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Estimation of genetic parameters for reproductive traits in multibreed cattle under tropical conditions

Estimación de parámetros genéticos de características reproductivas en ganado bovino multirracial en condiciones tropicales

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ABSTRACT

The estimation of genetic parameters is essential in breeding programs because it allows the development of appropriate selection criteria and prediction of correlated responses. This study aimed to estimate heritability and genetic correlations for age at first service (AFS), calving interval (CI), days open (DO), days to first postpartum service (DPS), gestation length (GL) and services per conception (SC) in multiracial cattle under tropical conditions. The data were analyzed with univariate and bivariate models by the MTDFREML program to obtain the covariance components. The heritabilities obtained were 0, 0.02, 0.03, 0.10, 0.25, and 0.29, for AFS, DO, SC, CI, FPS, and GL, respectively. The estimated genetic correlations were 1.00, 1.00, 0.90, 0.97, 0.79, 0.70, 0.99, -1.00, -0.59, -0.47, -0.36, -0.40, -0.15, -0.06, and -0. 05 for CI-DO, CI-AFS, FPS-CI, FPS-DO, FPS-AFS, GL-AFS, DO-AFS, SC-AFS, GL-CI, FPS-SC, GL-SC, CI-SC, GL-DO, FPS-GL and SC-DO, respectively. The heritabilities for GL, FPS, and CI represent an opportunity to improve these traits through a selection program; conversely, for AFS, DO, and SC the values were close to zero. Genetic associations between different traits simplify the design of breeding programs accounting for correlated responses.

KEY WORDS: Reproductive traits, heritability, genetic correlations, cattle, animal model.

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RESUMEN

La estimación de parámetros genéticos es esencial en programas de mejoramiento, porque permite desarrollar criterios de selección adecuados y predecir respuestas correlacionadas. El objetivo del estudio fue estimar la heredabilidad y correlaciones genéticas para edad a primer servicio (AFS), intervalo entre partos (CI), días abiertos (DO), días a primer servicio posparto (FPS), duración de la gestación (GL) y servicios por concepción (SC) en ganado multirracial en condiciones tropicales. Los datos se analizaron con modelos univariados y bivariados con el programa MTDFREML, para obtener los componentes de covarianza. Las heredabilidades obtenidas fueron 0, 0.02, 0.03, 0.10, 0.25 y 0.29, para AFS, DO, SC, CI, FPS, GL, respectivamente. Las correlaciones genéticas estimadas fueron 1.00, 1.00, 0.90, 0.97, 0.79, 0.70, 0.99, -1.00, -0.59, -0.47, -0.36, -0.40, -0.15, -0.06 y -0.05 para CI-DO, CI-AFS, FPS-CI, FPS-DO, FPS-AFS, GL-AFS, DO-AFS, SC-AFS, GL-CI, FPS-SC, GL-SC, CI-SC, GL-DO, FPS-GL y SC-DO, respectivamente. La heredabilidad para GL, FPS e CI representa una oportunidad para mejorar estas características a través de un programa de selección, contrariamente, para AFS, DO y SC los valores fueron cercanos a cero. Las asociaciones genéticas entre diferentes características facilitan el diseño de programas de mejoramiento genético que consideren las respuestas correlacionadas.

PALABRAS CLAVE: Características reproductivas, heredabilidad, correlaciones genéticas, bovinos, modelo animal.

Introduction

Livestock production is an important industry in many tropical countries, including Mexico (Casanova-Lugo, 2022). Tropical livestock farming is mainly based on grazing and is characterized by limitations in performance measurement and herd record keeping (Cavani *et al*., 2015; Eler *et al*., 2014; Pérez-Lombardini *et al*., 2021). However, due to the global demand for food products, it is important to promote the implementation of sustainable livestock intensification programs in tropical systems, based on genetic improvement (Fernandes Júnior *et al*., 2022). Genetically improving reproductive traits in females can not only increase profitability (König & May, 2019) but can also contribute to the long-term sustainability of the livestock industry (Fleming *et al*., 2019).

