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Genetic correlation estimates between calving ease in primiparous cows and economically important traits in Nellore cattle

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Abstract

This study aimed to estimate (co)variance components and genetic parameters for calving ease (CE) and their genetic correlations with growth, reproductive, carcass, and feed efficiency traits in Nellore cattle. Phenotypes for CE are scored in two categories: normal calving and assisted calving. The traits considered were probability of precocious calving, age at first calving, stayability, adjusted scrotal circumference at 365 days of age, accumulated cow productivity, age at puberty of males, gestation length, birth weight, adjusted weights at 210 and 450 days of age, adult cow weight, frame score, hip height, rib eye area, subcutaneous backfat thickness, rump fat thickness, intramuscular fat percentage, residual feed intake and dry matter intake. The estimation of genetic parameters was performed using a two-trait threshold-linear animal model, except for CE, stayability, and probability of precocious calving, which were evaluated through a two-trait threshold animal model. The direct (0.27) and maternal (0.19) heritability estimates for CE in heifers primiparous Nellore indicated that selecting for this trait is feasible. The selection to improve the female sexual precocity should consider CE during the selection and mating decisions to reduce calving problems. Genetic correlation estimates between CE and BW suggest that selecting low birth weight to reduce calving problems is not an appropriate strategy to improve calving ease in heifers Nellore. Therefore, adopting a multi-trait selection model with CE and BW in the Nellore breed would reduce calving difficulties, particularly in sexually precocious heifers, without impairing the growth, reproductive, feed efficiency conversion, and carcass indicator traits.

K E Y W O R D S

beef cattle, dystocia, genetic correlations, sexual precocity

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Growth-related traits are traditionally considered as selection criteria in beef cattle breeding programs due to their productive and economic importance and for being favourably correlated with slaughter and carcass weight. Further, growth-related traits favourably respond to selection when applied as selection criteria in beef cattle breeding programs. However, there is a growing concern about selecting for higher growth rates at young ages and their impact on the adult size, carcass composition, fertility and herd productivity in indicine (Bos taurus indicus) beef cattle breeding programs. Recently, quantitative genetic studies focused on sexual precocity and reproductive efficiency traits in indicine beef cattle (Fernandes Júnior et al., 2022; Kluska et al., 2018). In this sense, early heifer pregnancy is an economically relevant trait measured directly on females to improve fertility and sexual precocity, and it has been widely studied in indicine cattle (Eler et al., 2004; Silva et al., 2005; van Melis et al., 2010).

The heifer pregnancy is easy to assess, not requiring penalties for heifers that did not calve, and it showed moderate to high genetic additive variability, justifying their application as a selection criterion in beef cattle breeding programs (Silva et al., 2005). In this context, some indicine beef cattle breeding programs use the probability of precocious calving before 30 months (PP30) as a female early sexual precocity indicator trait. Many cattle breeders bring forward the heifer's first breeding season, and the proportion of precocious calving (<30 months) has increased due to of better nutritional management of females and direct selection for PP30. Despite the female sexual precocity genetic improvement in indicine herds, the incidence of calving problems has increased in recent years, probably due to higher calf birth weight and lower age at first calving of sexual precocious heifers, because of selection for higher growth rates and early sexual precocity.

The calving ease (CE) is an essential component of reproductive efficiency in taurine breeds (Bos taurus taurus), affecting herd profitability and animal welfare (Silvestre et al., 2019). Severe dystocia in heifers has unfavourable effects on fertility, providing lower re-conception rates, impairing viability and increasing the mortality rate of calves (Hossein-Zadeh, 2016; Lourenço et al., 2022). Despite the economic impact of CE, this trait has been widely evaluated only in dairy cattle (Hossein-Zadeh, 2016; Silvestre et al., 2019). The incidence of assisted births in primiparous 2-year-old heifers varies considerably between beef cattle breeds and herds (Hickson et al., 2010; Hogan et al., 2022). The Nellore breed and most of the indicine beef cattle breeds are recognized for a low frequency of calving problems (dystocia), and there are still no reports in the literature about the occurrence of dystocia. In Nellore cattle, CE is phenotypically favourable and associated with moderate to low calf birth weights (BW). In contrast, high birth weight calves are more susceptible to dystocia than low to median birth weight calves (Kamei et al., 2017).

The use of calf's BW to indicate calving difficulty in early sexually precocious heifers comprises selection and mating strategies that adopt low expected progeny difference (EPDs) for BW. Studies have corroborated a moderate to high genetic association between BW and calving problems. In taurine beef cattle breeds, Eriksson et al. (2004a) and Jamrozik and Miller (2014), reported moderate to high unfavourable genetic correlation estimates, varying from 0.62 to 0.80, between BW and calving difficulty. It is important to highlight that selection for low BW would interfere with animal development, impairing weight gain and live weight at later ages (Silveira et al., 2019). Although selection for low BW would improve CE, direct selection to reduce calving difficulty would be a better long-term alternative (Bennett et al., 2021). Recently, Saad et al. (2020) worked with the American Simmental breed to quantify the response to direct selection for CE versus selection for low BW and reported that direct selection for CE rather than low BW substantially improved CE and resulted in heavier animals.

