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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

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Abstract

The aim of this study was to estimate genetic parameters for different precocious calving criteria and their relationship with reproductive, growth, carcass and feed efficiency in Nellore cattle using the single-step genomic BLUP. The reproductive traits used were probability of precocious calving (PPC) at 24 (PPC24), 26 (PPC26), 28 (PPC28) and 30 (PPC30) months of age, stayability (STAY) and scrotal circumference at 455 days of age (SC455). Growth traits such as weights at 240 (W240) and 455 (W455) days of age and adult weight (AW) were used. Rib eye area (REA), subcutaneous fat thickness (SFT), rump fat thickness (RFT) and residual feed intake (RFI) were included in the analyses. The estimation of genetic parameters was performed using a bi-trait threshold model including genomic information in a single-step approach. Heritability for PPC traits was moderate to high (0.29–0.56) with highest estimates for PPC24 (0.56) and PPC26 (0.50). Genetic correlation estimates between PPC and STAY weakened as a function of calving age. Correlation with SC455, growth and carcass traits were low (0.25–0.31; −0.22 to 0.04; −0.09 to 0.18, respectively), the same occurs with RFI (−0.09 to 0.08), this suggests independence between female sexual precocity and feed efficiency traits. The results of this study encourage the use of PPC traits in Nellore cattle because the selection for such trait would not have a negative impact on reproductive, growth, carcass and feed efficiency indicator traits. Stayability for sexual precocious heifers (PPC24 and PPC26) must be redefined to avoid incorrectly phenotype assignment.

KEYWORDS
genetic correlations, genomic, Nellore, precocity, ssGBLUP

1 | INTRODUCTION

Female sexual precocity and reproductive indicator traits have a great impact on the productivity of cow–calf systems. In this regard, *Bos taurus indicus* cattle are likely to be less sexually precocious than *Bos taurus taurus* cattle constituting a bottleneck for profitability of zebu beef cattle systems restricting the genetic improvement (Day & Nogueira, 2013). Heifer pregnancy is an economically relevant trait measured directly on females for improving fertility and sexual precocity, and it

has been widely studied both in taurine (Morris et al., 2000) and indicine cattle (Van Melis, Eler, et al., 2010). The heifer pregnancy is easy to asses for all heifers, not requiring the use of penalties for heifers that did not calve and it showed moderate-to-high genetic additive variability which justifies their application as a selection criterion in beef cattle breeding programmes.

The use of precocious heifers aims to reduce the age at first calving (AFC) and increases the cattle herd profitability due to the ability to calve an extra calf per cow. This reduction also allows increasing the system's revenue by reducing the area for the heifer's growth, accelerating the capital turnover, decreasing the cow's rearing costs and the generation interval in breeding programmes (Morris et al., 2000). In addition, cows that calve earlier during the birth season are likely to wean heavier calves and have a longer post-partum recovery time, increasing the probability of early pregnancies in subsequent breeding seasons (Terakado, Pereira, Yokoo, & Albuquerque, 2015).

Heifer pregnancy is a binary trait which has been widely used to evaluate sexual precocity in Brazilian beef cattle breeding programmes, and such trait has already been used in sire evaluation catalogues for Nellore cattle. In this context, beef cattle breeding programmes use the probability of precocious calving at 30 months (PPC30) as a female sexual precocity indicator trait. It is noteworthy to highlight that in the last years, the proportion of precocious calving (<30 months) has increased because of better nutritional management of females and direct selection for this trait. Nowadays, many cattle breeders bring forward heifer's first breeding season; thus, there is a need to evaluate the redefinition of PPC30 and assess the genetic correlated impact of this change on other productive traits. There are few studies in beef cattle exploring the genetic associations of precocious heifer pregnancy with body weight (BW), carcass traits, stayability and feed efficiency traits (Boligon, De Albuquerque, Mercadante, & Lôbo, 2010; Grossi et al., 2009; Shiotsuki, Silva, Tonhati, & Albuquerque, 2009). Hence, the aim of this study was to estimate genetic parameters for different precocious calving criteria, which were probability of precocious calving at 24, 26, 28 and 30 months of age, and examine their genetic correlations with reproductive, growth, carcass and feed efficiency indicator traits in a Nellore cattle population using the single-step genomic BLUP method (ssGBLUP).