Reproductive traits are important indicators of productive efficiency (Stevenson & Britt, 2017). However, in tropical areas, reproductive performance represents a bottleneck for livestock efficiency, which directly affects the sustainability of productive systems (Fernandes Júnior *et al*., 2022). In recent decades, the main objective has been to genetically improve reproductive traits in most countries (Miglior *et al*., 2017; Sullivan *et al*., 2020). Genetic improvement is a key tool to improve the sustainability of livestock production because the results are permanent (Mueller & Eenennaam, 2022). However, most of the reproductive traits evaluated have low heritability (Cavani *et al*., 2015; Lopez *et al*., 2019), but demonstrate genetic variation, indicating good potential for direct selection for these (Miglior *et al*., 2017). Through selection of cows with superior genetic quality, this long-term goal can be achieved (Miglior *et al*., 2017; Martin *et al*., 2022).

The possibility of improving a trait is closely related to the genetic variability present in the population of interest, the greater the genetic variation, the greater the chances of improvement (Gebeyehu *et al*., 2014). Knowledge of genetic parameters is essential to ensure the success of breeding programs (Missanjo *et al*., 2013; Gebeyehu *et al*., 2014). Heritability and genetic correlations are the main genetic parameters required in practical breeding programs (Valsalan *et al*., 2022). Estimates of these parameters allow developing appropriate selection criteria and predicting correlated responses to traits of interest (Oliveira *et al*., 2021). This study aimed to estimate heritability and genetic correlations for gestation length, calving interval, number of services per conception, age at first service, days to first postpartum service, and days open in multiracial cattle under tropical conditions.

Material and Methods

The information was obtained from two herds, the first one located in Hueytamalco, Puebla, Mexico (20°00’10’’ N and 97°18’22’’ W), and the second in Ayotoxco de Guerrero, Puebla, Mexico (20°05’18’’ N and 97°24’46’’ W). The climate is classified as humid subtropical Af(c) (Garcia, 1998; Peel *et al*., 2007). No approval from the Bioethics and Animal Protection Committee was required for this study, as all data were obtained from an existing database.

Data and management

The reproductive traits correspond to 620 cows of Holstein, Brown Swiss, Simmental, and Brahman breeds, and different degrees of crossbreeding between these, born between 1996 and 2017 and calving between 1998 and 2021. Six reproductive traits were analyzed, namely: age at first service (AFS), which refers to the period from birth to the first recorded insemination; days to first postpartum service (FPS), which refers to the number of days elapsed from calving to their first service; days open (DO), represents the span in days from calving to conception; calving interval (CI) is the number of days separating two consecutive calvings in the same cow; gestation length (GL) defined as the number of days between conception and calving; and number of services per conception (SC) which refers to the number of attempts needed to achieve conception.

Cows with AFS between 515 and 1670 d, a GL between 257 and 305 d, an IC between 303 and 977 d, FPS between 22 and 462 d, DO between 22 and 574 d, and SC between 1 and 8 were kept for the final analyses since values outside these ranges may be physiologically abnormal or the result of erroneous recordings. Table 1 shows the descriptive statistics of the characteristics studied. The pedigree was the same for all traits analyzed and consisted of 1309 animals belonging to two generations.

Table 1. Descriptive statistics of reproductive traits in multibreed cattle.

Traits	n	Media	SD	Min	Max
AFS	341	1123.17	241.8	515	1670
CI	1124	480.2	101.22	303	977
DO	1344	173.33	105.16	22	574
FPS	1461	125.94	85.83	22	462
GL	1069	283.52	6.8	257	305
SC	1662	1.97	1.4	1	8

AFS= age at first service; DO= days open; FPS= days to first postpartum service; CI= calving interval; GL= gestation length; SC= number of services per conception; n: number of observations; SD= standard deviation; Min= minimum; Max= maximum.

Source: Authors own elaboration.

Three seasons were considered, corresponding to drought (November-February), rainy (March-June), and windy (July-October). A contemporary group (CG) was defined separately for each trait. For AFS, the CG was formed with herd, year of birth, and season of birth. For DO and FPS, the CG was formed with the herd, calving year, and calving season. For CI and GL, the CG was herd, year of conception, and season of conception. For SC, the CG was herd, year of service, and season of service. For all traits, only CG with at least four animals were retained.