The current beef cattle production scenario aims to increase herd profitability and reduce the incidence of problems related to calves' birth. Quantifying the genetic variability for CE in early sexually precocious primiparous cows and elucidating the genetic association between CE and other productive traits is necessary to assess the importance of using CE as large-scale selection criteria in indicine beef cattle production systems in tropical and subtropical regions. Thus, this study aimed to estimate (co)variance components and genetic parameters for CE in early sexually precocious primiparous cows and their genetic correlations with growth, reproductive, carcass and feed efficiency-related traits in Nellore cattle.

2 | MATERIALS AND METHODS

2.1 | Data

The phenotypic dataset used in this study belongs to the Nellore Brazil breeding program, coordinated by the National Association of Breeders and Researchers (ANCP, Ribeirão Preto, Brazil). A total of 4587 calving ease records of early sexually precocious primiparous Nellore cows born between 2010 and 2017, belonging to 21 farms in Brazil's Midwest, Southeast, Northeast and North regions were collected. Animals were raised in pasturebased production systems, with or without creep feeding and supplementation. The mating season varied from

average daily gain (kg/day) of each period is used to adjust the standard age.

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The FRAME is an index characterized by the relationship between height, sex, and age of the animal. The FRAME classification was proposed by Guimaraes (2020) for Nellore cattle and obtained from herds participating in the ANCP. The methodology used for these traits was the prediction of multiple linear regression and applied in 2 prediction equations, one of them for males and the other for females, as follows:

 $FRAME_{Males} = -20.35 + 0.1305 \times REA + 0.2633 \times BFT - 0.5901 \times RFT + 0.1139 \times HH + 0.0056 \times AGE$ (1)

 $FRAME_{Females} = -11.87 + 0.1316 \times REA - 0.2457 \times BFT - 0.6218 \times RFT + 0.1139 \times HH + 0.0009507 \times AGE$ (2)

2.2 | Reproduction traits

The reproductive traits evaluated in this study were calving ease (CE), probability of precocious calving (PP30), stayability (STAY), age at first calving (AFC), scrotal circumference adjusted at 365 days of age (SC365), accumulated cow productivity (ACP) and gestation length (GL).

February to April and mid-November to January, depending on the region. To evaluate early heifer pregnancy, heif-

ers were exposed to reproduction in their weaning year

(10–14 months), with a mating season period of 3 months.

Heifers were evaluated for pregnancy by rectal palpation

roughly 60 days after the end of the breeding season, and

those who did not conceive in the first mating season were

exposed to reproduction once again at 24 months of age.

The pedigree information included data from 137,467 ani-

mals, including 3183 sires and 25,442 dams.

For CE, only primiparous animals were considered and categorized into two groups. The category 1 consisted of animals that gave birth before 27 months, while category 2 included those that gave birth after 27 months. The CE records were collected shortly after birth and classified as success (2) for normal calving (non-assisted calving) or abnormal calving (1) with some assistance or intervention.

The ACP indicates the cow's production in kilograms of calves weaned per year. The ACP also evaluates the animal for precocity, reproductive periodicity, maternal ability and ability to wean calves with greater weight (Lobo et al., 2000). For PP30, all heifers with gestational confirmation and calved up to 30 months of age had their phenotypes categorized as success (2) or failure (1) otherwise. For STAY, cows with at least three calves calved up to 76 months of age had their phenotypes characterized as success (2) or failure (1) otherwise. The GL was considered as the number of days between conception and calving.

2.3 | Growth and carcass traits

Birth weight (BW), adjusted weights at 210 (W210) and 450 days of age (W450), adult cow weight (ACW) and frame score (FRAME) were analysed. The weight records were collected every 90 days until 18 months of age. After this period, weights were collected yearly until the age of 16 years. The weight was adjusted for age following the equation proposed by Garnero et al. (2001), in which the

where REA, BFT, RFT, HH and AGE are, respectively, rib eye area (cm²), subcutaneous backfat thickness (cm), rump fat thickness (cm), hip height (cm) and age (days) measured on the day of the ultrasound.

The carcass-related traits (REA, Intramuscular Fat Percentage (IMF), BFT, and RFT) were measured by ultrasound (between 15 and 18 months of age). The image scanning and analysis were performed by the ANCP technicians following the criteria of the Ultrasound Guidelines Council, according to the methodology of the Beef Improvement Federation (Hohenboken, 2002). The images for REA and IMF were obtained from the Longissimus thoracic muscle between the 12th and 13th ribs; for BFT on the Longissimus thoracic muscle at a point three-quarters of the ventral length of REA, and for RFT at the junction of the Biceps femoris and Gluteus medius between the ischium and ilium and parallel to the vertebrae (Greiner et al., 2003). A 3.5 MHz linear array transducer connected to a B-mode scanner (Aloka SSD 500; Tokyo, Japan) was used to measure the carcass traits.