2 | MATERIAL AND METHODS

2.1 | Animals and data

The data set used in this study comprises animals from the National Association of Breeders and Researchers (ANCP, Ribeirão Preto, Brazil), a Brazilian Nellore breeding programme. The data set encompasses records from 66,496 females and their relatives, totalling 176,069 phenotypic records for growth, carcass, reproductive and feed efficiency indicator traits. These females were exposed to reproduction since 10–14 months of age in an average 3 months of breeding season, if their no achieve a pregnancy are re-exposed at around 24 months of age. The pedigree contained information from 244,254 animals, born between 1977 and 2016.

A total of 8,652 animals were genotyped with the low-density panel (CLARIFIDE® Nellore 2.0) containing over 22,000 markers. Imputation was implemented using the FIMPUTE 2.2 software (Sargolzaei, Chesnais, & Schenkel, 2014), and all genotypes were imputed to a panel containing 735,044 markers. For imputation, a reference population with 963 founder animals genotyped with the Illumina BovineHD BeadChip (Illumina Inc., San Diego, CA, USA) was used. Prior imputation, markers for the genotyped and the reference populations were edited for call rate (<90%), minor allele frequency (<0.05%), mendelian conflicts (>1.0%) and SNPs with unknown position (<300 in CLARIFIDE® Nellore 2.0). Markers located on non-autosomal chromosomes were excluded. After editing, a total of 8,545 animals and 460,860 markers were retained for the analyses. The imputation accuracy was higher than 98%.

2.2 | Traits

The traits used in the analysis comprehend reproductive, growth, carcass and feed efficiency indicator traits. Reproductive traits such as probability of precocious calving (PPC) at 24 (PPC24), 26 (PPC26), 28 (PPC28) and 30 (PPC30) months of age, stayability (STAY), and scrotal circumference corrected at 455 days of age (SC455) were used. All heifers under PPC evaluations were exposed to reproduction in their weaning year to determine sexual precocity. Additionally, heifers which calved up to 24, 26, 28 or 30 months of age had their phenotypes characterized as success (2) or failure (1) otherwise. For STAY, dams with at least three calvings up to 76 months of age had their phenotypes categorized as success (2) or failure (1) otherwise.

Growth traits such as adjusted weight at 240 (W240) and 455 (W455) days of age, and adult cow weight (AW) were used. The AW was defined as the dam weight from weaning to 4 years of age. Carcass and feed efficiency indicator traits such as rib eye area (REA), subcutaneous fat thickness (SFT), rump fat thickness (RFT) and residual feed intake (RFI) were included. Carcass traits (REA, SFT and RFT) were measured using a 3.5 MHz linear-array transducer connected to a B-mode scanner (ALOKA SSD 500; Tokyo, Japan). SFT and RFT were measured in millimetres (mm) and REA in square centimetres (cm^2). The RFI was obtained by feed efficiency tests performed from 2011 to 2017. The animals were held in collective pens

equipped with GrowSafe® feeding system. In the growing phase, animals were kept in test during 70 days, preceded by a period of 21 days for adaptation, evaluation of the feed intake and average daily gain (ADG). Animals were weighted every 14 days. The diet was formulated with 67% of total digestible nutrients (TDN) and 13% of crude protein (CP), allowing an ADG of 1.0 kg/day.

To ensure ad libitum feed intake, food supply was adjusted daily, allowing refusals varying from 5% to 10% of offered. The following feed intake records were not considered in the analyses: Days when animals were handled outside of facilities for many hours, equipment failure (GrowSafe®) and when no refusals were found. Diet dry matter percentage was determined from weekly samples of offered and refusals. The ADG in each test was considered as the linear regression coefficient of BW on days in test (DIT):

$$y_i = \alpha + \beta * \mathrm{Dot}_i + \varepsilon_i$$

where, y_i = BW in i-th observation; α = intercept of regression equation corresponding to the initial BW; β = linear regression coefficient corresponding to ADG; Dot_i = days in test for i-th observation; and ε_i = random error associated with each observation. Metabolic weight (BW$^{0.75}$) was calculated as: BW$^{0.75}$ = $[\alpha + \beta \times (\mathrm{Dot}_i/2)]^{0.75}$, with α and β assuming the values obtained by the equation described above.

