

Genetic evaluation of oocyte and embryo production in dairy Gir cattle using repeatability and random regression models

Giovani Luis Feltes¹ , Renata Negri² , Fernanda Santos Silva Raidan³ , Luiz Fernando Rodrigues Feres⁴ , Virgínia Mara Pereira Ribeiro⁵ , Jaime Araújo Cobuci^{1*} 

¹ Universidade Federal do Rio Grande do Sul, Departamento de Zootecnia, Porto Alegre, RS, Brasil.

² Associação Brasileira dos Criadores de Girolando, Uberaba, MG, Brasil.

³ CSIRO Agriculture & Food, Brisbane, Queensland, Australia.

⁴ Universidade de Alfenas, Alfenas, MG, Brasil.

⁵ Universidade Federal de Minas Gerais, Escola de Veterinária, Departamento de Zootecnia, Belo Horizonte, MG, Brasil.

ABSTRACT - The objective of this work is to estimate genetic parameters and breeding values to improve embryo and oocyte production, using repeatability and random regression models (RRM) for Gir dairy cattle. We used 11,398 records of ovum pick-up from 1,747 dairy Gir donors and evaluated sixteen different models: the traditional repeatability model and fifteen RRM, each of which considered a different combination of Legendre polynomial regressors to describe the additive genetic and permanent environment effects. The 4G1P model (four regressors for the genetic effect and one regressor for the permanent environment effect) is the most suitable model to analyze the number of viable and total oocytes, while the 3G1P is the best model to analyze the number of cleaved and viable embryos, according to the values of the Akaike information criterion (AIC) and the Bayesian information criterion (BIC). The heritability estimated with the RRM was higher than that estimated with the repeatability model. The high repeatability reported for oocyte and embryo count traits indicates that donors, which had high oocyte and embryo counts in the first ovum pick-up, should maintain this result in the next ovum pick-up. Genetic correlations between adjacent ages were high and positive, while genetic correlations between extreme ages were weak. We observed a re-ranking of the top sires and females (heifers and cows) over the period evaluated. The reliability of the estimated breeding values by RRM showed changes across age, and the expected genetic gains by RRM are larger. This shows that RRM is most suitable alternative for the evaluation and selection of oocyte and embryo count traits.

*Corresponding author:

jaime.cobuci@ufrgs.br

Received: February 8, 2022

Accepted: September 12, 2022

How to cite: Feltes, G. L.; Negri, R.; Raidan, F. S. S.; Feres, L. F. R.; Ribeiro, V. M. P. and Cobuci, J. A. 2022. Genetic evaluation of oocyte and embryo production in dairy Gir cattle using repeatability and random regression models. *Revista Brasileira de Zootecnia* 51:e20220017. <https://doi.org/10.37496/rbz5120220017>

Copyright: This is an open access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.



Keywords: animal breeding, *Bos indicus*, dairy cattle, *in vitro* fertilization, ovum pick-up

1. Introduction

Selection for reproductive efficiency is an effective strategy to ensure the success of dairy and beef cattle industries (Watanabe et al., 2017). Reproductive biotechnologies began several decades ago, with the development of superovulation protocols and embryo transfer from the late 1940s. However, the use of these biotechnologies on a large scale started in the 1970s. Great advances such as the birth of the first calves via *in vitro* fertilization and the collection of oocytes from live donors were carried out in the 1980s, and new protocols for *in vitro* embryo production were developed in the 1990s (Moore and Hasler, 2017).

Reproductive technologies, including superovulation, *in vitro* fertilization, and embryo transfer are used to increase the reproductive rate of genetically superior females (Parker Gaddis et al., 2017). In Brazilian dairy herds, the increase in the use of embryo transfer in the 1995-2015 period was 2,261.7% (Viana et al., 2017). Several factors, including those related to animals and those that involve environment and management, contribute to the low success rates of embryo transfer (Fleming et al., 2018). However, it is well-known that there is a genetic component related to superovulation traits and that selection should be applied to improve embryo transfer rates (Merton et al., 2009; Jatón et al., 2016a; Perez et al., 2017a, 2016; Parker Gaddis et al., 2017; Cornelissen et al., 2017).

In terms of the genetic component, *Bos indicus* animals show better results in *in vitro* oocyte and embryo production than *Bos taurus* (Lacerda et al., 2020). That is why the investigation of methodologies that consider the selection and improvement of embryo production traits are necessary for a possible inclusion of these traits in future genetic evaluations of the Gir breed.

The genetic evaluation of embryo and oocyte traits is usually performed using repeatability models (Tonhati et al., 1999; Asada and Terawaki, 2002; Merton et al., 2009; Jatón et al., 2016a), in which the genetic and permanent environment correlations are assumed as perfect (= 1); therefore, it is not considered that, over time, changes in genetic and permanent environment effects might occur. However, random regression models (RRM) allow us to obtain individual estimated breeding value (EBV) curves and consider changes in genetic and residual variances over time, which can be applied to predict breeding values more accurately (Jamrozik and Schaeffer, 1997; Resende et al., 2001). In addition, they allow the prediction of breeding values for any desired age, even for ages of the animal that have not been recorded.

Considering the importance of dairy Gir breed for dairy farming, this work aimed to estimate genetic parameters and breeding values for embryo and oocyte production using repeatability and RRM to determine which model could result in greater genetic gains in oocyte and embryo production in dairy Gir animals.

2. Material and Methods

2.1. Data

The data used were from three herds of dairy Gir cattle, belonging to the same company, in the state of Minas Gerais – Brazil (19°55' S, – 43°57' W). The complete data set considered for genetic analysis consisted of 3,124 Gir cows, daughters of 250 sires and that calved between 2000 and 2015.

The available information consisted of traits of total oocytes (TO), viable oocytes (VO), cleaved embryos (CE), and viable embryos (VE), resulting from 13,217 collection sessions, which produced a total of 283,752 total oocytes, 211,963 viable oocytes, 157,107 cleaved embryos, and 60,092 viable embryos. The cows' age varies from one to 20 years at the time of ovum pick-up. The sessions were held between January 2005 and March 2017. The number of ovum pick-up sessions varied from one to 53 per donor, and the intervals between sessions for the same donor varied from seven to 120 days.

For this study, we excluded records of females with extreme age at ovum pick-up (<12 or >144 months) and number of TO equal to zero. For the other traits (VO, CE, and VE), the count records equal to zero were kept and considered in the analyses. Only healthy females subjected to ovum pick-up and donors with at least two individual records of ovum pick-up during age period were maintained (in 41.7% of cases, only one collection per donor was performed). The contemporary groups for all traits are defined by the concatenation of herd, year, and ovum pick-up season. Seasons were classified into wet (October until March) or dry (April until September). We eliminated contemporary groups that contained fewer than five observations.

Following these criteria, we analyzed 11,398 ovum pick-up records, collected from 2010 to 2017, from 1,747 dairy Gir heifers and cows from three farms where the same protocols and procedures are used. Semen from 212 different sires (Gir or Holstein) was used in *in vitro* fertilization procedures, of which 81.13% is sexed semen. We used the same database for all models evaluated. The pedigree file included 5,921 animals of eight generations.

2.2. Statistical analyses

The statistical program R version 3.4.2 (R Core Team, 2017) was used for data editing and descriptive statistics. Data used in this work were transformed using the common logarithmic transformation, $y_i = \log(y + 1.001)$, in which y_i is the log-transformed value of oocyte and embryo counts, and y is the original value of oocyte and embryo count.

2.3. Genetic analyses

The estimates of variance components for ovum pick-up traits at age in months were obtained using a random regression model. For all evaluated traits, the model considered contemporary groups, interval between collections, and number of collections as fixed effects. For VE, we added a fixed effect referring to sire used in artificial fertilization (Table 1).

Genetic parameters and breeding values were estimated using the model:

$$Y_{ijkl} = hys_i + iop_j + nop_j + \sum_{k=0}^n \Phi_k(mo_t)u_{jk} + \sum_{k=0}^n \Phi_k(mo_t)pe_{jk} + sa_i + e_{ijkl}$$

in which Y_{ijkl} is the vector of trait value (TO, VO, CE, and VE) in month t within the herd-year-season of ovum pick-up; hys_i is the fixed effect of herd-year-season of ovum pick-up; iop_j is the covariable effect of the interval between ovum pick-up in the same animal; nop_j is the covariable effect of number of animal ovum pick-up; sa_i is the fixed effect referring to sire used in artificial fertilization; u_{jk} and pe_{jk} are random regression coefficients that describe, respectively, the additive genetic and permanent environment effects on the performance of animal j ; $\Phi_k(mo_t)$ is the Legendre polynomial for registration in month of ovum pick-up of animal j in month t , in which k is Legendre polynomial coefficient; and e_{ijkl} is the random error.

For that we assume:

$$\text{Var} \begin{bmatrix} \mathbf{u} \\ \mathbf{pe} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{A} \otimes \mathbf{G} & 0 & 0 \\ 0 & \mathbf{I} \otimes \mathbf{P} & 0 \\ 0 & 0 & \mathbf{E} \end{bmatrix}$$

in which \mathbf{G} and \mathbf{P} are the covariance matrices of the random regression coefficients, \mathbf{A} is the kinship matrix, \mathbf{I} is the identity matrix, $\mathbf{E} = \sigma_e^2$ is a diagonal (residual) matrix, and \otimes is Kronecker product between the matrices.