The BFT and RFT were measured in millimetres (mm), REA in square centimetres (cm²) and IMF in percentage (%). In addition, the same day as the ultrasound examination was done, phenotypic data for hip height (HH) was collected using a tape measure, measuring the distance in meters from the ground to the tip of the ileum (Beef Improvement Federation [BIF], 2002).

2.4 | Feed efficiency traits

The feed efficiency-related traits were residual feed intake (RFI) and dry matter intake (DMI). The RFI was obtained in feed efficiency tests performed between 2011 and 2018. The animals were raised in individual or collective pens with automated feed intake measurement systems (GrowSafe[®] or Intergado[®]). The animals were evaluated under similar environments and management conditions to assess feed intake and average daily gain (ADG). The animals started the tests with a mean age of 13.5 ± 4.15 months and remained in the test for 70 days, after an adaptation period of 21 days. During the trial, the average weight of each animal was obtained by periodic weighing at the beginning and end of the evaluation period.

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The diets were formulated based on silage and commercial concentrate, with an average of 64% of total digestible nutrients, 13% of crude protein and 76% of dry matter for gains of 1.2 kg/day (Mendes et al., 2020). To ensure ad libitum feed consumption, the feed offer was adjusted daily, allowing refusals ranging from 5% to 10% of the offered feed.

Daily feed intake records that met the following criteria were excluded from the analyses: days when the animals were outside the premises for prolonged periods, instances of equipment failure and days where no feed refusal was observed. The percentage of dry matter in the diet was determined using weekly samples of both feed offered and refused. The ADG in each test was calculated as the linear regression coefficient of body weight on days in test (DIT):

$$y_{ij} = \alpha + \beta * \text{DIT} + \epsilon$$

where, y_{ii} is the body weight of the *i*-th observation in the *j*-th day; α = intercept of the regression equation corresponding to the initial body weight; β = coefficient of linear regression corresponding to ADG; DIT_i=test days for *i*-th observation; and ε_i = random error associated with each observation. The metabolic weight (MW) was calculated: MW = $[\alpha + \beta \times (DIT/2)]^{0.75}$, with α and β assuming the values obtained by the equation described above.

DMI (kg/day) was obtained by calculating the average of all valid daily intake values during the test period. This parameter was calculated in individual pens as the difference between the offered dry matter and the residue. In the collective pens, the DMI was obtained as the amount of feed consumed individually recorded automatically by the electronic systems.

The RFI was considered as the error of the multiple regression equation of DMI in ADG and metabolic weight, as shown below:

$$y = \beta_0 + \beta_1 * ADG + \beta_2 * MW + \epsilon$$

where, *y* is DMI; β_0 is the intercept, β_1 and β_2 are the linear regression coefficients for ADG and MW. respectively; and ϵ is the residual error (i.e., RFI). The number of data and

> TABLE 1 Number of records (Nr), number of common records with CE (Nc), number of contemporary groups (GC), mean and standard deviation (SD) for calving ease in primiparous cows, reproductive, growth, carcass traits, and feed efficiency indicator traits.

Abbreviations: ACP, Accumulated Cow Productivity; ACW, Adult Cow Weight; AFC, Age at First Calving; BFT, Subcutaneous Backfat Thickness; BW, birth weight; CE, calving ease; DMI, Dry Matter Intake; FRAME, Frame Score; GL, Gestation Length; HH, Hip Height; IMF, Intramuscular Fat Percentage; PP30, probability of precocious calving; REA, rib eye area; RFI, Residual Feed Intake; RFT, Rump Fat Thickness; SC365, Adjusted Scrotal Circumference at 365 days of age; STAY, stayability; W210, Adjusted weights at 210 days of age; W450, Adjusted weights at 450 days of age.

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Trait	Nr	Nc	CG	Mean ± SD
CE	4587		219	1.12 ± 0.32
PP30 (%)	42,386	648	1147	1.43 ± 0.49
STAY (%)	48,362	60	491	1.48 ± 3.73
AFC (months)	55,814	658	788	32 ± 6.35
ACP (kg of weaned calves/cow/year)	25,190	13	614	163.62 ± 32.77
SC365 (cm)	34,674	0	883	22.35 ± 2.74
GL (days)	47,757	1835	839	295.14 ± 6.05
HH	9974	326	319	136.89 ± 6.3
FRAME	10,717	372	432	5.73 ± 1.93
W210 (kg)	86,653	2223	2801	204.41 ± 31.97
W450 (kg)	72,330	1252	1847	324.64 ± 60.28
ACW (kg)	12,182	30	270	512.61 ± 69.29
BW (kg)	44,995	1051	1471	34.75 ± 4.88
REA (cm ²)	58,413	1297	1978	59.5 ± 11.42
BFT (mm)	58,104	1295	1975	3.53 ± 1.97
RFT (mm)	58,323	1295	1973	4.98 ± 2.74
IMF (%)	16,424	728	564	2.56 ± 0.94
RFI (kg of DM)	9525	429	154	-0.0035 ± 0.7
DMI (kg of DM)	9552	434	154	8.23 ± 1.82

descriptive statistics of the present study are presented in Table 1.