The RFI was considered as the error of linear regression equation of dry matter intake (DMI) on ADG and metabolic weight within each contemporary group (CG: sex, year of birth, and pen), as shown below:

$$\mathrm{DMI} = \beta T * \mathrm{TG} + \beta TA * \mathrm{TG} * \mathrm{ADG} + \beta TB * \mathrm{TG} * \mathrm{BW}^{0.75} + \varepsilon$$

where, βT, βTA and βTB are regression coefficients of classificatory variable test group (TG) and of interactions between TG and covariates ADG and BW$^{0.75}$, respectively; and ε is RFI.

For reproductive, growth and carcass traits, contemporary groups (CGs) were composed of herd, year and season of birth, sex, and management group. For RFI, CGs were composed of herd, year and season of birth, sex and management at the test. In all traits, CGs with less than three records were excluded, as those with records exceeding three standard deviations above or below the mean in continuous traits.

2.3 | Model

The covariance components and genetic parameters for SC455, W240, W455, AW, REA, SFT, RFT and RFI were estimated considering a linear animal model. A threshold animal model was used for STAY, PPC24, PPC26, PPC28 and PPC30. For all traits, a single-step genomic BLUP (ssGB-LUP) procedure was used (Aguilar et al., 2010). The general animal model used was as follows:

$$y = X\beta + Zu + Mm + Wc + e$$

where y is a vector of dependent variables; β is a vector of fixed effects, including the CG and age at calving class (varying from 1 to 10) for W240; X is the incidence matrix associating β with y; u is a vector of random effects of direct additive genetic effects; Z is the incidence matrix associating u with y; m is a vector of random effects of maternal additive genetic effects; M is the incidence matrix associating m with y, only for W240; c is a vector of random effects of maternal permanent environment effects for traits with maternal effects (W240); W is the incidence matrix associating c with y; and e is the residual effects. Genetic, maternal, permanent environment and residual effects were assumed to be normally distributed with mean equal to zero and variances $H\sigma_a^2$, $H\sigma_m^2$, $I\sigma_c^2$ and $I\sigma_e^2$, respectively. The covariance between direct and maternal genetic effects was set to zero.

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

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

where U is the vector of the base scale with order r (with r: number of animals); $\theta' = (\beta', u', m', c')$ is the parameters vector with order s (with s: number of class); β is a vector of fixed effects with order s; u, m and c are the additive genetic, maternal and CG random effects, respectively; W is the incidence matrix with order $r \times s$; I is the identity matrix with order $r \times r$; and σ_e^2 is the residual variance. The relationship matrix was computed using the ssGBLUP approach (Aguilar et al., 2010), as follows:

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

where H is the relationship coefficients matrix between the animal; G is the genomic relationship matrix; A is the additive relationship matrix; and A_{22} is a subset of the additive relationship matrix for the genotyped animals.

For the two-trait analysis under a threshold-linear model, it was assumed that the *prior* distributions of genetic and residual effects followed a normal multivariate distribution, as follows:

$$P\left(\begin{bmatrix} a_1 \\ a_2 \end{bmatrix}\middle| G\right) \sim N\left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, G = G_0 \otimes H\right);$$

$$P\left(\begin{bmatrix} e_1 \\ e_2 \end{bmatrix}\middle| R\right) \sim N\left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, R = R_0 \otimes I\right)$$

where G_0 are the genetic variances and covariances matrixes; R_0 is the residual variance matrix; $\otimes$ is the direct product operator; H is the relationship matrix and I is the identity matrix.

2.4 | Estimation of genetic parameters

The analyses were performed using the THRGIBBS1F90 software (Tsuruta & Misztal, 2006), and Gibbs chains of 500,000 iterations were generated with an initial burn-in of 50,000 and a sampling interval of 100. For RFI estimations, Gibbs chains of 800,000 iterations and initial burn-in of 400,000 were used. The convergence was tested using the Bayesian Output Analysis (BOA) (Smith, 2008) implemented in R (2010) programme. The convergence for all parameter estimates was verified by inspecting trace plots and using Geweke's (Geweke, 1992). Thus, the burn-in period considered was enough to reach convergence in all parameter estimates. Heritabilities and genetic correlation estimates were computed as the mean for each Gibbs sample. Posterior distributions are provided as Supporting information.

3 | RESULTS AND DISCUSSION

A low proportion (7.15%) of females calving before 24 months was observed, but it should be noted that the proportion of precocious heifers increased as a function of age (Table 1). This can be probably due to the effect of age on sexual maturation, and then with pregnancy (Day & Nogueira, 2013). Pregnancy rates in Nellore heifers reared under grazing conditions with bull exposure at 14–16 months of age ranged between 14.2% and 18.2% (Eler et al., 2002).