The additive genetic and permanent environment effects were estimated using Legendre polynomials (Kirkpatrick et al., 1994):

$$y_t = \sum_{i=0}^n \alpha_i \Phi_i(m_t^*)$$

in which m_t^* is the standardized time unit (months) ranging from -1 to $+1$; $mo_t^* = -1 + \frac{2(mo_t - mo_{min})}{mo_{max} - mo_{min}}$, wherein, mo_{min} and mo_{max} are, respectively, the lowest (12 months) and the highest (144 months) ages at ovum pick-up in months, reported in the data set after consistency edits; and m_t is the age at ovum pick-up.

The standardized age at ovum pick-up can be defined as:

$$\Phi(mo_t^*)k = \frac{1}{2^K} \sqrt{\frac{2K+1}{2}} \sum_{m=0}^{K/2} (-1)^m \binom{k}{m} \binom{2K+1}{r} (mo_t^*)^{r-2m}$$

Table 1 - Model design

Trait	Fixed effect				Regressor		Model
	CG	IVOP	NVOP	Sire	A	P	
TO, VO, CE	*	*	*	-	+	+	1G1P
	*	*	*	-	+	++	1G2P
	*	*	*	-	+	+++	1G3P
	*	*	*	-	+	++++	1G4P
	*	*	*	-	++	+	2G1P
	*	*	*	-	++	++	2G2P
	*	*	*	-	++	+++	2G3P
	*	*	*	-	++	++++	2G4P
	*	*	*	-	+++	+	3G1P
	*	*	*	-	+++	++	3G2P
	*	*	*	-	+++	+++	3G3P
	*	*	*	-	+++	++++	3G4P
	*	*	*	-	++++	+	4G1P
	*	*	*	-	++++	++	4G2P
	*	*	*	-	++++	+++	4G3P
	*	*	*	-	++++	++++	4G4P
VE	*	*	*	*	+	+	1G1P
	*	*	*	*	+	++	1G2P
	*	*	*	*	+	+++	1G3P
	*	*	*	*	+	++++	1G4P
	*	*	*	*	++	+	2G1P
	*	*	*	*	++	++	2G2P
	*	*	*	*	++	+++	2G3P
	*	*	*	*	++	++++	2G4P
	*	*	*	*	+++	+	3G1P
	*	*	*	*	+++	++	3G2P
	*	*	*	*	+++	+++	3G3P
	*	*	*	*	+++	++++	3G4P
	*	*	*	*	++++	+	4G1P
	*	*	*	*	++++	++	4G2P
	*	*	*	*	++++	+++	4G3P
	*	*	*	*	++++	++++	4G4P

TO - total oocytes; VO - viable oocytes; CE - cleaved embryos; VE - viable embryos; CG - contemporary group, IVOP - interval between ovum pick-up; NVOP - number of ovum pick-up.

* Considered; -: not considered; +: order of the Legendre polynomial.

in which mo_i^* is the i -th age at ovum pick-up, i is the order of the Legendre function, and m is the number of indices needed to determine the polynomial. The residual variance (σ_e^2) was considered homogeneous for all functions.

To assess which model had the best fit to be used in the genetic evaluation of traits of artificial reproduction, we sought to adjust the genetic and permanent environment effects using different polynomial functions from the first to the fourth order, totaling 16 different combinations between genetic and permanent environment effects. The models design can be seen in Table 1, e.g., 1G1P is a

traditional repeatability model and 4G3P is a random regression model that considers four regressors for the genetic additive effect and three regressors for the permanent environmental effect.

The estimated breeding value of animal i in month t was calculated as $EBV_{it} = z'_t \hat{\alpha}_i = \sum_{j=0}^{k_a-1} \alpha_{ij} \phi_j(mo_t)$, in which $\hat{\alpha}_i$ a vector ($k_a \times 1$) of estimates of the additive genetic random regression coefficients of animal i and z_t a vector of Legendre polynomial coefficients for month t .

All analyses were estimated through the maximum restricted likelihood method, using the program REMLF90 version 1.79 (Misztal et al., 2002). The quality of fit was carried out through comparison tests between models: Akaike's information criterion ($AIC = -2\log L + 2p$, in which p is the number of parameters in the model) and Schwarz's Bayesian information criterion ($BIC = -2\log L + p \log(\lambda)$, in which $\log(\lambda)$ is the natural logarithm of sample size (or dimension of y) and p is the number of parameters in the model).

In the heritability, $h_{mo}^2 = \frac{\sigma_{a(mo)}^2}{\sigma_{a(mo)}^2 + \sigma_{pe(mo)}^2 + \sigma_e^2}$, and repeatability, $R_{mo} = \frac{\sigma_{a(mo)}^2 + \sigma_{pe(mo)}^2}{\sigma_{a(mo)}^2 + \sigma_{pe(mo)}^2 + \sigma_e^2}$, $\sigma_{a(mo)}^2$ and $\sigma_{pe(mo)}^2$ are additive genetic and permanent environmental variances for months (mo) and were calculated and plotted graphically to check for possible differences between the repeatability model (1G1P) and the best-fit model selected by AIC and BIC.

The standard error of heritability was calculated according to the methodology of Meyer and Houle (2013), using the average information matrix with the AIREMLF90 program version 1.149 (Misztal et al., 2002).

The genetic correlation between two months in ovum pick-up, mo_{t1} and mo_{t2} , was calculated by dividing the additive genetic covariance between months in ovum pick-up, mo_{t1} and mo_{t2} , by the product of the square root of the genetic variances of months in ovum pick-up mo_{t1} and mo_{t2} :

$$r_{g(mo1,mo2)} = \frac{COV_{g(mo1,mo2)}}{\sqrt{var_{g(mo1,mo1)} + var_{g(mo2,mo2)}}}$$

in which $COV_{g(mo1,mo2)}$ is the genetic covariance between mo_{t1} and mo_{t2} months, and $var_{g(mo1,mo1)}$ and $var_{g(mo2,mo2)}$ are additive genetic variance of mo_{t1} and mo_{t2} months, respectively. The permanent environmental correlation was calculated in the same way as above, just replacing the genetic matrices with the permanent environment ones.

To verify the occurrence of changes in the ranking of the best animals at different ages at ovum pick-up, Spearman's ranking correlation was calculated between the classifications of the 5% best sires based on estimated breeding values (EBV) by the 1G1P model and by the best model by the AIC and BIC criteria. For the chosen model, the ranking by the EBV at six different ages (24, 48, 72, 96, 120, and 144 months) was used. The same procedure was performed for the 5% best females.

The reliabilities were calculated using the triangular matrices of prediction error (co)variances for random regression effects, from the inverse of the mixed model equations obtained in BLUPF90 program version 1.70 (Misztal et al., 2002).

The expected genetic gain was calculated through $\Delta G_{imo} = h_{imo}^2 * isel * \sigma_{imo}$, in which ΔG_{imo} is the genetic gain due to direct selection for trait i in month mo , h_{imo}^2 is the heritability of trait i in month mo , $isel$ is the selection intensity (default 5%), and σ_{imo} is the phenotypic standard deviation for trait i in month mo , after common logarithmic transformation.

3. Results

3.1. Data

The number of oocytes and embryos varied widely (Table 2) for all traits; the median was less than the mean, and the standard deviation showed high values, in some cases greater than the median, and

almost equal to the mean. The number of ovum pick-up varied over the age period studied (Figure 1); most collections were made in young animals; from the age of 72 months, a drastic reduction in the number of ovum pick-up was reported.

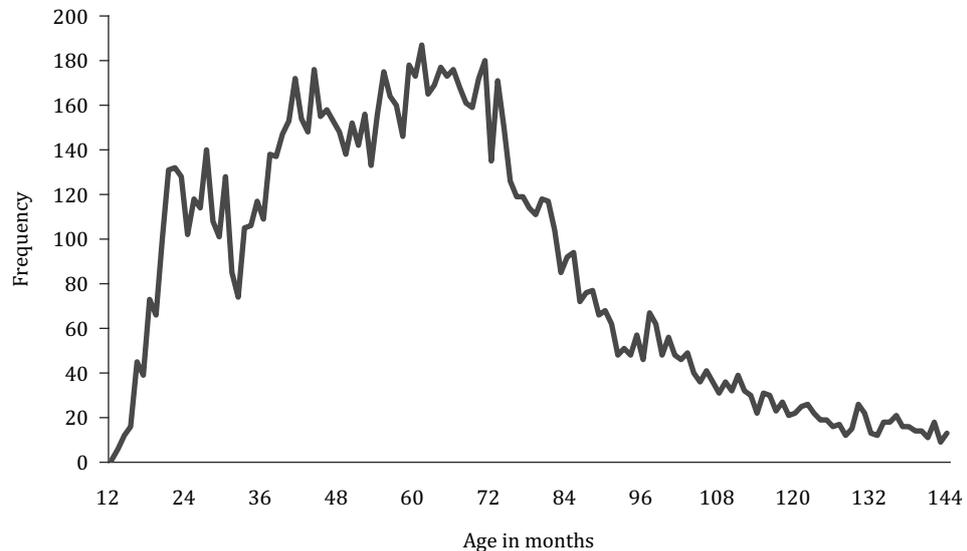


Figure 1 - Frequency of ovum pick-up in the age period evaluated.