2.5 | Statistical model

For CE, the contemporary group (CG) comprised farm, heifer birth year, calving year, calving month and calf sex. For growth and carcass traits, the CG was composed of the farm, management group, sex, year and season of birth (dry season from April to September and wet season from October to March). For STAY and PP30, the CG consisted of the farm, year, and season of birth. For traits related to feed efficiency, the CG was composed of farm, management group, sex, feed efficiency test identification, year and season of birth. For all the traits, records within the range of ± 3.5 standard deviations from the mean of the CG, and CG with at least three animals were kept in the analysis. The CG without phenotypic variability for STAY, PP30 and CE were excluded. Descriptive statistics, including the number of animals and contemporary group (CG) per trait analysed, are presented in Table 1.

The model included the direct additive genetic random effect and the fixed effects of GC for all the traits. For W210, GL and BW, the model included the maternal additive genetic and permanent environmental random effects. The dam calving age in years was included in the model as a fixed effect (classificatory effect) for GL, BW and W210.

For CE analyses, the model included the contemporary group and female age at calf birth (precocious females were those who gave birth within 27 months, while primiparous females were those who gave birth after 27 months) as fixed effects, and the direct and maternal additive genetic random effects.

A two-trait threshold-linear animal model was applied to estimate the (co)variance components between CE with W210, W450, ACW, FRAME, HH, ACP, AFC, SC365, GL, REA, BFT, RFT, RFI and DMI, and the (co)variance components between CE with STAY and PP30 were estimated using a two-trait threshold animal model, as follows:

$y = X\beta + Zg + Mm + Wmpe + \varepsilon$

where, **y** is a vector of dependent variables; $\boldsymbol{\beta}$ is a fixed effects vector, including CG and dam's age class at calving in years (ranging from 2 to 11) for W210, GL, and BW; **X** is the incidence matrix associating $\boldsymbol{\beta}$ with **y**; **g** is a random effects vector of direct additive genetic effects; **Z** is the incidence matrix that associates **g** with **y**; *m* is the random effects vector of maternal additive genetic effects (only for CE, GL, BW and W210); **M** is the incidence matrix that associates **m** with **y**; **mpe** is a vector of random maternal permanent

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environmental effects (only for BW and W210); W is the incidence matrix associating **mpe** with y; and ε is the residual random effects vector. It is assumed that $E[y] = X\beta$, genetic, maternal, permanent environment and residual effects were normally distributed with mean equal to zero for linear traits and variances $Var(g) = \mathbf{A} \bigotimes S_g$; $Var(m) = \mathbf{A} \bigotimes S_m$; $Var(mpe) = \mathbf{I} \bigotimes S_{mpe}; \quad Var(e) = \mathbf{I} \bigotimes S_{e},$ respectively, where: S_{σ} is the direct additive genetic covariance matrix; S_{m} is the matrix that maternal additive genetic variance, only for CE, GL, BW, and W210; S_{mpe} is the maternal permanent environment variance matrix; S_{e} is the residual covariance matrix, A is the relationship matrix and I is the identity matrix. For the threshold animal model, an underlying scale (Mrode & Tholmpson, 2005) with a normal distribution was assumed, as follows:

$$U \middle| \theta \sim N \bigl(W \theta, I \sigma_e^2 \bigr)$$

where **U** is the base scale vector with order *r* (with *r*: number of animals); $\theta = (\beta, \mathbf{u}, \mathbf{m}, \mathbf{mpe})$ is the array of parameters with order *s* (with *s*: class number); β is a fixed effects vector with order *s*; **u** is the vector of direct additive genetic effects; **m** is a vector of maternal additive genetic effects; **mpe** is a vector of maternal permanent environmental effects, **W** is the incidence matrix with the order $r \times s$; **I** is the identity matrix with order $r \times r$ and σ_e^2 is the residual variance. For threshold models, the residual variation is fixed at $\sigma_e^2 = 1$ (Sorense & Gianola, 2002). The link between the base and underlying scale was performed by the probability link function (Gianola & Foulley, 1983). For BW, W210, CE and GL the covariance between genetic direct and maternal random effects was set to zero.

The (co)variance components were obtained by the THRGIBBS1F90 software (Misztal et al., 2015). In the analysis, we used Gibbs sampling of 1,000,000 iterations generated with an initial burn-in of 50,000 and a sampling interval of 100. The mean heritability, (co)variance components and genetic correlations were calculated using the samples generated and stored every 100 Gibbs iterations, and subsequently, the mean of the samples was estimated.

For the convergence analysis, visual inspection with density and trace plots of variance components and a Geweke test were used, with the aid of the BOA package (Smith, 2005) in the R program (2023). The heritability estimates were classified as low (lower than 0.20), moderate (ranging from 0.20 to 0.40) and high (higher than 0.40), following the recommendation of Bourdon (1997). The genetic and phenotypic correlation estimates were classified as low (lower than 0.30), moderate (ranging from 0.30 to 0.70) and high (higher than 0.70), according to the recommendations of Hill (2013).