Statistical analysis

Data editing, as well as significance testing of fixed effects added to the model and CG training, were performed in SAS (SAS Institute, 2007). To estimate the variance components and genetic parameters of AFS, DO, FPS, CI, GL, and SC, the following univariate animal model was assumed (equation 1): $y = X\beta + Za + e$, and bivariate (equation 2): $\begin{bmatrix} y1 \\ y2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} * \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} * \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$. Where $y, y1, y2$ are vectors of observations for each one of the different traits. $\beta, \beta1, \beta2$ are fixed effects vectors (CG and cow age at calving on a linear and quadratic form). a, a_1, a_2 are unknown random vectors of direct additive genetic effects. e, e_1, e_2 are unknown random vectors of environmental effects. X, X_1, X_2 are known incidence matrices that relate phenotypic measures to the fixed effects in $\beta, \beta_1 y\, \beta_2$, respectively. Z, Z_1, Z_2 are known incidence matrices that relate records to additive genetic effects on $a, a_1\ y\ a_2$, respectively. The additive and residual genetic effects were assumed to be normally distributed with a mean of 0. For AFS, DO, FPS, CI, GL, and SC, the following structure of expected values (E) and (co) variances were assumed (equation 3):

$E\begin{bmatrix} a \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$, y $V\begin{bmatrix} a \\ \mathrm{e} \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 \\ 0 & I_n\,\sigma_e^2 \end{bmatrix}$. Where A is Wright's matrix of additive relationships among all animals in the pedigree, σ_a^2 is the additive genetic variance, σ_e^2 is the variance of the time environment, and I_n is an identity matrix of dimension equal to the number of cows and the number of observations.

Crossbreeding effects were included in the model as the direct breed effect, which was expressed as the percentage of the Holstein breed, the heterozygosity coefficient (equation 4): $HT = P_D * (1 - P_D) + P_D * (1 - P_S)$, and the recombination loss coefficient (equation 5): $RC = P_S * (1 - P_S) + P_D * (1 - P_D)$, for each European breed separately. Where PS and PD are the proportions of Holstein in the sire and dam, respectively. (Akbas *et al*., 1993; Román-Ponce *et al*., 2013).

Variance component estimation

Variance estimates were performed using the Derivative-Free Restricted Maximum Likelihood approach (Smith & Graser, 1986) through the MTDFREML software (Boldman *et al*., 1995). Convergence was assumed to be reached when the variance of minus two times the log-likelihood in the simplex was less than 10^{-8}. After the program reached initial convergence, several restarts were performed to ensure that a global maximum was obtained. In each subsequent iteration, the parameter estimators obtained in the previous analysis were used as initial values. The solutions corresponding to the random effects were derived from the last iteration cycle in which the global maximum was achieved.

Genetic parameter estimators

Estimators were obtained for phenotypic variance ($\sigma_p^2 = \sigma_a^2 + \sigma_e^2$), heritability for additive genetic effects ($h^2 = \sigma_a^2 / \sigma_p^2$), and residual variance as a proportion of phenotypic variance ($e = \sigma_e^2 / \sigma_p^2$). Standard errors of genetic parameter estimators were approximated and were calculated using the average information matrix and the Delta method (Dodenhoff *et al*., 1998), in both univariate and bivariate models (Johnson & Thompson, 1995).

Results and Discussion

Heritability (h^2) is considered one of the most important concepts for planning and establishing successful breeding programs since it represents the proportion of variation in the expression of a phenotype that is attributed to additive genetic factors. Variance components and estimated heritability's for reproductive traits using a univariate model are presented in Table 2. In general, the heritability for the different traits ranged from 0 to 0.29.

