. Pereira et al.[1] reported that the greater daily weight gain from weaning to puberty produced higher live weight and lower age at puberty, which can be related to an increase in follicular diameter[52].

The low genetic and phenotypic correlations obtained between AFCo with PREWWG and POSTWWG, and AFCa with PREWWG indicated that sexual precocity-indicator traits displayed a weak relationship with pre-weaning daily weight gain in Nellore cattle. However, these results are different from those observed between AFCa and POSTWWG. This result may be due to early post-weaning growth having a more profound effect on reproductive success in the first breeding season[53]. Therefore, post-weaning nutrition and daily weight gain are strategies to improve the economic and biological efficiency of cow-calf production systems, advancing the age of heifers at first calving[1].

The favorable (moderate and negative) genetic correlations between REA, BF, and RF with sexual precocity-indicator traits suggest that genetic selection for early heifer pregnancy would favorably improve performance for carcass traits. The phenotypic selection and environmental changes that aim to increase carcass fat thickness and ribeye area would increase sexual precocity, suggesting that the REA, BF, and RF of the heifers may be indicative of sexual precocity. The greater subcutaneous fat deposition could indicate earlier finishing and could result in animals being more sexually precocious[20]. Thus, it is possible to improve carcass quality and consequently decrease the age at first conception and calving. An extensive discussion about that can be found in Brunes et al.[45].

Similar results for genetic correlation between BF with AFCa[20] and AFCo, evaluated as a binary trait[17,54], and REA with AFCa[55] were reported in Nellore cattle. However, conflicting results have been reported by Bonamy et al.[6], Caetano et al.[20], de Paula et al.[56], Kluskaa et al.[17], and Portes et al.[57], who found low genetic and phenotypic correlations between carcass and sexual precocity-indicator traits in Nellore cattle. The results obtained in this study did not show this trend, probably due to differences in genetic population background and differences in the selection program since the evaluated herd is selected for sexual precocity, REA, BF, and RF.

Favorable (moderate and negative) genetic and phenotypic correlations between AFCo and AFCa with MAR indicate that an increase in marbling results in a reduction of age at first conception and calving. Similarly, Oyama[54] related favorable genetic correlations between marbling and AFCa, in beef cattle. The genetic association between MAR e sexual precocity-indicator traits corroborates results presented by Mota et al.[58], who reported that SNP markers with a specific effect on AFCa harbor QTL regions associated with important biological pathways, including marbling score. These results can be justified by a possible positive influence of the increase in marbling and carcass fat in reducing the onset of females' reproductive activity[59]. Adipose tissue deposition begins after bone and muscle tissue deposition is completed[60]. Thus, sexually precocious heifers reach maturity at a younger age, resulting in the beginning of carcass fat deposition[61], including intramuscular fat deposition, justifying the results obtained in this study.

Favorable (moderate) genetic and phenotypic correlations between HCW and EW with sexual precocity-indicator traits suggest that more precocious heifers selected based on AFCo and AFCa may display higher meat cut yields and carcass weight. The association between HCW and sexual precocity may be attributed to the same effects of their association with live weight since heifers with greater body development have a higher carcass weight. The EW variable indicates the amount of edible meat expected from the carcass, which in turn is associated with the rib-eye area and muscle deposition, a trait that is also associated with sexual precocity. According to Rosales Nieto et al.[62], sexual precocity is influenced by growth rate, which affects muscle deposition.

In general, a favorable and moderate genetic and phenotypic correlation between carcass and sexual precocity-indicator traits was expected. Since a positive body energy balance[63] regulates the ovulation rate of females, animals that mature earlier in carcass finishing are also expected to be more sexually precocious[55]. According to Pereira et al.[1], for every unit increase in BF, there was a reduction in 9.9 days to reach puberty in crossbred beef heifers.

5. Conclusions

The results of this study encourage the use of AFCo in Nellore cattle since this trait displayed enough genetic variability in this breed and can be used as a selection criterion to improve sexual precocity. In addition, considering the genetic correlation obtained between AFCo and AFCa, when the genetic selection objective is to increase heifer sexual precocity, we could use AFCo as a selection criterion, as the measurement of this trait occurs at a younger age compared to first calving, which implies reducing the time required for animal evaluation and decision-making. Long-term selection for animals with early ages at first conception and calving would improve carcass yield, fat deposition, and growth performance.

Declaration of conflict of interest

The authors declare no conflicts of interest.