3 | **RESULTS AND DISCUSSION**

The percentage of animals classified as successful calving was 88% (births with no assistance), and 12% required assistance. The incidence of dystocia presented in the present study agreed with previous studies in beef cattle. The reported incidences varied from 6.2% to 37.2% of assisted deliveries in beef cattle (Eriksson et al., 2004a; Hosono et al., 2020; Jamrozik & Miller, 2014; Phocas & Laloë, 2004; Silva et al., 2020).

The Highest Posterior Density (HPD) intervals were calculated based on direct and maternal heritability estimates (Table 2). For CE, the direct heritability estimate was of moderate magnitude (0.27), and the maternal was of moderate to low magnitude (0.19). Genetic parameter estimates for CE are still scarce in Nellore cattle. Silva et al. (2020) worked with a lower number of records of CE in early sexually precocious primiparous cows from two herds. They obtained lower direct heritability (0.18) and higher maternal heritability (0.39) estimates for CE applying a threshold sire-maternal grandsire model (S-MGS) single-step genomic BLUP than those obtained in this

study. The S-MGS model could overestimate the heritability estimates. Saad et al. (2020) worked with an American Simmental cattle population and estimated genetic parameters for CE using the S-MGS model and obtained lower direct heritability (0.23) and maternal heritability (0.14) estimates than those obtained in this study.

Bennett and Gregory (2001) evaluated a single herd of a composite beef cattle breed using the multi-trait animal model and reported moderate heritability estimates for direct (0.40) and maternal (0.22) heritability for CE, respectively. Eaglen and Bijma (2009) reported low direct (0.14) and maternal (0.06) heritability for CE using a linear animal model in Dutch Holstein-Friesian cattle. The heritability estimates reported in the literature for CE differ according to breed and the model used for estimation. Our results indicated that selection for CE in sexual precocious primiparous cows is feasible in Nellore cattle.

Although the maternal heritability is lower than the direct heritability, the maternal component should be considered to estimate the (co)variance components for CE. In this sense, Silva et al. (2020) showed genomic regions associated with CE in early sexual precocious Nellore

		HPD		HPD		
Trait	$h^2 \pm SD$	Upper	Lower	$h^2m \pm SD$	Upper	Lower
CE	0.27 ± 0.08	0.43	0.12	0.19 ± 0.07	0.33	0.07
PP30	0.16 ± 0.03	0.21	0.12			
AFC	0.08 ± 0.01	0.10	0.07			
ACP	0.12 ± 0.01	0.14	0.09			
SC365	0.47 ± 0.02	0.51	0.43			
GL	0.46 ± 0.02	0.43	0.49	0.26 ± 0.06	0.16	0.40
STAY	0.13 ± 0.01	0.16	0.11			
HH	0.32 ± 0.04	0.39	0.26			
FRAME	0.35 ± 0.03	0.41	0.3			
W210	0.18 ± 0.01	0.21	0.16	0.11 ± 0.01	0.12	0.09
W450	0.39 ± 0.03	0.41	0.36			
ACW	0.34 ± 0.03	0.39	0.29			
BW	0.24 ± 0.02	0.27	0.21	0.04 ± 0.01	0.05	0.0
REA	0.37 ± 0.01	0.39	0.35			
BFT	0.22 ± 0.01	0.24	0.21			
RFT	0.36 ± 0.01	0.38	0.34			
IMF	0.29 ± 0.02	0.33	0.25			
RFI	0.17 ± 0.02	0.22	0.13			
DMI	0.32 ± 0.03	0.38	0.26			

Abbreviations: ACW, Adult Cow Weight; AFC, Age at First Calving; BFT, Subcutaneous Backfat Thickness; BW, birth weight; CCP, Accumulated Cow Productivity; CE, calving ease; DMI, Dry Matter Intake.; FRAME, frame score; GL, Gestation Length, HH, Hip Height; IMF, Intramuscular Fat Percentage; PP30, probability of precocious calving; REA, rib eye area; RFI, Residual Feed Intake; RFT, Rump Fat Thickness; SC365, Adjusted Scrotal Circumference at 365 days; STAY, stayability; W210, Adjusted weights at 210 days of age; W450, p Adjusted weights at 450 days of age. **TABLE 2** Posterior mean and high probability density (HPD) interval for direct heritability with respective standard deviations ($h^2 \pm SD$) and HPD for maternal heritability and standard deviations ($h^2m \pm SD$) for calving ease, reproductive, growth, carcass, and feed efficiency indicators traits. primiparous cows. The authors reported that 0.5% of the additive genetic variance for CE varied between maternal and direct effects, suggesting that different sets of genes are responsible for this trait's direct and maternal effects.

