



Genetic parameters, correlations and trends of reproductive traits in Holstein cattle from Mexico



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Abstract:

The objective was to calculate the parameters, correlations and describe the genetic trends of reproductive traits in Holstein cattle from Mexico in three different periods of time, in females born between 2006 and 2019, using records of the Mexican Holstein association. The reproductive parameters calculated were: calving to first insemination interval (CFI), number of services per conception (NSC), days open (DO), interval between calving (IBC),

and age at first calving (AFC). The components of variance were estimated using restricted maximum likelihood in an animal model, to calculate genetic parameters (narrow-sense heritability (h^2), repeatability (r) and genetic correlations) and phenotypic correlations. Additive genetic variances and genetic values were also estimated in three periods of time (P1: 2006-2009, P2: 2010-2013 and P3: 2014-2017). The calculated heritabilities were from 4 to 9 % and the repeatabilities from 8 to 9 %, values close to previous reports for fertility traits. Phenotypic correlations were positive for almost all reproductive parameters and genetic correlations were positive over a wide range (0.13-0.99). Analyses by period showed changes, possibly derived from the influence of the import and use of germplasm from foreign bulls (mainly from the United States of America and Canada) which implement genomic selection and include fertility traits. The present research has made it possible to update the information on reproductive and genetic parameters in fertility traits that can be incorporated into national genetic evaluations.

Keywords: Reproductive traits, Holstein cattle, Genetic parameters, Heritability, Repeatability.

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Introduction

In domestic animals such as cattle, the study of reproduction is based on records of the reproductive events of herds, including dates of birth, insemination and calving, with which it is possible to calculate reproductive parameters (RPs)^(1,2). Examples of RPs are the days from calving to first service/insemination, the percentage of conception at first service, the interval between calvings, the days from calving to conception, the number of services per conception and the age at first calving, which may be correlated with each other^(3,4). The reproductive parameters that are used for the study of cow fertility differ between countries^(3,5).

In dairy cattle of the Holstein breed, there are several reports published worldwide on a reduction in fertility from the 80s to the early 2000s^(6,7), apparently due to the genetic improvement of milk production^(7,8), which is related to a negative genetic correlation reported between fertility and milk production^(9,10).

For dairy farmers, a reduction in fertility causes significant losses and economic impacts^(10,11). By requiring a greater number of inseminations for a cow to become pregnant, insemination costs increase and the interval between calvings lengthens^(7,9), decreasing the average milk production of the herd, as well as the number of calves per cow^(10,11). Likewise, fewer cows will become pregnant within the required period, which increases the “involuntary disposal” or slaughter of the cow due to low fertility^(10,11), increasing costs due to an additional replacement animal is bought or raised in the farm^(11,12).

Therefore, the fertility and the beginning of the productive life of the cow are priority factors in the lifetime productivity of dairy cattle^(2,12). Their study is important for the future profitability of production systems and reduction of slaughter generated by deficient fertilities^(9,11).

To increase milk production in cattle, genetic selection has been used, with methodologies developed and implemented from phenotypic and genealogical records^(13,14). For a little over 20 yr, the use of genome-wide genetic markers, such as single-nucleotide polymorphisms (SNPs), has been proposed to aid selection, through genomic selection (GS)⁽¹⁵⁾, first used in Holstein cattle from the United States in late 2009⁽¹⁶⁾.

For several generations in countries such as the United States of America and Canada, fertility traits in Holstein cattle have been evaluated and improved^(16,17), and the use of GS resulted in an increase in the rate of improvement, despite being generally low heritable traits^(16,17) and the possible impact that this selection has had on the genetic parameters and values of populations that import germplasm from these countries, such as Mexico, is not known. On the other hand, in Mexico there are few works with the aim of studying genetic aspects of fertility traits^(18,19,20), despite their high economic and functional impact on Mexican herds.

Therefore, the objective of the present study was to calculate the parameters, correlations and describe the genetic trends of reproductive traits in Holstein cattle from Mexico in three different periods of time.