Author contributions

Conceptualization: L. C. Brunes and C. U. Magnabosco*. Data curation*: L. C. Brunes, C. U. Magnabosco, F. Baldi and R. B. Lobo. *Formal analysis*: L. C. Brunes, C. U. Magnabosco and F. Baldi. *Investigation*: L. C. Brunes, C. U. Magnabosco, F. Baldi and R. B. Lobo. *Writing (original draft):* L. C. Brunes, C. U. Magnabosco and F. Baldi. *Writing (proof-reading & editing):* M. F. O. Costa and F. B. Lopes.

Acknowledgements

The authors thank the National Association of Breeders and Researchers (ANCP) for the help and support received during this project. We are also indebted to Vera Cruz Farm, EMBRAPA, CAPES and FAPEG for financial support.

References

1. Pereira GR, Barcellos JOJ, Sessim AG, Tarouco JU, Feijó FD, Braccini Neto J, Prates ER, Canozzi MEA. Relationship of post-weaning growth and age at puberty in crossbred beef heifers. Rev Bras Zootec. 2017;46(5):413–420. Disponível em: https://doi.org/10.1590/S1806-92902017000500007

2. Snelling WM, Kuehn LA, Thallman RM, Bennett GL, Golden BL. Genetic correlations among weight and cumulative productivity of crossbred beef cows. J Anim Sci. 2019;97(1):63–77. Disponível em: https://doi.org/10.1093/jas/sky420

3. Terry SA, Basarab JA, Guan LL, McAllister TA. Strategies to improve the efficiency of beef cattle production. Can J Anim Sci. 2021;101(1):1–19. Disponível em: https://doi.org/10.1139/cjas-2020-0022

4. Lopez BI, Santiago KG, Seo K, Jeong T, Park JEE, Chai HHH, Park W, Lim D. Genetic Parameters of Birth Weight and Weaning Weight and Their Relationship with Gestation Length and Age at First Calving in Hanwoo (Bos taurus coreanae). Animals. 2020;10(6):1083. Disponível em: https://doi.org/10.3390/ani10061083

5. Pegolo S, Cecchinato A, Savoia S, Di Stasio L, Pauciullo A, Brugiapaglia A, Bittante G, Albera A. Genome-wide association and pathway analysis of carcass and meat quality traits in Piemontese young bulls. Animal. 2020;14(2):243–52. Disponível em: https://doi.org/10.1017/s1751731119001812

6. Bonamy M, Kluska S, Peripolli E, de Lemos MVE, Amorim ST, Vaca RJ, Lobo RB, Castro LM de, Faria CU de, Ferrari FB, Baldi F. Genetic association between different criteria to define sexual precocious heifers with growth, carcass, reproductive and feed efficiency indicator traits in Nellore cattle using genomic information. J Anim Breed Genet. 2019;136:15–22. Disponível em: https://doi.org/10.1111/jbg.12366

7. Dias LT, Faro LE, Albuquerque LG. Estimativas de herdabilidade para idade ao primeiro parto de novilhas da raça Nelore. Rev Bras Zootec. 2004;97–102. Disponível em: https://doi.org/10.1590/S1516-35982004000100013

8. Meirelles SL, Espasandin AC, Mattar M, Queiroz SA de. Genetic and environmental effects on sexual precocity traits in Nellore cattle. Rev Bras Zootec. 2009;38(8):1488–1493. Disponível em: https://doi.org/10.1590/S1516-35982009000800012

9. Setiaji A, Oikawa T. Genetics of heifer reproductive traits in Japanese Black cattle. Asian-Australasian J Anim Sci. 2020;33(2):197–202. Disponível em: https://doi.org/10.5713%2Fajas.19.0118

10. Terakado APN, Pereira MC, Yokoo MJ, Albuquerque LG. Evaluation of productivity of sexually precocious Nelore heifers. Animal. 2015;9(6):938–43. Disponível em: https://doi.org/10.1017/S1751731115000075

11. Fernandes Júnior GA, Silva DA, Mota LFM, de Melo TP, Fonseca LFS, Silva DB dos S, Carvalheiro R, Albuquerque LG. Sustainable Intensification of Beef Production in the Tropics: The Role of Genetically Improving Sexual Precocity of Heifers. Animals. 2022;12(2):174. Disponível em: https://doi.org/10.3390/ani12020174