Table 2 - Number of observations (N), medians, means, standard deviations (SD), minimum (Min) and maximum (Max) (untransformed variables)

Trait	N	Median	Mean	SD	Min	Max
Total oocytes	11398	13.00	21.72	15.38	1.00	182.00
Viable oocytes	11398	13.00	16.24	13.01	0.00	182.00
Cleaved embryos	11398	10.00	11.99	8.87	0.00	98.00
Viable embryos	11398	3.00	4.55	4.53	0.00	43.00

3.2. Selection criteria

The AIC indicated more than one model as the best (Table 3). However, the BIC, which is more discerning, indicated only one model for each trait. That said, the 4G1P model was chosen for the TO and VO traits, and for CE and VE, the best fit model was the 3G1P. The models with a higher number of coefficients for additive genetic effect were preferred compared with models with a higher number of coefficients for permanent environmental effect by the AIC and BIC criteria.

3.3. Heritability

The estimated genetic parameters varied according to the age at ovum pick-up (Figure 2). Using RRM, the highest heritability (h^2) values (\pm standard error) were estimated at the lowest and highest ages (extremes) at ovum pick-up. The h^2 for TO ranged from 0.46 ± 0.06 (72 months) to 0.72 ± 0.07 (144 months) using 4G1P model and 0.37 ± 0.03 using 1G1P model. For VO, h^2 varied from 0.43 ± 0.06 (84 months) to 0.66 ± 0.08 (144 months) using the 4G1P model and 0.34 ± 0.06 using 1G1P model.

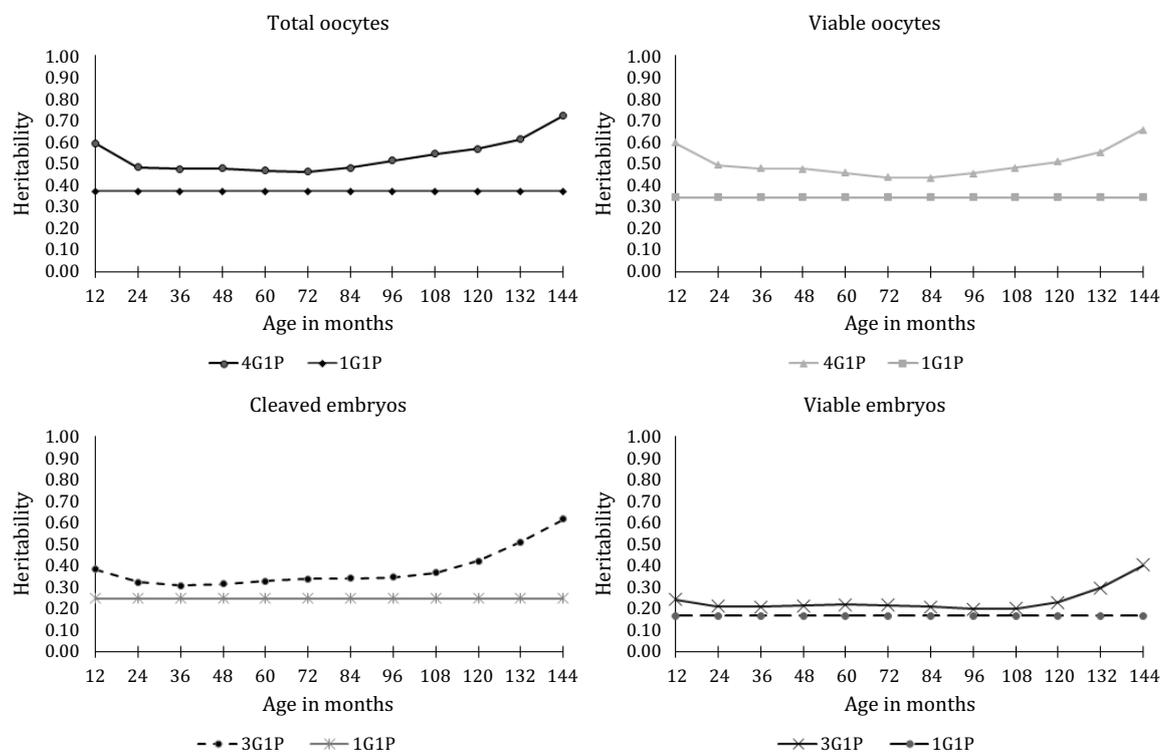
In the case of CE, using the 3G1P model, h^2 ranged from 0.31 ± 0.05 (36 months) to 0.62 ± 0.06 (144 months) and 0.25 ± 0.05 with 1G1P. For VE, h^2 varied from 0.20 ± 0.04 (96 months) to 0.40 ± 0.08 (144 months) using 3G1P and 0.17 ± 0.05 with 1G1P model.

Table 3 - Selection criteria based on values of goodness-of-fit tests obtained by repeatability and random regression models in Brazilian dairy Gir cattle

Model	Total oocytes		Viable oocytes		Cleaved embryos		Viable embryos	
	AIC	BIC	AIC	BIC	AIC	BIC	AIC	BIC
1G1P	-1,450*	-1,444*	1,461*	1,467*	2,023*	2,030*	7,036*	7,043*
1G2P	-1,623	-1,613	1,327	1,337	1,945	1,955	7,019	7,029
1G3P	-1,648	-1,632	1,306	1,322	1,928	1,944	7,006	7,022
1G4P	-1,673	-1,648	1,288	1,313	1,920	1,945	7,005	7,030
2G1P	-1,717	-1,707	1,257	1,267	1,899	1,909	7,014	7,024
2G2P	-1,720	-1,705	1,256	1,270	1,899	1,913	7,016	7,030
2G3P	-1,743	-1,722	1,235	1,256	1,883	1,904	7,002	7,023
2G4P	-1,761	-1,733	1,222	1,251	1,878	1,907	7,001	7,030
3G1P	-1,764	-1,748	1,213	1,230	1,876*	1,892*	7,001*	7,017*
3G2P	-1,764	-1,743	1,215	1,236	1,878	1,899	7,003	7,023
3G3P	-1,764	-1,738	1,214	1,241	1,879	1,906	7,001	7,028
3G4P	-1,774	-1,739	1,208	1,243	1,875	1,910	7,000	7,035
4G1P	-1,782*	-1,758*	1,200*	1,225*	1,870	1,895	7,001	7,026
4G2P	-1,782	-1,753	1,201	1,230	1,871	1,900	7,004	7,033
4G3P	-1,782	-1,747	1,200	1,235	1,873	1,908	7,003	7,037
4G4P	-1,777	-1,734	1,204	1,247	1,874	1,918	7,003	7,046

AIC - Akaike's information criterion; BIC - Bayesian information criterion.

* The lowest values of AIC and BIC and values of the repeatability model (1G1P).

**Figure 2** - Heritability estimates for the *in vitro* embryo production traits using random regression model and repeatability models in Brazilian dairy Gir cattle.

In summary, the 1G1P model produced the lowest heritability estimates for all traits. The RRM captured the highest proportions of additive genetic effects, producing the highest h^2 values for all traits, especially in the initial and final evaluated periods, in which there is a smaller number of observations (Figure 1). The highest h^2 estimates were reported in the first months of ovum pick-up and after 84 months of age, in which, after that period, there is a linear increase in the h^2 value.

3.4. Repeatability

There is little difference in repeatability (R) estimates between months 24 and 96 for models 1G1P and RRM. In the initial period, 12 to 24 months, the R of models considering random regression for genetic effect was greater than the 1G1P model (Figure 3). From 96 months onwards, there was a linear increase in R until the end of the period.

For TO, R was 0.54 using the 1G1P model, while with the 4G1P model, R ranged from 0.54 (72 months) to 0.76 (144 months), with the highest values reported in the late age period and the lowest values in the intermediate period. The VO trait showed R of 0.51, considering the 1G1P model, and varied between 0.50 (84 months) and 0.70 (144 months), with the highest values also found in final period and the lowest values in the intermediate period.

The CE presented R of 0.42 with 1G1P model and varied between 0.41 (36 months) and 0.67 (144 months) with 3G1P, with the highest values also being found in final ages and lowest values from 24 to 48 months. The VE presented R of 0.35 with 1G1P and ranged from 0.35 (96 months) to 0.51 (144 months) with 3G1P, with the highest values reported for age in the last months (132-144 months) and the lowest values in intermediate ages.

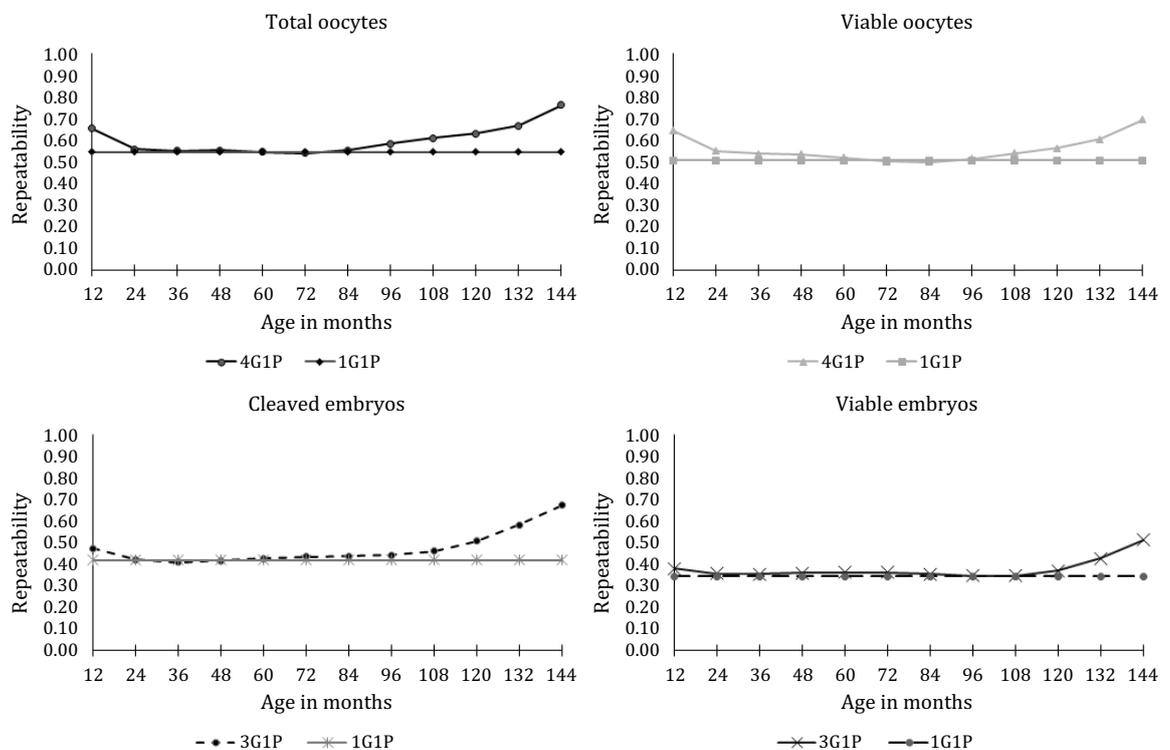


Figure 3 - Repeatability estimates for the *in vitro* embryo production traits in Brazilian dairy Gir cattle.