The mean values for W240 (188.87 kg), W455 (280.25 kg) and AW (466.62 kg) were higher than those reported by Grossi et al. (2009) (262 kg for W455), and closer to that reported by Klusca et al. () (195 and 293 kg for W240 and W455, respectively) study in Nellore cattle. The mean for SC455 was higher than those reported by Buzanskas et al. (2017). The same was observed for RFT and SFT, but not for REA (Buzanskas et al., 2017). Based on the results, differences in mean between the studies could be associated with sampling population, because heifers exposed earlier to bulls and related animals were used in the present study.

The heritabilities estimates for PPC traits were from moderate-to-high magnitude, with values ranging from 0.29 to 0.56 (Table 2). The highest estimates were obtained for PPC24 (0.56) and PPC26 (0.50) traits. These results are in agreement with those reported by Eler et al. (2002) for probability of pregnancy in heifers bull-exposed at 14 months of age. The results obtained here suggest that a response to selection is expected for heifer sexual precocity at PPC24 or PPC26. It is worth to highlight that an additional care is necessary when rebreeding primiparous precocious heifers (PPC24 and PP26) under extensive range conditions. Subsequent rebreeding of primiparous heifers is influenced by non-genetic effects, that is, climate and nutrition, which highly affect the beef cattle reproductive performance. Additionally, the large physiological demands imposed by lactation and growth on young

TABLE 1 Number (n) and percentage (%) of animals within each category for different criteria for sexual precocious heifers, and descriptive statistic for reproductive, growth, carcass and feed efficiency indicator traits in Nellore cattle

Trait	Animals (n)	CG (n)	Categories (n, %)	
			1 (Failure)	2 (Success)
PPC24	66,496	1,497	61,744 (92.85)	4,752 (7.15)
PPC26	66,496	1,497	57,447 (86.39)	9,049 (13.61)
PPC28	66,496	1,497	54,967 (82.66)	11,529 (17.34)
PPC30	66,496	1,497	52,664 (79.20)	13,832 (20.8)
STAY	57,289	605	31,084 (54.26)	26,205 (45.74)
			Mean ± SD	
W240	122,067	1,123	188.87 ± 27.76	
W455	90,230	3,317	280.25 ± 48.33	
AW	102,984	3,181	466.62 ± 75.34	
SC455	13,133	391	25.03 ± 3.26	
REA	32,865	1,321	52.60 ± 10.40	
SCF	32,357	1,311	3.08 ± 1.75	
RFT	32,623	1,310	4.61 ± 2.44	
RFI	2,112	88	−0.004 ± 0.71	

AW: adult weight (kg); CG: contemporary group; PPC24: probability of precocious calving at 24 months of age; PPC26: probability of precocious calving at 26 months of age; PPC28: probability of precocious calving at 28 months of age; PPC30: probability of precocious calving at 30 months of age; REA: rib eye area (cm^2); RFI: residual feed intake; RFT: rump fat thickness (cm); SC455: scrotal circumference at 455 days of age (cm); SFT: subcutaneous fat thickness (cm); STAY: stayability; W240: weight at 240 days of age (kg); W455: weight at 455 days of age (kg).

primiparous females are associated with low subsequent re-breeding rates on heifers.

The heritability estimated for STAY was low (0.16 ± 0.01; Table 2), indicating that this trait is highly influenced by environmental components. STAY is a sex-limited and late measured trait with low heritability estimate, and all these factors together limit the genetic improvement of the trait. These results were in accordance with previous reports in Nellore cattle (Van Melis, Oliveira, et al., 2010), whose findings described estimates ranging from 0.11 to 0.17. Van Melis et al. (2007) reported higher heritability estimates for Nellore cattle, with values varying from 0.22 to 0.28. Despite the low heritability, STAY is an economically relevant trait and its inclusion in breeding programmes could allow the selection of sires whose daughters have a greater probability of remaining productive in the herd for a long period of time. In this sense, the use of this trait as a selection criterion is likely to reduce costs since longer-lived cows tend to be more profitable as the replacement rate may be reduced (Van Melis et al., 2007); on the other hand, it increases the generational interval and then, delays the genetic improvement.