12. Fernandes Júnior GA, Garcia DA, Hortolani B, de Albuquerque LG. Phenotypic relationship of female sexual precocity with production and reproduction traits in beef cattle using multivariate statistical techniques. Ital J Anim Sci. 2019;18(1):182–188. Disponível em: https://doi.org/10.1080/1828051X.2018.1503570

13. Irano N, De Camargo GMF, Costa RB, Terakado APN, Magalhães AFB, Silva RMDO, Dias MM, Bignardi AB, Baldi F, Carvalheiro R, Oliveira, HN de, Albuquerque LG. Genome-wide association study for indicator traits of sexual precocity in Nellore cattle. PLoS One. 2016;11(8):1–14. Disponível em: https://doi.org/10.1371/journal.pone.0159502

14. Novakovic Z, Sretenovic L, Aleksic S, Petrovic MM, Pantelic V, Ostojic-Andric D. Age at first conception of high yielding cows. Biotechnol Anim Husb. 2011;27(3):1043–1050. Disponível em: http://www.doiserbia.nb.rs/Article.aspx?ID=1450-91561103043N

15. Lopes MV de O, Silva VM da, Araujo TL de. A análise de diagnósticos de enfermagem sob uma perspectiva bayesiana. Rev da Esc Enferm da USP. 2012;46(4):994–1000. Disponível em: https://doi.org/10.1590/S0080-62342012000400030

16. Aguilar I, Misztal I, Johnson D, Legarra A, Tsuruta S, Lawlor T. Hot topic: A unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of Holstein final score. J Dairy Sci. 2010;93:743–52. Disponível em: https://doi.org/10.3168/jds.2009-2730

17. Kluskaa S, Olivieria BF, Bonamy M, Chiaiaa HLJ, Feitosaa FLB, Bertona MP, Peripolli E, Lemos MVA, Tonussi RL, Lobo RB, Magnabosco CU, Di Croce F, Osterstock J, Pereira ASC, Munari DP, Bezerra LA, Lopes FB, Baldi F. Estimates of genetic parameters for growth, reproductive, and carcass traits in Nelore cattle using the single step genomic BLUP procedure. Livest Sci. 2018;216:203–9. Disponível em: https://doi.org/10.1016/j.livsci.2018.08.015

18. Pires BC, Tholon P, Buzanskas ME, Sbardella AP, Rosa JO, Campos da Silva LO, Torres Junior RA de A, Munari DP, Alencar MM de. Genetic analyses on bodyweight, reproductive, and carcass traits in composite beef cattle. Anim Prod Sci. 2017;57(3):415–421. Disponível em: https://doi.org/10.1071/AN15458

19. Buzanskas ME, Pires PS, Chud TCS, Bernardes PA, Rola LD, Savegnago RP, Lobo RB, Munari DP. Parameter estimates for reproductive and carcass traits in Nelore beef cattle. Theriogenology. 2017;92:204–209. Disponível em: https://doi.org/10.1016/j.theriogenology.2016.09.057

20. Caetano SL, Savegnago RP, Boligon AA, Ramos SB, Chud TCS, Lôbo RB, Munari DP. Estimates of genetic parameters for carcass, growth and reproductive traits in Nellore cattle. Livest Sci. 2013;155(1):1–7. Disponível em: http://dx.doi.org/10.1016/j.livsci.2013.04.004

21. Szenci O, Cyulai G, Nagy P, Kovács L, Varga J, Taverne MAM. Effect of uterus position relative to the pelvic inlet on the accuracy of early bovine pregnancy diagnosis by means of ultrasonography. Vet Q. 1995;17(1):37–39. Disponível em: https://doi.org/10.1080/01652176.1995.9694528

22. Garnero AV, Lôbo RB, Bezerra LAF, Oliveira HN. Comparação entre alguns critérios de seleção para crescimento na raça Nelore. Rev Bras Zootec. 2001;30(3):714–718. Disponível em: https://doi.org/10.1590/S1516-35982001000300016

23. BIF - Beef Improvement Federation. Guidelines for uniform beef improvement programs. Athens: BIF. Beef Improvement Federation. 2016. Disponível em: https://beefimprovement.org/wp-content/uploads/2013/07/BIFGuidelinesFinal_updated0916.pdf

24. Lobo RB, Bezerra LAF, Magnabosco CU, Faria CU, Bergmann JAG, Castro LM, Negreiros MP, Baena MM, Oliveira DMC, Nakabashi LRM, Assagra WLO, Baldi F. Sumário de Touros. Ribeirão Preto: ANCP; 2023. 116 p. Portuguese. Disponível em: https://www.ancp.org.br/wp/wp-content/uploads/2023/08/Suma%CC%81rio-ANCP-2023_230823.pdf

25. R Core Team. R: A language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing, 2021.

26. Roso VM, Schenkel FS. AMC – A computer program to assess the degree of connectedness among contemporary groups. In: 8 th World Congress on Genetics Applied to Livestock Production. Belo Horizonte: UFMG; 2006. p. 26-27.