3.5. Genetic and permanent environment correlation

Genetic correlations ranged from 0.98 to -0.24 for TO, 0.98 to -0.19 for VO, 0.99 to -0.03 for CE, and 0.99 to -0.04 for VE (Figure 4). Strong and positive correlations were reported at adjacent ages, and the lowest and negative correlations were observed at the extreme ages.

The models 4G1P and 3G1P indicated that only a linear coefficient (1P) is efficient to evaluate the effect of permanent environment, so the correlation of permanent environment is equal to 1, because no change in the value of variance of permanent environment was observed across ages.

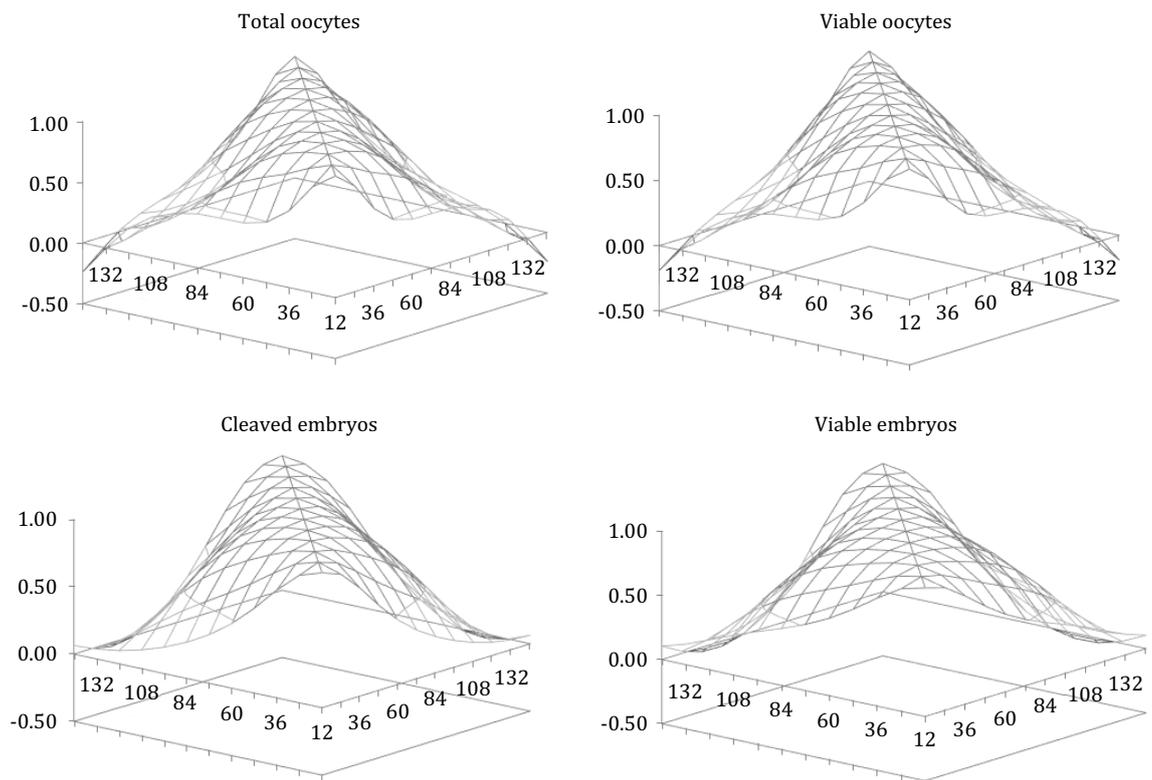


Figure 4 - Genetic correlation estimates between the different collection months for total oocytes (4G1P), viable oocytes (4G1P), cleaved embryos (3G1P), and viable embryos (3G1P) using random regression models in Brazilian dairy Gir cattle.

3.6. Spearman's rank correlation

The magnitude of the estimated coefficient of Spearman's rank correlations confirmed the reranking of the top 5% sires and females in most comparisons (Tables 4, 5, 6, and 7). Altogether, 168 rank correlations were calculated, and only five of these (2.97%) presented value above 0.80. This demonstrates a reranking of the best animals when considering repeatability versus random regression over the evaluated age period (12-144 months) using RRM.

In TO, the rank correlation of 0.86 was reported among the top 5% best sires (Table 4) between the 4G1P_24 (random regression model with four coefficients for genetic effect, one for permanent environment effect, and regressed for age at ovum pick-up at 24 months) and 4G1P_120 model. In the case of the top 5% best females, no rank correlation greater than 0.80 was reported (Table 4) for this trait.

For VO, no rank correlation greater than 0.80 was reported in the top 5% best sires (Table 5), but in top 5% best females, the rank correlation of 0.80 was reported by the 1G1P (repeatability model) with those ranked at 4G1P_48 (Table 5).

In the case of CE, no rank correlation greater than 0.80 was reported both among the top 5% best sires and the top 5% best females (Table 6). For VE, rank correlations of 0.84 and 0.85 were reported between 3G1P_24 and 3G1P_144, and between 3G1P_48 and 3G1P_72 for the top 5% best sires (Table 7). In addition, for VE, a rank correlation of 0.84 was estimated between 3G1P_48 and 3G1P_72 (Table 7) for the top 5% best females.

Table 4 - Spearman's rank correlation between estimated breeding values for total oocytes obtained by 1G1P and 4G1P models at different ages at ovum pick-up, considering the 5% best sires (above diagonal) and 5% best females (below diagonal)

Model	1G1P	4G1P_24	4G1P_48	4G1P_72	4G1P_96	4G1P_120	4G1P_144
1G1P		0.71	0.49	0.66	-0.17	0.08	0.02
4G1P_24	0.67		0.58	0.58	0.02	0.86	0.2
4G1P_48	0.76	0.76		0.78	0.27	0.40	-0.02
4G1P_72	0.65	0.56	0.72		0.50	0.22	0.15
4G1P_96	0.01	-0.17	-0.01	0.33		0.74	0.44
4G1P_120	-0.13	-0.42	-0.25	0.06	0.67		0.53
4G1P_144	0.12	-0.08	0.11	0.12	0.57	0.69	

Table 5 - Spearman's rank correlation between estimated breeding values for viable oocytes obtained by 1G1P and 4G1P models at different ages at ovum pick-up, considering the 5% best sires (above diagonal) and 5% best females (below diagonal)

Model	1G1P	4G1P_24	4G1P_48	4G1P_72	4G1P_96	4G1P_120	4G1P_144
1G1P		0.79	0.49	0.67	0.50	0.25	0.31
4G1P_24	0.69		0.61	0.58	0.3	0.16	0.58
4G1P_48	0.80	0.74		0.71	0.28	-0.18	0.34
4G1P_72	0.68	0.57	0.76		0.54	0.09	0.43
4G1P_96	0.09	0.06	0.18	0.38		0.63	0.61
4G1P_120	-0.14	-0.25	0.04	0.25	0.62		0.73
4G1P_144	-0.12	0.19	0.33	0.25	0.48	0.68	

Table 6 - Spearman's rank correlation between estimated breeding values for cleaved embryos obtained by 1G1P and 3G1P models at different ages at ovum pick-up, considering the 5% best sires (above diagonal) and 5% best females (below diagonal)

Model	1G1P	3G1P_24	3G1P_48	3G1P_72	3G1P_96	3G1P_120	3G1P_144
1G1P		0.22	0.48	0.52	0.59	0.60	0.57
3G1P_24	0.68		0.59	0.40	-0.25	0.19	0.5
3G1P_48	0.75	0.72		0.63	0.34	0.34	0.54
3G1P_72	0.60	0.45	0.78		0.69	0.44	0.19
3G1P_96	0.30	0.18	0.38	0.63		0.69	0.40
3G1P_120	0.05	-0.13	0.01	0.14	0.55		0.69
3G1P_144	-0.16	0.00	0.09	0.21	0.47	0.67	

Table 7 - Spearman's rank correlation between estimated breeding values for viable embryos obtained by 1G1P and 3G1P models at different ages at ovum pick-up, considering the 5% best sires (above diagonal) and 5% best females (below diagonal)

Model	1G1P	3G1P_24	3G1P_48	3G1P_72	3G1P_96	3G1P_120	3G1P_144
1G1P		0.73	0.68	0.73	0.74	0.59	0.38
3G1P_24	0.65		0.73	0.55	0.38	0.52	0.84
3G1P_48	0.79	0.79		0.85	0.51	0.43	0.40
3G1P_72	0.77	0.56	0.84		0.77	0.61	0.61
3G1P_96	0.72	0.32	0.56	0.75		0.62	0.35
3G1P_120	0.27	-0.13	0.16	0.21	0.42		0.53
3G1P_144	0.30	0.30	0.17	0.06	0.18	0.60	

3.7. Reliability

The average reliability of EBV for TO of the top 5% sires (Figure 5) and all sires (Figure 6) using 1G1P model was 0.38 and 0.11, while the reliability of EBV using the 4G1P model varied from 0.15 (144 months) to 0.38 (72 months) and 0.05 (144 months) to 0.11 (72 months), respectively; the highest reliability values were reported at intermediate ages (60 to 84 months). For the top 5% females (Figure 5) and all females (Figure 6), the average reliability of EBV of TO using 1G1P model was 0.61 and 0.30, while with the 4G1P model, it varied from 0.20 (144 months) to 0.64 (48 months) and 0.11 (144 months) to 0.30 (60 months), respectively; the highest reliability values were reported at the initial intermediate ages (36 to 72 months).