For SC455, heritability estimated was close to values reported in the literature for Nellore cattle (Boligon, Rorato, & De Albuquerque, 2007; Van Melis, Eler, et al., 2010), with

TABLE 2 Posterior mean and high probability density interval (HPD) of heritability (h^2) for different criteria of precocious heifers, reproductive, growth, carcass and feed efficiency indicator traits in Nellore cattle

| Trait | Mean $h^2 \pm SD$ | HPD[a] | |
		Upper	Lower
PPC24	0.56 ± 0.02	0.53	0.61
PPC26	0.50 ± 0.02	0.46	0.54
PPC28	0.46 ± 0.02	0.43	0.5
PPC30	0.29 ± 0.02	0.26	0.33
STAY	0.16 ± 0.01	0.13	0.18
SC455	0.48 ± 0.03	0.43	0.59
W240	0.23 ± 0.01	0.21	0.25
W455	0.37 ± 0.01	0.35	0.39
AW	0.32 ± 0.02	0.29	0.36
REA	0.32 ± 0.01	0.29	0.35
SFT	0.21 ± 0.01	0.19	0.24
RFT	0.34 ± 0.01	0.31	0.36
RFI	0.36 ± 0.08	0.22	0.52

[a]Credibility intervals at 95%; AW: adult weight (kg); PPC24: precocious calving at 24 months of age; PPC26: probability of precocious calving at 26 months of age; PPC28: probability of precocious calving at 28 months of age; PPC30: probability of precocious calving at 30 months of age; REA: rib eye area (cm²); RFI: residual feed intake; RFT: rump fat thickness (cm); SC455: scrotal circumference at 455 days of age (cm); SFT: subcutaneous fat thickness (cm); STAY: stayability; W240: weight at 240 days of age; W455: weight at 455 days of age.

values ranging from 0.40 to 0.65. Heritabilities for weight traits (W240, W455, and AW) were similar to those reported for Nellore cattle [Boligon et al., 2010 (W240: 0.28 ± 0.02, W455: 0.30 ± 0.03, AW:0.36 ± 0.04); Eler, Van Vleck, Ferraz, & Lobo, 1995 (W240: 0.23 ± 0.03)]. For carcass traits, heritability obtained for REA was close to those reported by Buzanskas et al. (2017) (0.29 ± 0.03–0.31 ± 0.03). Higher heritability estimates for SFT and RFT were reported by Yokoo et al. (2010), with values of 0.50 ± 0.09 and 0.39 ± 0.09 for SFT and RFT, respectively.

Heritability estimated for RFI was close to those reported by Arthur et al. (2001) study in Angus cattle (0.39), and Grion et al. (2014) in Nellore cattle (0.33). In beef cattle systems, feed efficiency has a major influence on the unit cost of production, and it is one of the main reasons for the inefficiency of the productive chain since it stands for the most important expense. In this regard, the heritability estimates obtained in this research suggest that selection for more efficient animals would increase the feed efficiency of the herd according to Arthur et al. (2001).

Genetic and phenotypic correlations between PPC and reproductive, growth, carcass and feed efficiency indicator traits are described in Table 3. Overall, weak phenotypic correlations were estimated between PPC traits with reproductive, growth, carcass and feed efficiency indicator traits, indicating that these traits are poor phenotypic indicators of early heifer pregnancy. The genetic correlation estimates between PPC and STAY varied from low-to-moderate magnitude and decreased as a function of precocious calving age. In this respect, the selection for precocious heifers (PPC24, PPC26 and PPC28) would not have a significant effect on STAY. Meanwhile, the genetic correlation estimate between PPC30 with STAY was moderate, indicating that selection for higher PPC30 would increase the proportion of dams that remain longer in the herd. Moreover, higher genetic gains per year are expected applying indirect selection for STAY through direct selection in PPC30. Similar findings were reported by Kluska et al. (2018) working with the same traits in Nellore cattle. This result is expected because STAY displayed lower heritability estimates than PPC30 and also is necessary almost threefold more time to measure the STAY. It is important to highlight that both traits are sex-limited; thereby, a progeny test is necessary for young sire genetic evaluation for both traits. Roy (1976) had shown that a reduce in calving age from 36 to 24 months of age decreased the replacement rate by 33% and increased the herd profitability by 20% in dairy systems.