A heritability of 0.29 was estimated for GL, this result is higher than 0.14 (0.01) reported by Lopez *et al*. (2019), calculated from 49,748 observations in Hanwoo cattle in South Korea. On the other hand, Kumar *et al*. (2016) notified 0.24 ± 0.08 in multiracial cattle in India, a value similar to the present study. However, Domínguez-Castaño *et al*. (2021) mentioned a lower value (0.11 ± 0.02) from Holstein cows, in Brazil. Inoue *et al*. (2020) informed 0.11 ± 0.03 in Japanese black cattle, however, this value was estimated with data from the first calving. In fact, Zhu *et al*. (2024) noted a different heritability value for gestation length in cows (0.12 ± 0.01) and heifers (0.04 ± 0.03) of Holstein in China.

The estimated heritability for FPS was 0.25; a value that is higher than those reported in previous studies with Holstein (0.057 ± 0.011) and Nordic Red (0.049 ± 0.011) cattle from Denmark, Finland, and Sweden (Muuttoranta *et al*., 2019). Also, in Holstein cattle (0.10 ± 0.008) from China (Liu *et al*., 2017) and in Holstein, Brown Swiss, and Simmental cattle (0.10, 0.10, and 0.08, respectively) from northeastern Italy (Martinez-Castillero *et al*., 2020). However, Muuttoranta *et al*. (2019) suggest that reproductive performance between heifers and cows should not be considered in a joint analysis, but should be differentiated (Þórarinsdóttir *et al*., 2021; Liu *et al*., 2017; Muuttoranta *et al*., 2019). However, in the this study, this differentiation could not be considered due to the limited number of available observations. Likewise, in the study of Muuttoranta *et al*. (2019) a more restricted range of SPF was used, retaining only data between 20 and 230 days and fixing those values above 181, at 180 d. Whereas in this study all values that were between 22 and 462 days postpartum were considered, so this difference in the selection of the range of SPF could have generated variation in heritability estimates.

Table 2. Variance components and heritability estimates of reproductive traits of multiracial cattle under tropical conditions, estimated using univariate models.

Traits	σ_a^2	σ_{pe}^2	σ_p^2	$h^2(ee)$
AFS	0.10	517338.73	517338.83	0 (0.00)
CI	913.19	8633.47	9546.66	0.10 (0.3)
DO	3867.32	219659.88	223527.20	0.02 (0.015)
FPS	1636.79	5025.90	6662.70	0.25 (0.03)
GL	12.66	31.57	44.23	0.29 (0.03)
SC	1583.46	45516.31	47099.77	0.03 (0.017)

σ_a^2: additive genetic variance; σ_{pe}^2: permanent environmental variance; σ_p^2: phenotypic variance; h^2: heritability; *ee*: standard error; AFS: age at first service; DO: days open; FPS: days at first service; CI: calving interval; GL: gestation length; SC: number of services per conception.

Source: Authors own elaboration.

The estimated heritability for CI was 0.10 (0.3), a value similar to that reported for Brahman cattle in Colombia (0.11 ± 0.03) (Duitama *et al*., 2013). In that study, the estimated heritability was for the interval between the first and second calving, while for the present study, all records of intervals between one and eight calvings were considered together, which could explain the differences in the results obtained. In another study, with multiracial cattle, the h^2 for CI was estimated to be 0.20 (Kumar & Mandal, 2021), which is twice the heritability estimated in the present study. In more recent research, h^2 values of 0.04 (0.05) have been reported in Simmental cattle from Colombia (Amaya *et al*., 2020) and 0.02 (0.01) in Hanwoo cattle from Korea (Lopez *et al*., 2019), the latter estimated from a much larger database with 32,599 CI records. The present study has a limited database, with information from only 620 cows and 1124 CI records.

The estimated heritability for SC was 0.03. This estimate is lower than 0.11 (0.03) reported in zebu cattle from Cuba by Palacios *et al*. (2019) but is similar to 0.02 (0.002) reported in Brahman cattle in Brazil (Cavani *et al*., 2015). Importantly, Cavani *et al*. (2015) attributed the low heritability estimate to the low number of observations available for this trait. Recently, Þórarinsdóttir *et al*. (2021) reported heritability of 0.01 (0.005) and 0.02 (0.008), based on data from heifers and cows up to three calvings, respectively. The heritability estimated in the present study is within this range of values reported by Þórarinsdóttir *et al*. (2021), considering that no distinction was made between heifers and cows in the present study.