For VO, the average reliability of EBV of the top 5% sires (Figure 5) and all sires (Figure 6) using 1G1P was 0.34 and 0.11, while using the 4G1P, it ranged from 0.13 (144 months) to 0.35 (72 months) and 0.05 (144 months) to 0.11 (72 months), respectively; the highest values were reported at intermediate ages (48 to 72 months). In the top 5% females (Figure 5) and all females (Figure 6), the average reliability using the 1G1P model was 0.59 and 0.29, and when using the 4G1P model, it varied from 0.20 (144 months) to 0.63 (48 months) and 0.11 (144 months) to 0.31 (60 months), respectively; the highest values were reported at intermediate ages (36 to 60 months).

In the case of CE, the average reliability of EBV for CE of the top 5% sires (Figure 5) and all sires (Figure 6) using the 1G1P model was 0.26 and 0.10, and when using the 3G1P model, it ranged from 0.20 (36 months) to 0.41 (120 months) and 0.09 (36 months) to 0.37 (120 months), respectively; the highest values were reported at advanced ages (96 to 132 months). The average reliability of EBV for CE of the top 5% females (Figure 5) and all females (Figure 6) using 1G1P model was 0.51 and 0.26, and when using the 3G1P model, it varied from 0.41 (12 months) to 0.52 (96 months) and 0.23 (36 months) to 0.42 (120 months), respectively; the highest values were reported at the final intermediate ages (84 to 108 months).

In relation to VE, the average reliability of EBV of the top 5% sires (Figure 5) and all sires (Figure 6) using the 1G1P model was 0.20 and 0.08, and using the 3G1P model, it ranged from 0.07 (144 months) to 0.20 (72 months) and 0.04 (144 months) to 0.08 (60 months), respectively; the highest values were reported at intermediate ages (48 to 84 months). In the case of the top 5% females (Figure 6) and all females (Figure 6), the average reliability of EBV using 1G1P model was 0.42 and 0.22 and, using the 3G1P model, it varied between 0.16 (144 months) and 0.44 (48 months) and between 0.09 (144 months) and 0.22 (60 months), respectively; the highest values were reported at intermediate ages (48 to 72 months).

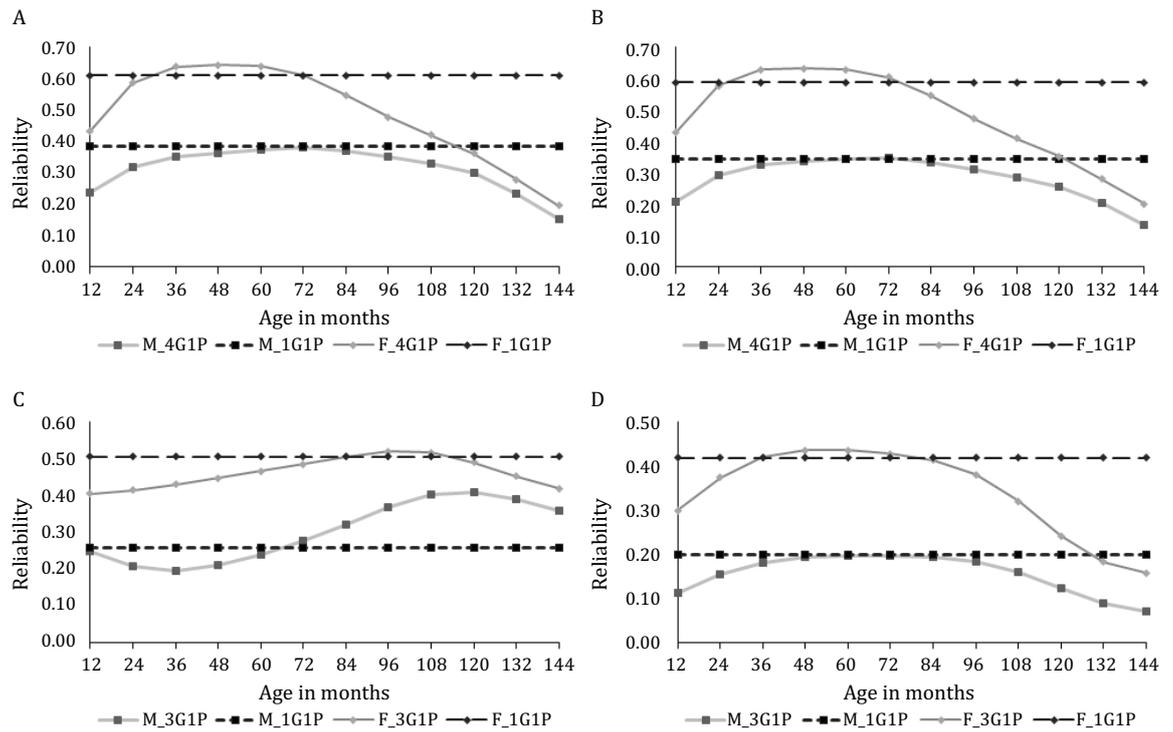


Figure 5 - Reliability of estimated breeding value of the 5% best sires (M_4G1P, M_3G1P, M_1G1P), and the 5% best females (F_4G1P, F_3G1P, F_1G1P) for total oocytes (A), viable oocytes (B), cleaved embryos (C), and viable embryos (D) in Brazilian dairy Gir cattle.

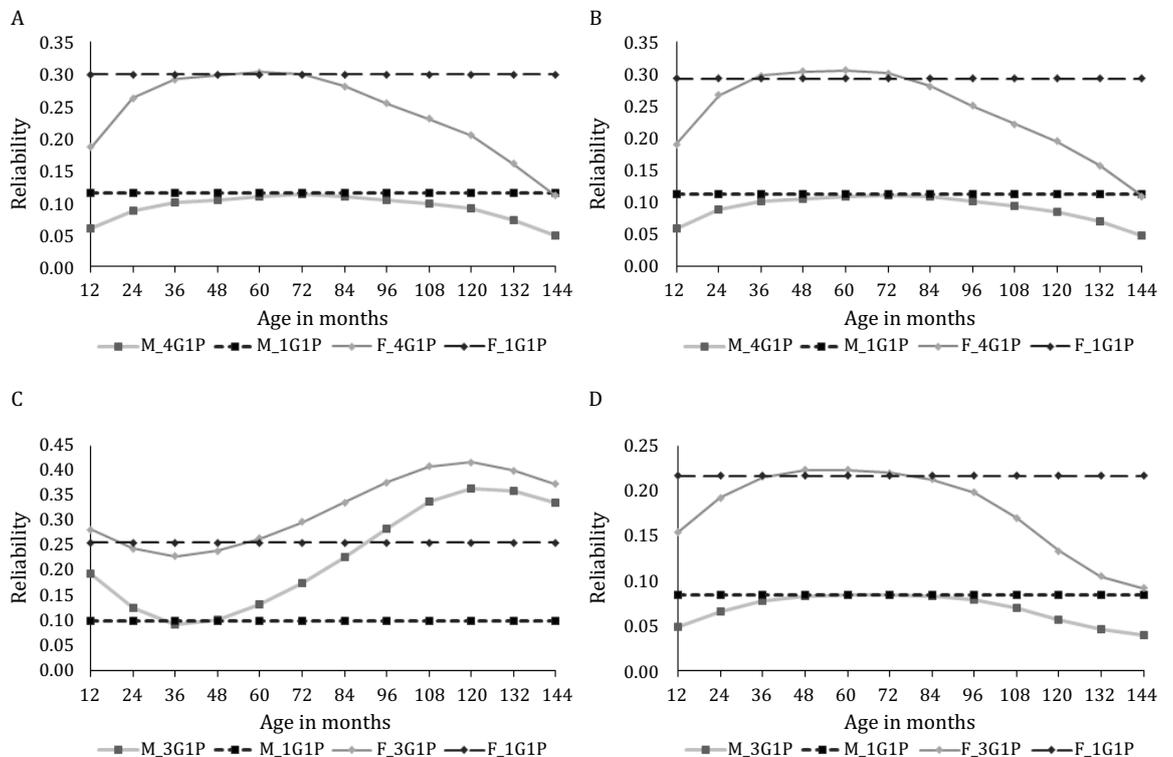


Figure 6 - Reliability of estimated breeding value of all sires (M_4G1P, M_3G1P, M_1G1P) and all females (F_4G1P, F_3G1P, F_1G1P) for total oocytes (A), viable oocytes (B), cleaved embryos (C), and viable embryos (D) in Brazilian dairy Gir cattle.