27. Misztal I, Tsuruta S, Lourenco DAL, Aguilar I, Legarra A, Vitezica Z. Manual for BLUPF90 family of programs. Athens: University of Georgia; 2019. 125 p. Disponível em: http://nce.ads.uga.edu/wiki/lib/exe/fetch.php?media=blupf90_all1.pdf

28. Meyer K, Houle D. Sampling based approximation of confidence intervals for functions of genetic covariance matrices. In: association for the advancement of animal breeding and genetics conference. In: Association for the advancement of animal breeding and genetics conference. Napier: AAABG; 2013. p. 523–526. Disponível em: http://www.aaabg.org/aaabghome/AAABG20papers/meyer20523.pdf

29. Araujo CV de, Lobo RB, Figueiredo LGG, Mousquer CJ, Laureano MMM, Bittencourt TCB dos SC de, Araujo SI. Estimates of genetic parameters of growth traits of Nellore cattle in the Midwest region of Brazil. Rev Bras Saude e Prod Anim. 2014;15(4):846–853. Disponível em: https://www.scielo.br/j/rbspa/a/HTwK5jxChbfHCNRWGfN5ygz/?lang=en

30. Kamei LM, De Azambuja Ribeiro EL, Fonseca NAN, De Souza Dantas Muniz CA, Camiloti TV, Koritiaki NA, Albieri N, Fortaleza AP de S. Genetic parameters of growth traits in Nellore cattle. Semin Ciências Agrárias. 2017;38(3):1513. Disponível em: http://dx.doi.org/10.5433/1679-0359.2017v38n3p1513

31. Hohnholz T, Volkmann N, Gillandt K, Waßmuth R, Kemper N. Risk Factors for Dystocia and Perinatal Mortality in Extensively Kept Angus Suckler Cows in Germany. Agriculture. 2019;9(4):85-96. Disponível em: https://doi.org/10.3390/agriculture9040085

32. Manuel M, Cavani L, Millen DD, Andrighetto C, Lupatini GC, Fonseca R da. Estimation of genetic parameters for weight traits and Kleiber Index in a Brahman cattle population. Sci Agric. 2019;76(6):459–462. Disponível em: https://doi.org/10.1590/1678-992X-2018-0062

33. Lira TS de, Pereira L de S, Lopes FB, Ferreira JL, Lôbo RB, Santos GC de J. Tendências genéticas para características de crescimento em rebanhos nelore criados na região do trópico úmido do Brasil. Cienc Anim Bras. 2013;14(1):23–31. Disponível em: https://doi.org/10.5216/cab.v14i1.16785

34. Gordo DGM, Espigolan R, Bresolin T, Fernandes Júnior GA, Magalhães AFB, Braz CU, Fernandes WB, Baldi F, Albulquerque LG. Genetic analysis of carcass and meat quality traits in Nelore cattle. J Anim Sci. 2018;96(9):3558–64. Disponível em: https://academic.oup.com/jas/article/96/9/3558/5051832

35. Tonussi RL, Espigolan R, Gordo DGM, Magalhães AFB, Venturini GC, Baldi F, Oliveira HN, Chardulo LAL, Tonhati H, Albuquerque LG. Genetic association of growth traits with carcass and meat traits in Nellore cattle. Genet Mol Res. 2015;14(4):18713–18719. Disponível em: https://doi.org/10.4238/2015.december.28.20

36. Weik F, Hickson RE, Morris ST, Garrick DJ, Archer JA. Genetic Parameters for Growth, Ultrasoundand Carcass Traits in New Zealand Beef Cattle and Their Correlations with Maternal Performance. Animals. 2022;12(25):1-19. Disponível em: https://doi.org/10.3390/ani12010025

37. Claus LAM, Koetz Júnior C, Roso VM, Borges MHF, Barcellos JOJ, Ribeiro EL de A. Genetic parameters of age at first calving, weight gain, and visual scores in Nelore heifers. Rev Bras Zootec; 2017;46(4):303–308. Disponível em: https://doi.org/10.1590/S1806-92902017000400005