When STAY is performed using the traditional definition, which is taken at 76 months of age with at least three calving per cow, it turns out not to be an appropriate approach for PPC24 and PPC26. In precocious production systems, heifers calving for the first time at 24 months of age should calve up to five calves when attaining 76 months of age, otherwise it exists the possibility of failure two times in their productive

TABLE 3 Mean and high probability density (HPD[a]) for genetic and phenotypic correlation for different criteria of sexual precocious heifers, reproductive, growth, carcass and feed efficiency indicator traits in Nellore cattle

	PPC24	PPC26	PPC28	PPC30
STAY				
Genetic	0.09 (−0.01; 0.22)	0.20 (0.09; 0.31)	0.23 (0.13; 0.34)	0.42 (0.29; 0.54)
Phenotypic	0.14 (0.09; 0.19)	0.17 (0.14; 0.20)	0.18 (0.15; 0.20)	0.18 (0.16; 0.20)
SC455				
Genetic	0.30 (0.14; 0.44)	0.25 (0.11; 0.38)	0.31 (0.18; 0.43)	0.31 (0.20; 0.42)
Phenotypic	0.10 (0.04; 0.14)	0.09 (0.04; 0.14)	0.11 (0.07; 0.16)	0.12 (0.07; 0.16)
W240				
Genetic	−0.22 (−0.31; −0.14)	−0.22 (−0.30; −0.15)	−0.18 (−0.26; −0.11)	−0.07 (−0.17; 0.02)
Phenotypic	−0.09 (−0.13; −0.06)	−0.09 (−0.12; −0.06)	−0.07 (−0.10; −0.04)	−0.02 (0.05; 0.01)
W455				
Genetic	−0.08 (−0.15; −0.01)	−0.06 (−0.13; 0.01)	−0.07 (−0.13; −0.01)	0.04 (−0.04; 0.12)
Phenotypic	0.13 (0.11; 0.16)	0.15 (0.13; 0.17)	0.15 (0.13; 0.17)	0.17 (0.15; 0.19)
AW				
Genetic	−0.08 (−0.22; 0.07)	−0.11 (−0.23; 0.01)	−0.10 (−0.21; 0.01)	−0.08 (−0.19; 0.03)
Phenotypic	−0.02 (−0.07; 0.02)	−0.03 (−0.07; 0.01)	−0.02 (−0.06; 0.01)	−0.03 (−0.07; 0.01)
REA				
Genetic	−0.05 (−0.14; 0.04)	0.02 (−0.07; 0.11)	0.02 (−0.08; 0.11)	0.09 (−0.02; 0.20)
Phenotypic	0.03 (−0.01; 0.06)	0.05 (0.02; 0.08)	0.06 (0.03; 0.10)	0.10 (0.06; 0.12)
SFT				
Genetic	0.13 (0.04; 0.22)	0.18 (0.08; 0.26)	0.14 (0.04; 0.23)	0.17 (0.06; 0.27)
Phenotypic	0.10 (0.08; 0.13)	0.16 (0.13; 0.18)	0.16 (0.13; 0.19)	0.15 (0.13; 0.18)
RFT				
Genetic	0.13 (0.04; 0.21)	0.13 (0.04; 0.22)	0.08 (−0.01; 0.17)	0.14 (0.04; 0.24)
Phenotypic	0.13 (0.11; 0.16)	0.19 (0.17; 0.22)	0.19 (0.16; 0.22)	0.20 (0.18; 0.23)
RFI				
Genetic	−0.03 (−0.32; 0.35)	0.08 (−0.19; 0.42)	−0.09 (−0.36; 0.21)	−0.04 (−0.31; 0.24)
Phenotypic	−0.10 (−0.21; 0.01)	0.08 (−0.13; 0.27)	0.09 (−0.14; 0.31)	0.13 (−0.17; 0.35)

[a]Credibility intervals at 95%; AW: adult weight (kg); PPC24: probability of precocious calving at 24 months of age; PPC26: probability of precocious calving at 26 months of age; PPC28: probability of precocious calving at 28 months of age; PPC30: probability of precocious calving at 30 months of age; REA: rib eye area (cm); RFI: residual feed intake; RFT: rump fat thickness (cm); SC455: scrotal circumference at 455 days of age (cm); SFT: subcutaneous fat thickness (cm); STAY: stayability; W240: weight at 240 days of age; W455: weight at 455 days of age.

life, increasing productive cost by feed unproductive cows. In this regard, dissimilarities among the number of calves per cow can arise depending on the approach used to measure STAY. Thus, developing an adequate method to measure and define STAY in precocious heifers is necessary.