3.8. Expected genetic gain

When comparing the 4G1P and 3G1P models to 1G1P (Figure 7), the expected genetic gain was greater throughout the age period evaluated, and the greatest difference was found in the initial and final periods.

The difference between the expected genetic gains for TO obtained by 4G1P and 1G1P models were at least 0.05 (72 months) and maximum of 0.23 (144 months), and in the case of VO, this difference between expected genetic gain obtained by the cited models was at least 0.05 (84 months) and maximum of 0.22 (144 months).

When comparing the expected genetic gain for CE and VE, the difference was at least 0.04 (36 months) and 0.02 (96 months) and maximum of 0.26 (144 months) and 0.17 (144 months), respectively.

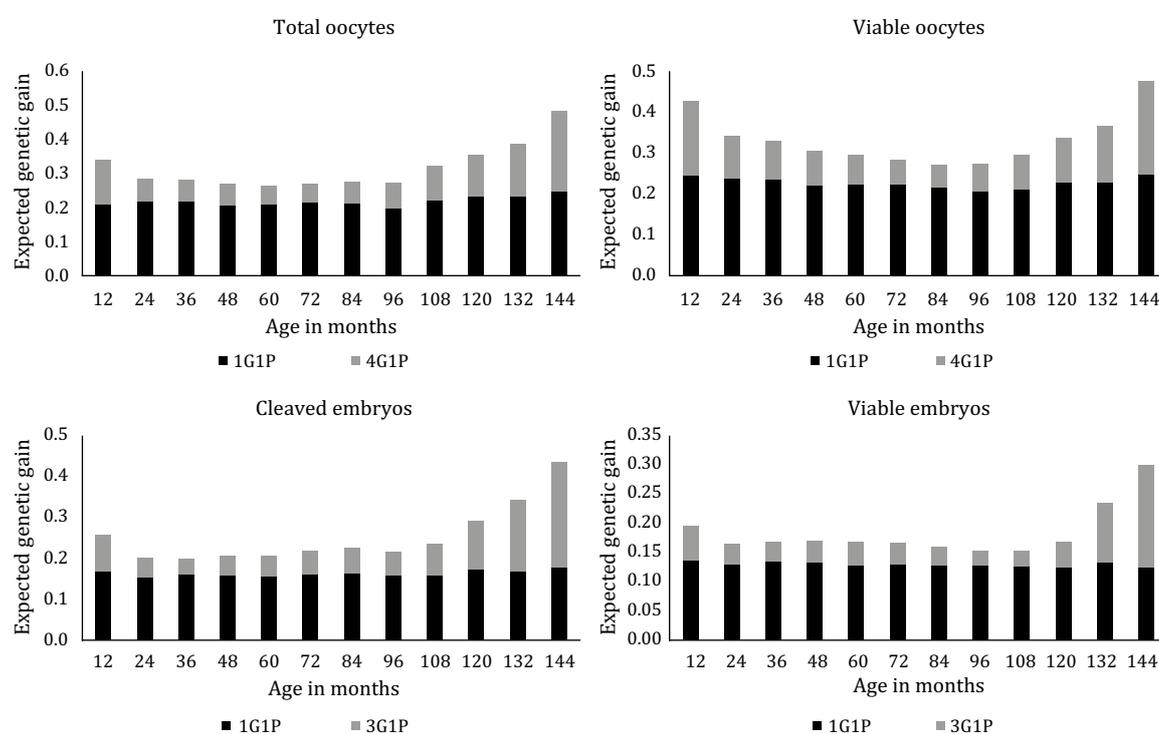


Figure 7 - Expected genetic gain for total oocytes, viable oocytes, cleaved embryos, and viable embryos in Brazilian dairy Gir cattle.

4. Discussion

4.1. Data

In all traits, the mean value was higher than the median, indicating that there are animals with high counts and that, thereby, could increase the mean value. The high standard deviation values, in some cases higher than the median, indicate that there is great variance in these traits.

The performance of *Bos indicus* and *Bos taurus* cows under *in vitro* embryo production technology has been reported in the literature, and the results indicate that there are significant differences between genetic groups (Vizoná et al., 2020). However, there is no obvious biological explanation for the greater number of oocytes recovered in *Bos indicus* (Pontes et al., 2011). Based on this information, we compared the phenotypic values reported in this work only with those of *Bos indicus* animals.

For VO, the values of our work are higher than the reports of 15.6 ± 12.7 by Perez et al. (2017b) for the Guzerá breed, and of 12.39 ± 10.04 by Vizoná et al. (2020) for dairy Gir breed. Results for VE are similar to those of Vizoná et al. (2020), 4.59 ± 4.64 , and lower than the values of Perez et al. (2017b), 6.1 ± 5.7 . For the CE trait, values of 12.2 ± 10.0 (Perez et al., 2017b) are similar to the mean, but with greater standard deviation. None of these authors worked with TO, but it is likely that this value would be a little higher than the value of VO, both on average and in standard deviation. In general, these reported differences are not of great magnitude.

4.2. Selection criteria

Among the sixteen models tested, only two of them were best for fit using AIC and BIC criteria, thus forming two pairs of traits evaluated by each model, TO and VO by the 4G1P model and CE and VE by the 3G1P model, which indicates subtle differences between traits, that is, only one more degree to adjust the genetic effect.

More parameterized models usually adapt better to the data. However, this greater parameterization increases the computational demands and often does not substantially alter the result. The use of criteria that penalize more parameterized models and that give preference to more parsimonious models is indicated. In the case of traits studied in this paper, the use of a greater number of regressors for the additive genetic effect was indicated. In other traits, such as milk yield, some studies point to the need to use a greater number of coefficients to model the permanent environmental effect, compared with additive genetic effect (Canaza-Cayo et al., 2015).

4.3. Heritability

For all traits, using RRM, the h^2 curve along the age presented a "U" shape. Usually, only a few records were collected at extreme ages as presented in Figure 1, and higher h^2 values at the beginning and end of the curve may be related to the number of records (Meyer, 1999).

Heritability for TO reported in the literature ranges from 0.13 in Holstein cattle raised in United States (Parker Gaddis et al., 2017) to 0.31 also in Holstein raised in the Netherlands (Cornelissen et al., 2017). These values are below those reported in this study, for both 1G1P and 4G1P models, indicating that this trait will respond more quickly to selection in the Gir than in Holstein herds. The use of RRM (4G1P) could also respond more quickly to the selection than the repeatability model (1G1P).

For VO, h^2 ranges from 0.16 to 0.25 in Brazilian Guzerá breed depending on the type of distribution used (Perez et al., 2017b). Using a Bayesian model with Poisson distribution, Vizoná et al. (2020) reported h^2 of 0.32. In studies using information from MOET (multiple ovulation and embryo transfer), e.g., Merton et al. (2009) and Perez et al. (2017a), there can be a pre-selection of animals that will be subjected to collection, which can result in lower h^2 (Vizoná et al., 2020).

In the case of CE, h^2 varies between 0.10 (Parker Gaddis et al., 2017) and 0.23 (Perez et al., 2017b), and in the case of VE, it varies from 0.10 (Perez et al., 2016) to 0.56 (Peixoto et al., 2004). According to Merton et al. (2009) and Cornelissen et al. (2017), the h^2 for TO is higher than the h^2 for CE and VE. Comparing the estimates between the traits, the VE has the lowest h^2 , which must be because this trait has a large number of non-genetic factors that can influence the result and affect service sire (Vizoná et al., 2020).

The higher h^2 recorded for the population of this study, compared with most of the works reported in the literature, are probably related to the fact that the farms present similar conditions, are located in the same region, and have the same technical support and animal husbandry techniques that standardizes management and highlights genetic differences between animals.

4.4. Repeatability

The R estimates were similar between the models for each trait in intermediate ages. The highest values recorded in the initial and final periods are due to the higher estimates of the genetic variance in these months, which is related to the ability of the Legendre polynomials to make predictions in the ends of the curve and the number of ovum pick-up in that period.

The R for TO at intermediate ages at measurement was close to that reported by Parker Gaddis et al. (2017) for Holstein donors, but in general, it was higher than that reported in other works in the literature. The R values for VO, except in the final period, was close to that reported by Perez et al. (2017b) for Guzerá breed using a Bayesian model that considered Poisson distribution for data.

The R for CE was also within the values reported in the literature, except after the 120th month of age at ovum pick-up. Perez et al. (2017b) reported R of 0.60 for this trait when using a Bayesian model, and Peixoto et al. (2004) reported R of 0.47 for Nellore donors when using untransformed data.

For these traits, these R estimates can be explained by the high R of the number of follicles per follicular wave (Jaton et al., 2016b). A study on the average number of follicles per single donor wave reported an extremely high R of 0.89 (Ireland et al., 2007). Due to the dependency relationship between the production of embryos and the number of follicles, it makes sense that the number of embryos per procedure can also be repeated in a donor (Jaton et al., 2016b).

The R is a useful tool for quantifying the extent to which an individual's performance remains consistent over time. The high R reported for oocyte and embryo count traits indicates that donors, which had high counts of oocytes and embryos in the first ovum pick-up, should maintain this result in the next ovum pick-up. Therefore, donors can be selected after the first ovum pick-up, with special attention to puncturing young females (even in pre-puberty); this procedure should give good indications of life potential of these animals (Vizoná et al., 2020).