38. da Silva Neto JB, Peripolli E, da Costa e Silva EV, Espigolan R, Neira JDR, Schettini G, Costa Filho LCC, Barbosa FB, Macedo GG, Brunes LC, Lobo RB, Pereira ASC, Baldi F. Genetic correlation estimates between age at puberty and growth, reproductive, and carcass traits in young Nelore bulls. Livest Sci. 2020;241:104266. Disponível em: https://doi.org/10.1016/j.livsci.2020.104266

39. Pereira E, Eler JP, Ferraz JBS. Análise genética de características reprodutivas na raça Nelore. Pesq agropec bras. 2002;37(5):703–8. Disponível em: https://doi.org/10.1590/S0100-204X2002000500016

40. Boligon AA, Rorato PRN, De Albuquerque LG. Correlacoes geneticas entre medidas de perimetro escrotal e caracterissticas produtivas e reprodutivas de femeas da raça Nelore. Rev Bras Zootec. 2007;36(3):565–571. Disponível em: https://doi.org/10.1590/S1516-35982007000300007

41. Heise J, Stock KF, Reinhardt F, Ha NT, Simianer H. Phenotypic and genetic relationships between age at first calving, its component traits, and survival of heifers up to second calving. J Dairy Sci. 2018;101(1):425–432. Disponível em: https://doi.org/10.3168/jds.2017-12957

42. Shiotsuki L, Silva JA, Tonhati H, Albuquerque LG. Genetic associations of sexual precocity with growth traits and visual scores of conformation, finishing, and muscling in Nelore cattle. J Anim Sci. 2009;87(5):1591–1597. Disponível em: https://doi.org/10.2527/jas.2008-1173

43. Boligon AA, Albuquerque LG. Genetic parameters and relationships of heifer pregnancy and age at first calving with weight gain, yearling and mature weight in Nelore cattle. Livest Sci. 2011;141(1):12–16. Disponível em: http://dx.doi.org/10.1016/j.livsci.2011.04.009

44. Freetly HC, Ferrell CL, Jenkins TG. Timing of realimentation of mature cows that were feed-restricted during pregnancy influences calf birth weights and growth rates. J Anim Sci. 2000;78:2790–2796. Disponível em: https://doi.org/10.2527/2000.78112790x

45. Brunes LC, Baldi FS, Costa MFO e, Quintans G, Banchero G, Lôbo RB, Magnabosco CU. Early growth, backfat thickness and body condition has major effect on early heifer pregnancy in Nellore cattle. An Acad Bras Cienc. 2022;94(1):1-18. Disponível em: https://doi.org/10.1590/0001-3765202120191559

46. Vaz RZ, Lobato JFP, Restle J, Costa PT, Eloy LR, Ferreira OGL, Costa JLB. Calving month and calf sex on the production and efficiency of herds. Ciência Anim Bras. 2020;21:1-13. Disponível em: https://doi.org/10.1590/1809-6891v21e-61977

47. Gregianini HAG, Carneiro Junior JM, Pinto Neto A, Costa Filho LCC da, Gregianini JTF, Pinheiro AK, Trenkel CKG. Precocidade sexual de novilhas Nelore em rebanho sob seleção no Estado do Acre. Res Soc Dev. 2021;10(4):e16310413945. Disponível em: http://dx.doi.org/10.33448/rsd-v10i4.13945

48. Andrade EF, Ferreira DF, Santos PEF dos, Eustáquio Filho A. Principais fatores que afetam a precocidade de novilhas nelores e a classificação do sistema de produção precoce: uma revisão. Recital. 2020;2(57):73. Disponível em: https://doi.org/10.46636/recital.v2i3.132

49. Funston RN, Martin JL, Larson DM, Roberts AJ. Physiology and Endocrinology Symposium: Nutritional aspects of developing replacement heifers. J Anim Sci. 2012;90(4):1166–1171. Disponível em: https://doi.org/10.2527/jas.2011-4569

50. Boligon AA, Albuquerque LG de. Correlações genéticas entre escores visuais e características reprodutivas em bovinos Nelore usando inferência bayesiana. Pesqui Agropec Bras. 2010;45(12):1412–1408. Disponível em: https://doi.org/10.1590/S0100-204X2010001200011