The estimated heritability for DO was 0.02 (0.015), a value similar to 0.02 (0.01) reported by Lopez *et al*. (2019) in Hanwoo beef cattle in South Korea, estimated on 15,355 reproductive data collected between 1997 and 2016. However, it is lower than 0.04 (0.004) reported in Holstein cows in Iran (Solemani-Baghshah *et al*., 2014) and 0.09 (0.121) obtained from a database with different cattle breeds (Holstein Friesian, Sahiwal x Friesian, Jersey, Jersey x Achai and Achai) under subtropical conditions in Pakistan (Ali *et al*., 2019), both previous studies used data from dairy cows as in the present study, even so, their heritability is higher. Higher values than these (0.09 ± 0.12) have also been obtained in Multiracial cattle under subtropical conditions of Pakistan (Ali *et al*., 2019) and in Karan-Fries cattle (0.07 ± 0.02) from Karnal, India (Worku *et al*., 2021). Likewise, a heritability of 0.10 (0.03) was estimated in Zebu cattle in Cuba, but using a large database with 55, 220 calving records from 21,909 cows (Palacios *et al*., 2019), much higher than the number of data used in this study. In addition, it was shown that combining a trait with a high level of heritability, such as weaning weight, with a reproductive trait, can have significant benefits since it increases the heritability values and, thus, more accurate genetic values are obtained (Fernandes *et al*., 2015; Palacios *et al*., 2019), and it is even proposed as a way to improve genetic evaluations of reproductive traits (Johnston, 2014). In another study, Lopez *et al*. (2019) reported a heritability of 0.02 ± 0.01, in Hanwoo cattle from South Korea, and Kumar & Mandal (2021) reported 0.14 in multiracial cattle from West Bengal, India.

AFS is an indicator of age at puberty; however, the heritability obtained through univariate analysis was 0 (0.00). This result is lower than reported by Gathura *et al*. (2020) in a meta-analysis of genetic parameters in beef cattle. The meta-analysis included data published between 1986 and 2018 on 32 breeds in tropical areas, and an average heritability of 0.03 (0.04) was reported. Comparatively, Ríos-Utrera *et al*. (2013) reported a heritability of 0.31 (0.152), which is considered high, in reproductive traits; it is important to keep in mind that these authors analyzed calving interval in months, unlike the present study where it was analyzed in days. This factor could have influenced the heritability estimation since the interval in days provides greater variability. Therefore, the change in the magnitude of heritability is not an indication of a real change in the genetic influence on the variation of the variable, but rather a consequence of the scale of the variable.

The type of model used, whether univariate or multivariate, can have an impact on the estimation of heritabilities. Univariate analysis considers a single trait at a time, whereas multivariate analysis involves two or more traits simultaneously. The use of multivariate analysis may be advantageous in allowing the estimation of genetic correlations between related traits, which can result in more accurate heritability estimates. However, it can also introduce complexity into the analysis and require a larger number of data to obtain reliable estimates. Therefore, it is important to consider the type of model used when interpreting and comparing heritability estimates in different studies (Domínguez-Castaño *et al*., 2021). Table 3 presents the heritabilities obtained through the bivariate model in the present study.

Heritabilities increased for all traits. This could be due to the unbalanced number of observations between the traits analyzed, e.g., for AFS there are 341 data vs. 1662 for SC. On the other hand, Worku *et al*. (2021) report heritabilities of 0.07 ± 0.02 and 0.06 ± 0.01 for DO and IC, respectively, estimated from a multivariate model. It is important to note that few and especially current studies, perform h^2 estimations through multivariate models using only reproductive traits.