4.5. Genetic and permanent environment correlation

Positive and high genetic correlations indicate that the selection to increase oocyte or embryo production at each age at measurement may have a positive influence on oocyte and embryo production at another age at ovum pick-up.

The production of oocytes and embryos in cows at ages at ovum pick-up between 84 and 96 months was positively correlated with all other ages, and in some cases, this association varied from moderate to weak, allowing us to infer that the period between 84 and 96 months is more appropriate to carry out the selection of animals due to the possibility of a greater correlated response than in other periods. However, to accelerate the genetic gain, the selection should be carried out at ages at ovum pick-up under 12 to 48 months, prioritizing genetic gains at the beginning of the cow's productive life.

In distant periods, such as 12 and 144 months, low correlations have been reported, and in some cases even negative, -0.19 , for TO. These correlation values are not expected in biological terms, but have already been reported for other traits and have been attributed to the poor fit of the RRM using Legendre polynomials at the extreme points of the curve, which is probably associated with the lower number of observations during these periods (Meyer, 1999).

In Brazilian dairy Gir cattle, negative genetic correlations between the initial and final periods of lactation were reported by Pereira et al. (2010) and Pereira et al. (2013), both stating that these correlations are not biologically expected. Results like this may be related to a pre-selection, in which animals had productions registered. Kern et al. (2018) reported that within a herd, not all animals are evaluated for type-traits in Brazil, so some kind of bias can be found in genetic evaluation. Another important factor is the extent of the period evaluated for counting oocytes and embryos, 132 months, a much longer period than the lactation period, which is usually 305 days (or 10 months). This long

period can explain, in part, these correlations, but it makes it difficult for comparisons with small periods. However, this large period that has been evaluated demonstrates that there is considerable variation over time, especially when it comes to the genetic component that affects these traits, and this variation should not be overlooked.

The genetic correlations between the traits of oocyte and embryo production are high and positive, e.g., genetic correlation between number of VO and CE of 0.90, VO and VE of 0.72, and between CE and VE of 0.79 in animals of the Guzerá breed (Perez et al., 2016). In animals of the Holstein breed, Parker Gaddis et al. (2017) reported a genetic correlation equal to 1, between the total structures recovered and the number of good embryos estimated from the bivariate analysis, and justified that high correlations were expected because the number of good embryos is a subset of the total number of structures recovered. Thus, high genetic correlations between traits are also expected in the Gir breed, and therefore, it would not be necessary to select for all traits, but for the one with the highest correlations with the others and with greater commercial interest, even though all these traits are routinely collected in the procedure.

4.6. Spearman's rank correlation

Livestock decision-making depends mainly on the level of genetic superiority of the animal, and the correlation between the EBV of different models is an important issue to be considered in an animal breeding program (Perez et al., 2017b).

The differences in magnitude of rank correlations between EBV can be explained, mainly, by the approach of each methodology in modeling productions in each measure (El Faro and Albuquerque, 2005). González Herrera et al. (2008), comparing repeatability model with RRM, reported a ranking correlation of 0.74 for all animals and 0.65 for sires with progeny for 305-day milk yield in dairy Gir cattle.

In Guzerá herds, Santos et al. (2014) reported moderate to high correlations, indicating the possibility of differences in the ranking of animals, once RRM are adopted in place of the conventional model used in the genetic evaluations for milk yield. Variations in ranking correlations are probably due to differences in data consistency requirements, the functions used to adjust random effects, and the fixed effects included in random regression models (Pereira et al., 2019).

Alteration between the rankings of the best animals with the variation in age of ovum pick-up indicates that there is no well-defined relationship between the genes that influence oocyte and embryo production throughout the female's life. For this reason, changes in the choice of sires and donors in different periods must happen, since high selection intensities are used in this case. It is necessary to define only a period on which the selection should be based; the best would be right after puberty to improve these traits in young animals and to shorten the generation interval.

4.7. Reliability

The reliability estimated by the 4G1P and 3G1P models, in some periods, was higher than that estimated by the 1G1P model. In general, for TO, VO, and VE, the highest reliability values were reported in intermediate periods; in the initial and final periods, the reliability of these selected animals was lower, which may be related to the amount of collections that is higher in the intermediate period. In contrast, the reliability for the EBV of CE was higher in the intermediate period until the end.

The replacement of the repeatability model with RRM resulted in an increase in reliability of the EBV for 305-day milk yield (Padilha et al., 2016). In our study, the gains in reliability occurred in the period when the greatest number of collections occurs. In the initial and final parts of the evaluated period, the reliability estimated by the 4G1P and 3G1P models was lower than that estimated by the 1G1P model. The increase in the number of collections (Figure 1) is related to reliability (Figures 5 and 6); therefore, increasing the number of collections in young animals favors the EBV reliability at an early age.

Low reliability values are associated with the lower number of collections in young and older animals, in which a low number of phenotypes can have a negative effect on the reliability of EBV (Gonzalez-Recio et al., 2014). Thus, thinking only about the increase in reliability of the EBV, it could be useful to increase the number of collections in young and in older animals; however, the collection in older animals, which would possibly have lower EBV, would not be viable.

4.8. Expected genetic gain

Although the results indicate that the selection using the 4G1P and 3G1P models would be more efficient to improve of oocyte and embryo production in dairy Gir, mainly in young animals, the lower reliability of the EBV in the initial period may be a factor limiting the use of these models.

The increase in the number of ovum pick-up in young animals is recommended, due to the possibility that reliability is associated with the number of ovum pick-up, which, in future evaluations, using RRM could result in increased EBV reliability in the initial period.

5. Conclusions

The use of a more accurate model that allows an increase in productive gains is of great importance. In this sense, the use of the random regression models to replace the repeatability model in the genetic evaluation of total oocytes, viable oocytes, cleaved embryos, and viable embryos increases the genetic gains in these traits in dairy animals; the same can be expected in other breeds. These traits have high repeatability values, indicating that the same counts must be repeated in different observations for the selection of animals after the first ovum pick-up with precision. The reliability of the estimated breeding value by random regression models is greater in the periods when the greatest number of ovum pick-up occurs; therefore, increasing ovum pick-up in young animals increases the reliability of estimated breeding values at an early age.

Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Conceptualization: G.L. Feltes, R. Negri and J.A. Cobuci. Data curation: G.L. Feltes, F.S.S. Raidan, L.F.R. Feres and V.M.P. Ribeiro. Formal analysis: G.L. Feltes, R. Negri and F.S.S. Raidan. Funding acquisition: J.A. Cobuci. Investigation: G.L. Feltes, R. Negri and F.S.S. Raidan. Methodology: G.L. Feltes and R. Negri. Project administration: J.A. Cobuci. Resources: L.F.R. Feres, V.M.P. Ribeiro and J.A. Cobuci. Software: G.L. Feltes. Supervision: J.A. Cobuci. Visualization: F.S.S. Raidan, L.F.R. Feres and V.M.P. Ribeiro. Writing – original draft: G.L. Feltes. Writing – review & editing: G.L. Feltes, R. Negri, F.S.S. Raidan and J.A. Cobuci.

Acknowledgments

The authors thank the Fazendas do Basa for kindly providing the data for this study and the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) and the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES; Finance Code 001) – Brazil, for partially funding this study.

References

Asada, Y. and Terawaki, Y. 2002. Heritability and repeatability of superovulatory responses in Holstein population in Hokkaido, Japan. *Asian-Australasian Journal of Animal Sciences* 15:944-948. <https://doi.org/10.5713/ajas.2002.944>