Moderate heritability estimates for HH (0.32), FRAME (0.35), W450 (0.39) and ACW (0.34) were obtained, indicating the feasibility of selection for these traits. Similar estimates were reported for Nellore cattle by Negreiros et al. (2022), whose values were FRAME (0.30), ACW (0.27) and W450 (0.26). Schmidt et al. (2019) obtained moderate heritability for the yearling weight (0.44) and height (0.34) in the Nellore breed. Boligon et al. (2011) reported higher heritability estimates for hip height at weaning (0.51) and hip height at post-weaning (0.54) in the Nellore breed.

The direct (0.24) and maternal (0.04) heritability estimates for BW were moderate and low, respectively, and similar to previous studies in the Nellore breed. Kamei et al. (2017) and Silveira et al. (2019) worked with Nellore cattle and reported estimates for BW direct (0.17) and (0,29), whereas maternal heritability was 0.11 and 0.07, respectively. Studies involving taurine beef cattle breeds displayed higher heritability estimates for BW. Saad et al. (2020) worked with the Simmental breed reported a high direct heritability (0.52) for BW. Herrera-Ojeda et al. (2019) worked with the Charolais breed and obtained high direct (0.51) and moderate maternal (0.32) heritability estimates for BW.

For W210, low direct (0.18) and maternal (0.11) heritability estimates were obtained. The heritability estimates for W210 obtained were within the range presented in the literature for the Nellore breed. For direct effect, the estimates ranged from 0.17 to 0.32, and for maternal effect ranged from 0.09 to 0.29 (Kamei et al., 2017; Lopes et al., 2017; Pedrosa et al., 2014).

High-magnitude heritability estimates were obtained for reproductive traits such as SC365 (0.47) and GL (0.46). The heritability estimate for SC365 was within the range (0.33 to 0.48) reported for the Nellore breed (Carvalho et al., 2020; Kluska et al., 2018; Negreiros et al., 2022). For GL, the heritability estimates reported in Nellore cattle were lower than those obtained in the present study, whose values range from 0.18 to 0.23 (Brunes et al., 2020; Schmidt et al., 2019). The heritability

TABLE 3 Posterior mean and high probability density (HPD) interval for direct genetic correlations with the respective standard deviations ($rg \pm SD$) and HPD for maternal genetic correlations and the respective standard deviations ($rm \pm SD$) between calving ease with growth, reproduction, carcass and feed efficiency related traits.

		HPD			HPD m		
Trait	rg±SD	Upper	Lower	rm±SD	Upper	Lower	
ACP	-0.04 ± 0.26	-0.55	0.44				
AFC	0.36 ± 0.25	0.71	0.05				
GL	-0.16 ± 0.14	0.08	-0.39	-0.24 ± 0.15	-0.05	0.51	
SC365	0.11 ± -0.11	-0.27	0.49				
STAY	-0.26 ± 0.23	0.14	-0.74				
PP30	-0.49 ± 0.24	-0.01	-0.9				
REA	-0.08 ± 0.16	-0.38	0.24				
BFT	0.12 ± 0.12	-0.12	0.36				
RFT	0.22 ± 0.13	-0.02	0.49				
BW	-0.66 ± 0.13	-0.9	-0.4	-0.20 ± 0.21	-0.65	0.16	
W210	-0.31 ± 0.13	-0.59	-0.08	-0.03 ± 0.11	-0.25	0.18	
ACW	-0.27 ± 0.27	-0.72	0.18				
W450	-0.25 ± 0.15	-0.53	0.03				
FRAME	-0.20 ± 0.17	-0.55	-0.55				
HH	0.11 ± 0.26	-0.42	0.55				
DMI	-0.3 ± 0.21	-0.69	0.14				
RFI	0.14 ± 0.25	-0.36	0.62				
IMF	-0.04 ± 0.18	-0.38	0.32				

Abbreviations: ACP, Accumulated Cow Productivity; ACW, Adult Cow Weight; AFC, Age at First Calving; BFT, Subcutaneous Backfat Thickness; BW, birth weight; DMI, Dry Matter Intake.; FRAME, frame score; GL, Gestation Length; HH, Hip Height; IMF, Intramuscular Fat Percentage; PP30, probability of precocious calving; REA, rib eye area; RFI, Residual Feed Intake; RFT, Rump Fat Thickness; SC365, Adjusted Scrotal Circumference at 365 days of age; STAY, stayability; W210, Adjusted weights at 210 days of age; W450, Adjusted weights at 450 days of age.

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estimates for PP30, STAY, ACP and AFC were low, 0.16, 0.13, 0.12 and 0.08, respectively. These results reflect the high environmental influence on these traits. Low heritability estimates were also reported for these traits in previous studies in Nellore cattle (Bonamy et al., 2019; da Silva Neto et al., 2020; Kluska et al., 2018; Schmidt et al., 2018).

The heritability estimates for the carcass traits were moderate for REA (0.37), BFT (0.22), and RFT (0.36). Similar REA, BFT and RFT results were reported in Nellore by Bonamy et al. (2019) and Kluska et al. (2018), with estimates ranging from 0.17 to 0.34. For IMF, the heritability estimate was low (0.17) and it was within the range of heritability estimate of previous studies with Nellore (Feitosa et al., 2016; Magalhães et al., 2016).