Weak genetic correlation estimates between PPC and SC455 were observed. The beneficial effect of scrotal circumference selection and its impact on females' precocity have been widely described both in taurine and indicine breeds (Van Melis, Eler, et al., 2010). This trait is one of the most useful in breeding programmes regarding indirect selection for sexual precocity due to their moderate-to-high heritability estimates, ease of measurement and interpretation, and it also allows to improve the bull's fertility and male and female sexual precocity (Toelle & Robison, 1985).

The genetic correlations between PPC and growth traits (W240, W455, and AW) were weak. Similar results were described by Boligon et al. (2010) for AFC and weaning weight (−0.18) and by Shiotsuki et al. (2009) between yearling weight and heifer pregnancy (0.08). For AW, an increase in weight is undesired for extensive production systems because larger animals have greater requirements for maintenance and reproduction rates. Additionally, these animals will not thrive in environments in which food sources are limited, that is, extensive systems in tropical regions. Thus, the results of the present study show that selection for higher early heifer pregnancy would not affect the mature cow size. Similar findings were reported by Terakado et al. (2015), in which sexually precocious Nellore heifers had similar mature weight to those non-precocious.

Carcass traits were low correlated with PPC (Table 3). Similar results were reported by Buzanskas et al. (2017) between AFC and RFT (-0.08 ± 0.09) and AFC and REA (-0.12 ± 0.08) traits in Nellore cattle populations. Low genetic correlation estimates between heifer pregnancy and muscling or finishing scores were reported by Shiotsuki et al. (2009); nevertheless, negative correlation has been reported between carcass traits and precocity in Brahman (-0.36 ± 0.18, -0.29 ± 0.16 -0.35 ± 0.16 for REA, SFT and RFT, respectively; Johnston et al., 2009).

Nowadays, the animals' efficiency measure as RFI is drawing more attention and reports of such impact in selected population are incipient. It is suggested that RFI allows us to detect differences in maintenance requirements, independently of the animal's BW and weight gain (Arthur, Pryce, & Herd, 2014). Genetic correlations between PPC and RFI were of low magnitude, suggesting independence between female sexual precocity and feed efficiency traits. Controversy about the relationship between heifer sexual precocity and feed efficiency does exist. In this sense, Shaffer, Turk, Wagner, and Felton (2011) reported a negative correlation between RFI and AFC in British females, and Johnston et al. (2009) in Brahman steers and related females. Conversely, Basarab et al. (2011) stated that RFI adjusted for backfat thickness is not correlated with fertility traits, indicating the importance of fat deposition. Our results suggest that improving heifer's precocity would not affect feed efficiency and *vice versa*. This result could be due to the fact that *Bos taurus indicus* cattle have lower requirements for basal metabolism, use the energy more efficiently and require lower feed intake (Schutt, Arthur, & Burrow, 2009) than *Bos taurus taurus*.

Several studies have emphasized a favourable correlated response between early heifer's pregnancy and growth, carcass and reproductive traits (Boligon et al., 2010; Grossi et al., 2009; Shiotsuki et al., 2009), in which the selection for high early heifer's pregnancy would increase the productive response in several traits. The results obtained in this study did not show this trend, probably, due to differences in genetic population background and differences in the criteria used to edit the phenotypic data set for PPC. In the present study, all heifers under PPC evaluations were exposed to reproduction in their weaning year to determine sexual precocity, different from the criteria used in the previous studies, in which a sexual precocious heifer was defined according to the AFC, that is, if a heifer calved up to 28 and 30 months, then it was considered as precocious.

The improvement of heifer sexual precocity should combine genetic selection, adequate nutrition planification and prebreeding examination that encompass the herd as a whole. In this regard, the heifer's nutrition is one of the main aspects to consider in both pre- and postweaning stages.

4 | CONCLUSIONS

Higher response to selection for early heifer pregnancy is expected when females are challenged to their first mating season at younger ages. The results of this study are encouraging for the use of PPC in Nellore cattle since the selection for such trait would not affect negatively the reproductive, growth, carcass and feed efficiency indicator traits. STAY for sexual precocious heifers must be redefined to avoid incorrectly phenotype assignment.

CONFLICT OF INTEREST

Authors declare no conflict of interest.

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