For example, Ali *et al*. (2019) report heritability of 0.09 (0.121) and 0.14 (0.211) for DO and CI, respectively. The values are approximate to those estimated in this study, but, as well as this one, the vast majority analyze reproductive traits in conjunction with growth traits (Amaya *et al*., 2020; Eler *et al*., 2014; Palacios *et al*., 2019), related to milk production and traits (Ali *et al*., 2019; Recinos *et al*., 2017) and even with survival traits (Heise *et al*., 2018) and new reproductive traits (Martin *et al*., 2022). On the other hand, estimating genetic correlations between reproductive traits is of utmost importance, especially when seeking to know joint behavior with easily measured traits (Júnior *et al*., 2018). Genetic and phenotypic covariances between reproductive traits are presented below (Table 4).

Table 3. Variance components and heritability estimates of reproductive traits in multiracial cattle under tropical conditions, estimated using a bivariate model.

Traits	σ_a^2	σ_{pe}^2	σ_p^2	$h^2(ee)$
AFS	1154.79	8894.42	8700.02	0.09 (0.25)
CI	613.33	6841.70	7009.72	0.26 (0.10)
DO	1317.21	7930.80	9177.99	0.13 (0.03)
FPS	2349.16	4222.24	6571.39	0.34 (0.17)
GL	652.82	629.15	1281.97	0.47 (0.25)
SC	0.13	1.51	1.64	0.08 (0.08)

σ_a^2: additive genetic variance; σ_{pe}^2: permanent environmental variance; σ_p^2: phenotypic variance; h^2: heritability; *ee*: standard error; AFS: age at first service; DO: days open; FPS: days at first service; CI: calving interval; DL: gestation length; SC: number of services per conception.

Source: Authors own elaboration.

Table 4. Genetic (above diagonal) and phenotypic (below diagonal) covariances between reproductive traits of multi-breed cattle under tropical conditions, estimated using a bivariate model.

Traits	AFS	CI	DO	FPS	GL	SC
AFS		9.69	8.65	2100.94	34.69	-19.99
CI	9087.03		1629.62	1107.78	-128.70	-17.94
DO	ne	8230.37		1465.66	-17.13	-0.74
FPS	6413.06	4185.47	5432.17		-8.33	-7.37
GL	13.06	-198.91	3.76	-14.25		-0.44
SC	52.35	49.34	60.07	-12.49	-0.13	

AFS: age at first service; DO: days open; FPS: days at first service; CI: calving interval; GL: gestation length; SC: number of services per conception; ne=not estimated.

Source: Authors own elaboration.

The estimation of covariances allows quantifying the degree of relationship between the characteristics being evaluated, and the genetic correlation can be estimated through the covariances. Table 5 shows the genetic correlations between reproductive traits.

In general, genetic correlations between traits are between -1.0 to 1.0. Strong positive correlations were observed between CI and DO (1.00) and with AFS (1.00), indicating that as DO increases, CI will also increase, and as AFS increases, DO will also increase. This is understandable, as the calving interval also includes the days from calving until a new gestation is achieved, similarly Worku *et al*. (2021) reported 0.99 ± 0.00, between CI and DO. High genetic correlations indicate that both traits may be regulated by a similar gene number (Easa *et al*., 2022).

Table 5. Estimators of genetic correlations and standard error (in parentheses) between reproductive traits of multi-breed cattle under tropical conditions.

Traits	DF	CI	SC	DO	AFS
FPS	-0.06 (0.13)	0.90 (0.42)	-0.47 (0.22)	0.97 (037)	0.79 (1.91)
GL		-0.59 (0.77)	-0.36 (0.21)	-0.15 (0.16)	0.70 (0.09)
CI			-0.40 (0.25)	1.00 (0.46)	1.00 (ne)
SC				-0.05 (0.21)	-1.00 (1.52)
DO					0.99 (ne)

AFS: age at first service; DO: days open; FPS: days at first service; CI: calving interval; GL: gestation length; SC: number of services per conception; ne=not estimated.

Source: Authors own elaboration.

The genetic correlation between SC and AFS is also strong but negative (-1.00), indicating that as AFS increases, SC will decrease. From a physiological point of view, this is consistent, as a mature female is more likely to become pregnant, especially in tropical conditions, where young females rarely reach the desired body size and therefore require more time to reach maturity.