- Canaza-Cayo, A. W.; Lopes, P. S.; Silva, M. V. G. B.; Torres, R. A.; Martins, M. F.; Arbex, W. A. and Cobuci, J. A. 2015. Genetic parameters for milk yield and lactation persistency using random regression models in Girolando cattle. *Asian-Australasian Journal of Animal Sciences* 28:1407-1418. <https://doi.org/10.5713/ajas.14.0620>
- Cornelissen, M. A. M. C.; Mullaart, E.; Van der Linde, C. and Mulder, H. A. 2017. Estimating variance components and breeding values for number of oocytes and number of embryos in dairy cattle using a single-step genomic evaluation. *Journal of Dairy Science* 100:4698-4705. <https://doi.org/10.3168/jds.2016-12075>
- El Faro, L. and Albuquerque, L. G. 2005. Predição de valores genéticos para a produção de leite no dia do controle e para a produção acumulada até 305 dias. *Revista Brasileira de Zootecnia* 34:496-507. <https://doi.org/10.1590/s1516-35982005000200017>
- Fleming, A.; Abdalla, E. A.; Maltecca, C. and Baes, C. F. 2018. Invited review: Reproductive and genomic technologies to optimize breeding strategies for genetic progress in dairy cattle. *Archives Animal Breeding* 61:43-57. <https://doi.org/10.5194/aab-61-43-2018>
- Gonzalez-Recio, O.; Coffey, M. P. and Pryce, J. E. 2014. On the value of the phenotypes in the genomic era. *Journal of Dairy Science* 97:7905-7915. <https://doi.org/10.3168/jds.2014-8125>
- González Herrera, L. G.; El Faro, L.; Albuquerque, L. G.; Tonhati, H. and Machado, C. H. C. 2008. Estimativas de parâmetros genéticos para produção de leite e persistência da lactação em vacas Gir, aplicando modelos de regressão aleatória. *Revista Brasileira de Zootecnia* 37:1584-1594. <https://doi.org/10.1590/S1516-35982008000900009>
- Ireland, J. J.; Ward, F.; Jimenez-Krassel, F.; Ireland, J. L. H.; Smith, G. W.; Lonergan, P. and Evans, A. C. O. 2007. Follicle numbers are highly repeatable within individual animals but are inversely correlated with FSH concentrations and the proportion of good-quality embryos after ovarian stimulation in cattle. *Human Reproduction* 22:1687-1695. <https://doi.org/10.1093/humrep/dem071>
- Jamrozik, J. and Schaeffer, L. R. 1997. Estimates of genetic parameters for a test day model with random regressions for yield traits of first lactation Holsteins. *Journal of Dairy Science* 80:762-770. [https://doi.org/10.3168/jds.S0022-0302\(97\)75996-4](https://doi.org/10.3168/jds.S0022-0302(97)75996-4)
- Jaton, C.; Koeck, A.; Sargolzaei, M.; Malchiodi, F.; Price, C. A.; Schenkel, F. S. and Miglior, F. 2016a. Genetic analysis of superovulatory response of Holstein cows in Canada. *Journal of Dairy Science* 99:3612-3623. <https://doi.org/10.3168/jds.2015-10349>
- Jaton, C.; Koeck, A.; Sargolzaei, M.; Price, C. A.; Baes, C.; Schenkel, F. S. and Miglior, F. 2016b. Short communication: Genetic correlations between number of embryos produced using in vivo and in vitro techniques in heifer and cow donors. *Journal of Dairy Science* 99:8222-8226. <https://doi.org/10.3168/jds.2016-11356>
- Kern, E. L.; Cobuci, J. A.; Costa, C. N. and Ducrocq, V. 2018. Phenotypic relationships between type traits and productive life using a piecewise Weibull proportional hazard model. *Scientia Agricola* 75:470-478. <https://doi.org/10.1590/1678-992x-2017-0153>
- Kirkpatrick, M.; Hill, W. G. and Thompson, R. 1994. Estimating the covariance structure of traits during growth and ageing, illustrated with lactations in dairy cattle. *Genetical Research* 64:57-69. <https://doi.org/10.1017/s0016672300032559>
- Lacerda, I. P.; Dode, M. A. N.; Lima, M. M. S.; Guerra, B. F.; Costa, E. S.; Moreira, G. R. and Carvalho, J. O. 2020. Cattle breed affects in vitro embryo production in a large-scale commercial program on dairy farms. *Livestock Science* 240:104135. <https://doi.org/10.1016/j.livsci.2020.104135>
- Merton, J. S.; Ask, B.; Onkundi, D. C.; Mullaart, E.; Colenbrander, B. and Nielen, M. 2009. Genetic parameters for oocyte number and embryo production within a bovine ovum pick-up-in vitro production embryo-production program. *Theriogenology* 72:885-893. <https://doi.org/10.1016/j.theriogenology.2009.06.003>
- Meyer, K. 1999. Estimates of genetic and phenotypic covariance functions for postweaning growth and mature weight of beef cows. *Journal of Animal Breeding and Genetics* 116:181-205. <https://doi.org/10.1046/j.1439-0388.1999.00193.x>
- Meyer, K. and Houle, D. 2013. Sampling based approximation of confidence intervals for functions of genetic covariance matrices. *Proceedings Association Advancement of Animal Breeding and Genetics* 20:523-526.
- Misztal, I.; Tsuruta, S.; Strabel, T.; Auvray, B.; Druet, T. and Lee, D. H. 2002. Blupf90 and Related Programs (Bgf90). In: *Proceedings of the 7th World Congress on Genetics Applied to Livestock Production*. Montpellier, France.
- Moore, S. G. and Hasler, J. F. 2017. A 100-Year Review: Reproductive technologies in dairy science. *Journal of Dairy Science* 100:10314-10331. <https://doi.org/10.3168/jds.2017-13138>
- Padilha, A. H.; Cobuci, J. A.; Costa, C. N. and Braccini Neto, J. 2016. Random regression models are suitable to substitute the traditional 305-day lactation model in genetic evaluations of Holstein cattle in Brazil. *Asian-Australasian Journal of Animal Sciences* 29:759-767. <https://doi.org/10.5713/ajas.15.0498>
- Parker Gaddis, K. L.; Dikmen, S.; Null, D. J.; Cole, J. B. and Hansen, P. J. 2017. Evaluation of genetic components in traits related to superovulation, in vitro fertilization, and embryo transfer in Holstein cattle. *Journal of Dairy Science* 100:2877-2891. <https://doi.org/10.3168/jds.2016-11907>
- Peixoto, M. G. C. D.; Pereira, C. S.; Bergmann, J. A. G.; Penna, V. M. and Fonseca, C. G. 2004. Genetic parameters of multiple ovulation traits in Nelore females. *Theriogenology* 62:1459-1464. <https://doi.org/10.1016/j.theriogenology.2004.02.019>

- Pereira, R. J.; Ayres, D. R.; El Faro, L.; Vercesi Filho, A. E.; Verneque, R. S. and Albuquerque, L. G. 2013. Genetic parameters for production traits of dairy Gyr (*Bos indicus*) × Holstein cattle estimated with a random regression model. *Livestock Science* 158:24-31. <https://doi.org/10.1016/j.livsci.2013.10.003>
- Pereira, R. J.; Ayres, D. R.; Santana Júnior, M. L.; El Faro, L.; Vercesi Filho, A. E. and Albuquerque, L. G. 2019. Test-day or 305-day milk yield for genetic evaluation of Gir cattle. *Pesquisa Agropecuária Brasileira* 54:e00325. <https://doi.org/10.1590/S1678-3921.pab2019.v54.00325>
- Pereira, R. J.; Lopes, P. S.; Verneque, R. S.; Santana Júnior, M. L.; Lagrotta, M. R. and Torres, R. A. 2010. Funções de covariância para produção de leite no dia do controle em bovinos Gir leiteiro. *Pesquisa Agropecuária Brasileira* 45:1303-1311. <https://doi.org/10.1590/S0100-204X2010001100011>
- Perez, B. C.; Balieiro, J. C. C.; Ventura, R. V.; Bruneli, F. A. T. and Peixoto, M. G. C. D. 2017a. Inbreeding effects on *in vitro* embryo production traits in Guzerá cattle. *Animal* 11:1983-1990. <https://doi.org/10.1017/s1751731117000854>
- Perez, B. C.; Peixoto, M. G. C. D.; Bruneli, F. T.; Ramos, P. V. B. and Balieiro, J. C. C. 2016. Genetic analysis of oocyte and embryo production traits in Guzerá breed donors and their associations with age at first calving. *Genetics and Molecular Research* 15:gmr.15027583. <https://doi.org/10.4238/gmr.15027583>
- Perez, B. C.; Silva, F. F.; Ventura, R. V.; Bruneli, F. A. T.; Balieiro, J. C. C. and Peixoto, M. G. D. C. 2017b. Count Bayesian models for genetic analysis of *in vitro* embryo production traits in Guzerá cattle. *Animal* 11:1440-1448. <https://doi.org/10.1017/s175173111700012x>
- Pontes, J. H. F.; Melo Sterza, F. A.; Basso, A. C.; Ferreira, C. R.; Sanches, B. V.; Rubin, K. C. P. and Seneda, M. M. 2011. Ovum pick up, *in vitro* embryo production, and pregnancy rates from a large-scale commercial program using Nelore cattle (*Bos indicus*) donors. *Theriogenology* 75:1640-1646. <https://doi.org/10.1016/j.theriogenology.2010.12.026>
- Resende, M. D. V.; Rezende, G. D. S. P. and Fernandes, J. S. C. 2001. Regressão aleatória e funções de covariância na análise de medidas repetidas. *Revista de Matemática e Estatística* 19:21-40.
- Santos, D. J. A.; Peixoto, M. G. C. D.; Aspilcueta Borquis, R. R.; Panetto, J. C. C.; El Faro, L. and Tonhati, H. 2014. Predicting breeding values for milk yield of Guzerá (*Bos indicus*) cows using random regression models. *Livestock Science* 167:41-50. <https://doi.org/10.1016/j.livsci.2014.05.023>
- Tonhati, H.; Lôbo, R. B. and Oliveira, H. N. 1999. Repeatability and heritability of response to superovulation in Holstein cows. *Theriogenology* 51:1151-1156. [https://doi.org/10.1016/S0093-691X\(99\)80018-1](https://doi.org/10.1016/S0093-691X(99)80018-1)
- Viana, J. H. M.; Figueiredo, A. C. S. and Siqueira, L. G. B. 2017. Brazilian embryo industry in context: pitfalls, lessons, and expectations for the future. *Animal Reproduction* 14:476-481. <https://doi.org/10.21451/1984-3143-ar989>
- Vizoná, R. G.; Perez, B. C.; Peixoto, M. G. C.; Viana, J. H. M.; Ventura, R. V.; Vercesi Filho, A. E. and Balieiro, J. C. C. 2020. Genetic analysis of *in-vitro* embryo production traits in Dairy Gir cattle. *Theriogenology* 148:149-161. <https://doi.org/10.1016/j.theriogenology.2020.02.014>
- Watanabe, Y. F.; Souza, A. H.; Mingoti, R. D.; Ferreira, R. M.; Batista, E. O. S.; Dayan, A.; Watanabe, O.; Meirelles, F. V.; Nogueira, M. F. G.; Ferraz, J. B. S. and Baruselli, P. S. 2017. Number of oocytes retrieved per donor during OPU and its relationship with *in vitro* embryo production and field fertility following embryo transfer. *Animal Reproduction* 14:635-644. <https://doi.org/10.21451/1984-3143-AR1008>