The genetic correlation estimates between CE and reproductive, growth, carcass and feed efficiency traits are presented in Table 3. The estimated genetic correlation between CE and female sexual precocity indicator traits was moderate, PP30 (-0.49) and AFC (+0.36), suggesting that selection for early sexual precocity and anticipation of parturition in heifers would increase the incidence of calving problems in primiparous cows. Lower age at first calving in heifers was also related to calving difficulty in subsequent calving's, both in beef and dairy cattle (López-Paredes et al., 2018; Nix et al., 1998). The genetic relationship between these traits was also confirmed in genomic association studies in Nellore heifers. In this sense, Mota et al. (2020) performed a genome-wide association study in Nellore cattle and reported that the SNPs statistically associated with AFC also harboured QTLs related to calving ease, pointing out that there are biological relationships between calving ease and sexual precocity. These results pointed out that selection for early sexual heifer precocity would be genetically associated with the occurrence of calving problems, which has negative consequences for fertility, reinforcing the importance of selection for ease of parturition as an auxiliary selection criterion, mainly in herds that have been selected for early sexual precocity.

The estimated genetic correlation between CE and SC365 was low and close to zero (0.11), indicating that selection for scrotal circumference at 12 months would not interfere with CE. The genetic correlation estimate between CE and STAY (-0.26) was also low. The genetic correlation HPD interval included zero, indicating that the occurrence of calving problems would not have an unfavourable effect on cows' longevity. Even so, studies in beef and dairy cattle reported that calving difficulties in heifers with calving interventions negatively impacted longevity, which triggered a higher probability of slaughter and lower herd longevity (Rogers et al., 2004; Sewalem et al., 2008). The genetic correlation between CE and ACP was low and close to zero (-0.04), and the genetic

correlation HPD interval includes zero. Thus, the occurrence of calving problems would not affect productivity.

The genetic correlation between CE and GL (-0.16) indicates a low-genetic association between both traits and the genetic correlation HPD interval includes zero. Burfening et al. (1978), Kemp et al. (1988) and Jamrozik and Miller (2014) reported low-genetic correlation estimates between GL and CE (-0.06, 0.12, and -0.21), respectively. Mujibi and Crews (2009), reported moderate genetic correlation estimates between CE, GL (-0.38), and BW (0.43), pointed out that longer pregnancies are associated with higher birth weight. However, in the present study, the genetic association estimates between CE and GL were weak, so there is no suggestion that GL genetically interferes with CE.

Moderate and negative genetic correlation estimates were obtained between CE with the direct effect of BW (-0.66) and low with the maternal effect of BW (-0.20). The moderate direct genetic correlation obtained between CE and BW shows that selection for lower birth weight would reduce the incidence of dystocia. However, selection for low BW would impair calf health and survival, weight gain and weight at later ages. The genetic correlation obtained between BW and CE was within the estimates reported by other authors. McGuirk et al. (1999) for the Holstein breed reported a higher genetic correlation estimate between birth weight and the occurrence of dystocia (0.81).

Bennett and Gregory (2001) obtained high (0.81) and moderate (0.34) genetic correlations between calving difficulty scores and BW with direct and maternal effects, respectively. Eriksson et al. (2004a) obtained moderate genetic correlations between birth weight and direct calving difficulty of 0.62 and 0.71 and maternal correlations of 0.46 and -0.28 for Charolais and Hereford breeds, respectively. Mujibi and Crews (2009) in Charolais cattle, reported a high-genetic correlation between BW and CE for direct (-0.93) and maternal effects (-0.69). For Simmental cattle, moderate to high estimates of direct genetic correlation between BW and CE were reported, varying from 0.67 to -0.85 (Jamrozik & Miller, 2014; Saad et al., 2020).

Based on the findings reported in the literature and the results obtained herein, the BW should be adopted as an indicator trait of dystocia. Despite the moderate genetic correlation with CE (-0.66), the estimate is not high enough to be able to state that the BW trait can replace or be an indicator trait of CE in Nellore cattle, and the selection for low BW would have a more substantial negative impact on subsequent weights after weaning. In addition, the birth weight record is more challenging to get or access in extensive conditions since it requires a scale, while CE is an observational measure. Thus, it is possible to infer that CE is a crucial component to be considered to reduce calving problems in primiparous cows of Nellore cattle.