51. Regatieri IC, Boligon AA, Costa RB, de Souza FRP, Baldi F, Takada L, Venturini Gc, de Camargo GMF, Júnior GGA, Tonhati H, de Oliveira HN, de Albuquerque LG. Association between single nucleotide polymorphisms and sexual precocity in Nellore heifers. Anim Reprod Sci. 2017;177:88–96. Disponível em: http://dx.doi.org/10.1016/j.anireprosci.2016.12.009

52. Barcellos JOJ, Pereira GR, Dias EA, McManus C, Canellas L, Bernardi ML, Tarouco A, Prates ER. Higher feeding diets effects on age and liveweight gain at puberty in crossbred Nelore × Hereford heifers. Trop Anim Health Prod. 2014;46(6):953–960. Disponível em: https://doi.org/10.1007/s11250-014-0593-6

53. Roberts AJ, Geary TW, Grings EE, Waterman RC, MacNeil MD. Reproductive performance of heifers offered ad libitum or restricted access to feed for a one hundred forty-day period after weaning. J Anim Sci. 2009;87(9):3043–3052. Disponível em: https://doi.org/10.2527/jas.2008-1476

54. Oyama K, Katsuta T, Anada K, Mukai F. Genetic Parameters For Reproductive Performance Of Breeding Cows And Carcass Traits Of Fattening Animals In Japanese Black (Wagyu) Cattle. Anim Scie. 2004; 78(2):195-201. Disponível em: https://doi.org/10.1017/S1357729800053984

55. Yokoo MJ, Lôbo RB, Magnabosco CU, Rosa GJM, Forni S, Sainz RD, Albuquerque LG. Genetic correlation of traits measured by ultrasound at yearling and 18 months of age in Nellore beef cattle. Livest Sci. 2015;180:34–40. Disponível em: http://dx.doi.org/10.1016/j.livsci.2015.07.003

56. De Paula EJH, Martins EN, De Oliveira CAL, Magnabosco CDU, Sainz RD, Geron LJV, Souza Neto EL, Porto E de P, Miguel GZ. Associations between reproductive and carcass traits in Nellore. Semin Agrar. 2015;36(6):4423–4434. Disponível em: http://dx.doi.org/10.5433/1679-0359.2015v36n6Supl2p4423

57. Portes JV, Menezes GRO, MacNeil MD, da Silva LOC, Gondo A, Braccini Neto J. Selection indices for Nellore production systems in the Brazilian Cerrado. Livest Sci. 2020;242:104309. Disponível em: https://doi.org/10.1016/j.livsci.2020.104309

58. Mota LFM, Lopes FB, Fernandes Júnior GA, Rosa GJM, Magalhães AFB, Carvalheiro R, Albuquerque LG. Genome-wide scan highlights the role of candidate genes on phenotypic plasticity for age at first calving in Nellore heifers. Sci Rep. 2020;10(1):6481. Disponível em: https://doi.org/10.1038/s41598-020-63516-4

59. Oyama K, Mukai F, Yoshimura T. Genetic relationships among traits recorded at registry judgment, reproductive traits of breeding females and carcass traits of fattening animals in Japanese Black cattle. Anim Sci Technol. 1996;67:511–518. Disponível em: https://www.jstage.jst.go.jp/article/chikusan1924/67/6/67_6_511/_pdf

60. Magnabosco CU, Brito Lopes F, de Magalhaes Rosa GJ, Sainz RD. Bayesian estimates of genetic parameters for reproductive traits in Nellore cows raised on pasture in tropical regions. Rev Colomb Ciencias Pecu. 2016;29(2):119–129. Disponível em: https://doi.org/10.17533/udea.rccp.v29n2a05

61. Faria CU, Pires BC, Vozzi AP, Magnabosco CU, Koury Filho W, Viu MAO, Oliveira HN, Lobo RB. Genetic correlations between categorical morphological traits in Nelore cattle by applying Bayesian analysis under a threshold animal model. J Anim Breed Genet. 2010;127:377–384. Disponível em: https://doi.org/10.1111/j.1439-0388.2010.00860.x

62. Rosales Nieto CA, Ferguson MB, Macleay CA, Briegel JR, Martin GB, Thompson AN. Selection for superior growth advances the onset of puberty and increases reproductive performance in ewe lambs. Animal. 2013;7(6):990–997. Disponível em: https://doi.org/10.1017/s1751731113000074

63. Bronson FH, Manning JM. The Energetic Regulation of Ovulation: A Realistic Role for Body Fat. Biol Reprod. 1991;44(6):945–950. Disponível em: https://doi.org/10.1095/biolreprod44.6.945