SPF showed a strong positive correlation with CI (0.90), DO (0.97), and AFS (0.79). These results are convenient, as it implies that as SPF decreases, DO also decreases, which in turn leads to a decrease in calving interval. The result obtained is consistent with the value of 0.7 reported by Liu *et al*. (2017) in a previous study conducted on Holstein cattle in China. The genetic correlation between AFS and FPS (0.79) indicates that as the female increases the age at first service the days to first service after calving also increases.

GL also had a moderate negative correlation with CI (-0.59), indicating that as CI increases GL decreases, however, negative correlations of low magnitude (-0.02) have also been reported (Lopez *et al*., 2019). The strong positive genetic correlation of AFS and GL (0.70) indicates that the lower the AFS the lower the GL. The genetic correlations of SC were moderate and negative with FPS (-0.47), GL (-0.36), and CI (-0.40), these correlations indicate that the lower the FPS, GL, and CI, the higher the number of services needed to get a cow pregnant. The results seem logical, since the greater the number of days to first service after calving, the longer the time for the reproductive tract to recover properly after parturition and be ready for a new gestation. The results of Þorarinsdóttir *et al*. (2021) show a genetic correlation of 0.56 between SC and CI, which is similar in magnitude, but different in direction with respect to the results (-0.40). Similarly, genetic correlations ranging from moderate and positive (0.35) according to Liu *et al*. (2017), to weak and negative (-0.17) according to Þorarinsdóttir *et al*. (2021), between FPS and SC have been reported in previous studies. Weak and negative correlations were also estimated between DO and GL (-0.15), and close to zero for DO and SC (-0.05) and GL and FPS (-0.06). The genetic correlation of DO and GL is similar in direction, but lower in magnitude than -0.03 ± 0.0) reported by Domínguez-Castaño *et al*. (2021) in Holstein cattle in Brazil.

When an inappropriate asymptotic approximation is employed, especially in small sample sizes, the sample variance is likely to show a bias (Thai *et al*., 2013), which potentially could have influenced the estimates made in this study, particularly in cases where features had a limited number of data, as in the case of AFS. However, it is still unclear what amount of data constitutes a sufficiently large sample size (Walsh & Lynch 2018). In many instances, not enough data are available to meet the conditions necessary for optimal likelihood estimates, yet parameter estimates are critical for genetic improvement of reproductive traits (Roy *et al*., 2024). On the other hand, it should always be considered that variance components and heritabilities are simply estimation points of the population under study (Rameez *et al*., 2022). In fact, if the results of the present study are compared with values reported in the scientific literature, it can be observed that the values of genetic parameters are heterogeneous, this is attributed to the fact that they are obtained from different locations, variable sample sizes, and by distinctive estimation methods (Akanno *et al*., 2013; Ndung'u *et al*., 2020), as well as by effects of biological variations among different populations (Zhang & Schumacher, 202). Still, being a population parameter, estimates have a direct impact on genetic progress within the population under study (Gathura *et al*., 2020).

Conclusions

The heritabilities obtained for GL, FPS, and CI are considered moderate, which represents an opportunity to improve the reproductive traits through a selection program, while for SC, DO, and AFS the heritabilities values found are considered low and would imply a lower response to selection. Genetic correlations between reproductive traits make it feasible to propose genetic improvement programs that can consider the different traits studied simultaneously. It is recommended to estimate the genetic values of the animals and observe their correlated response to selection.

Authors' contribution

Conceptualization of the work, LAGB, VVEM; methodology development, LAGB; software management, LAGB, VEVM; experimental validation, JAVC, ORLO, JPZM, RCCR, ARU, MMB, GMV; analysis of results, LAGB, VEVM; data management, LAGB, VEVM, ARU; manuscript writing and preparation, LAGB, JAVC; drafting, revising and editing, LAGB, VEVM, JAVC, ORLO, JPZM, RCCR, ARU, MMB, GMV; project manager, VEVM, JAVC; fund acquisition, VEVM, JPZM, RCCR, ARU, MMB, GMV.

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Conflict of interest

The authors declare that they have no conflicts of interest.

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