The direct genetic correlation obtained between CE and W210 was moderate to low (-0.31), whereas for maternal effects, the genetic correlation was close to zero (0.03). Bennett and Gregory (2001) reported higher direct genetic correlation estimates for composite cattle breeds between calving difficulty scores with weaning weight and post-weaning gain at 168 days (0.41 and 0.36, respectively). Phocas and Laloë (2004) estimated genetic parameters between calving difficulty and weaning weight for specialized beef breeds (Charolais, Limousin, Blonde D'Aquitaine and Maine Anjou) and obtained estimates of genetic correlations of moderate magnitude for direct effects (0.30-0.40) and for maternal effects (0.30). The results of the present study and previous studies suggest a moderate genetic association between higher weight at weaning and the occurrence of calving difficulties. The maternal genetic correlation between CE and W210 was of low magnitude, close to zero, indicating a low influence of the maternal component of weaning weight on CE. Bennett et al. (2021) analysed animals selected for calving ease and reported that calves from the chosen line were nursed longer and gained 10% more weight than calves from the control line.

For after-weaning growth traits, the genetic correlation estimates were low and close to zero, and the genetic correlation HPD interval includes zero. The estimated genetic correlation between CE with W450 (-0.25) and ACW (-0.27) was low, and the genetic correlation HPD interval includes zero, indicating that selection for postweaning weight performance would not influence CE. Low-to-moderate genetic correlation estimates between calving difficulty and yearling weight were also presented by Roughsedge et al. (2005) for Aberdeen Angus (-0.20), South Devon (0.46), Limousine (0.33) and Simmental (0.19) cattle breeds.

The genetic correlation estimates between CE with FRAME (-0.20) and HH (0.11) were low and near zero, and the genetic correlation HPD interval includes zero, pointing out that selection to improve CE would not have an unfavourable impact on the frame and animal height. Similarly, the findings for growth traits suggested that selection for CE would not interfere with growth performance. To reduce calving problems in primiparous Nellore cows, the selection for CE instead of BW might be advantageous because selection for BW could potentially delay the animal's growth, given the solid and favourable genetic correlation between BW with weaning and year-ling weight (Silveira et al., 2019).

For carcass traits, genetic correlation estimates between CE and REA (-0.08), BFT (0.12), RFT (0.22) and IMF (-0.04) were low. The genetic correlation HPD interval includes the zero, suggesting that selection for ease of calving would not affect the yield of meat cuts, Animal Breeding and Genetics

intramuscular fat deposition or subcutaneous and rump fat thickness. Our results agree with Hosono et al. (2020), who reported a weak genetic association between ease of calving and traits related to carcass fatness and REA. These authors estimated genetic parameters in Japanese beef cattle for CE and obtained low-genetic correlation estimates between CE with BFT and IMF (0.09-0.28). The authors also reported close to zero estimates between CE and REA (0.06-0.08). Bennett et al. (2021) worked with a composite beef cattle breed selected for CE and studied the influence of selection for CE on carcass traits and reported that animals from the strain selected for CE were heavier and displayed 11% more fat thickness. Eriksson et al. (2004b) worked with Hereford and Charolais cattle. The authors stated that carcass traits and traits related to calving performance should be included as selection criteria in beef cattle since these traits showed unfavourable correlations.

The genetic correlation estimate obtained between CE with DMI (-0.30) and RFI (0.14) was low. The genetic correlation HPD interval included zero, indicating that selection for calving ease would not interfere with feed conversion and dry matter intake. Feed intake is genetically and phenotypically correlated with body weight (Brunes et al., 2021). Thus, generally, smaller animals tend to eat less. The relationship between feed efficiency and the performance of Irish beef cows was reported by Crowley et al. (2011), who obtained low and close to zero genetic correlation estimates between calving efficiency, feed conversion rate and residual feed intake, with calving difficulty, being -0.02 and -0.1, respectively.

Selection for CE in early sexually precocious primiparous cows is an important criterion to be considered in indicine beef cattle breeding programs, given the impact of both direct and maternal genetic effects on this trait. To reduce calving problems, direct selection for CE is more adequate than selecting for low BW since BW is not a replacement trait. However, with such a solid direct genetic correlation between BW and CE (-0.66), an alternative to select favourable CE values corrected for high BW calves is considering a multi-trait selection model including BW and CE with direct and maternal effects. Furthermore, combining CE selection with reproductive and growth traits would improve the selection for sexual precocity, resulting in higher reproductive success with minimal performance losses, lower incidence of calving problems and higher growth rates at older ages.

4 | CONCLUSION

The direct and maternal heritability estimates for CE in sexual precocious primiparous Nellore cows indicated

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that selecting for this trait is feasible. The selection to improve the female sexual precocity should account for CE during the selection and mating decisions to reduce calving problems. The genetic correlation estimates between CE and BW pointed out that solely selecting for low birth weight to reduce calving problems is not the appropriate strategy to increase the calving easy in sexual precocious primiparous Nellore cows, given the moderate genetic correlation between CE and BW. Therefore, adopting a multi-trait selection model with CE and BW as a selection criterion would reduce calving difficulties, particularly in sexually precocious primiparous cows, without impairing the Nellore cattle's growth, reproductive, feed efficiency conversion and carcass indicator traits.

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CONFLICT OF INTEREST STATEMENT

The authors declare that they do not have any conflict of interest.

DATA AVAILABILITY STATEMENT

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 and due to belonging to the National Association of Breeders and Researchers (ANCP).

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