Material and methods

Data and reproductive parameters analyzed

This study included 415,859 reproductive records of Holstein cows (*Bos taurus taurus*) that had information on milk production, insemination events (artificial (AI) or natural mounting

(NM)) and calving, occurred between January 2006 and December 2019; information provided by the Holstein association of Mexico.

The RPs calculated and included in the present study were: calving to first insemination interval (CFI), measured as the days elapsed between calving and the first service/insemination; number of services per conception (NSC), it corresponds to the number of services/inseminations until gestation; days open (DO), are the days elapsed between the calving and the new gestation of the cow, the interval between calvings (IBC), measured as the number of months between two consecutive calvings, and finally, the age at first calving (AFC), which corresponds to the recorded age on which each cow has its first calving. The first four RPs together indicate the ability of cows to conceive and restore the estrous cycle; and the ability of farmers to detect estrus and insemination⁽⁵⁾. The last RP (age at first calving) is a measure of the female calf's ability to grow and conceive at an early age.

To ensure the quality of the data of the RPs studied, biologically feasible limits were applied to prevent the use of misinformation (outliers), considering the values reported by the International Bull Evaluation Service (INTERBULL)⁽²¹⁾. Thus, the following records were excluded: days from calving to first service < 20 or > 365 d, when the number of services per conception was greater than 10, when the days open were <20 or > 365, when the intervals between calving were outside the range of 290 to 762 d and when the age at first calving was <18 or > 40 mo, the descriptive statistics of the variables studied are shown in Table 1. After quality control, the dataset consisted of 202,545 records for CFI and NSC; 194,816 records for DO; 139,901 for IBC and 103,467 for AFC. The pedigree files included between 103,467 and 202,545 animals, depending on the trait evaluated and included up to three generations of ancestors of animals with reproductive records.

Estimation of variance components

The variance components for CFI, NSC, DO and IBC were estimated with a repeatability animal model, separately for each characteristic to take advantage of as much information as possible. In the animal model, the availability of individual records allows the prediction of genetic values for all individuals in the population (even if they do not have phenotypic information but genealogical information). The genetic values are calculated with the best linear unbiased predictor, with a mixed equation model (equation 1)⁽¹³⁾, where the random effect refers to the animal that has records and its ancestors, and the fixed effects are all those environmental effects, such as the year of birth⁽¹⁴⁾.

In order to control sources of variation other than those studied in the models of the RPs, the following were included as fixed effects: the subclasses of herd/year/season of calving or herd-year season of birth for AFC, with four seasons defined according to the month of calving (January to March, April to June, July to September and October to December); the level of production (classified into four levels for all farms from 1 to 4, seeking to assign cows to the quartile that describes their level of production within their herd/year/season of calving, with 1 being the one with the lowest production and 4 being the one with the highest production); the number of calving (grouping cows with four lactations or more in a single class) and age at calving. The animal and the cow's permanent environment were included as random effects. In the case of AFC, there was no permanent environment.

The general animal model used was:

$$y = Xb + Zu + e \quad \text{[equation 1]}$$

Where:

y=variable of interest (vector of records of: CFI, NSC, DO, IBC, AFC);

b= vector of fixed effects (herd-year-season of calving (hys) or herd-year season of birth (hysb) for AFC, production level (pl), number of calving (noc) and age at calving (ac));

u= vector of random effects (effect of animal and permanent environment when applicable);

X= incidence matrix that relates observations to fixed effects;

Z= incidence matrix that relates observations to random effects (animal and permanent environment);

e= vector of the effects of the error or residuals.

No transformations of the studied variables were performed because previous studies⁽¹²⁾ showed that they are not necessary. Estimates of variance components were made by means of restricted maximum likelihood⁽²²⁾, using the BLUPF90 software⁽²³⁾.

Multivariate analyses

In order to estimate the genetic covariances and correlations for each pair of traits, bivariate analyses were performed using the models described above.

The general model used was:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} u_1 \\ u_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

where subindices 1 and 2 identify the pair of traits to be evaluated (CFI, NSC, DO, IBC, AFC) with their respective fixed and random effects.

Genetic parameters and correlations

Narrow-sense heritabilities (h^2), repeatability (r) and genetic correlations⁽²⁴⁾ between the RPs were obtained based on the estimates of the variance components using the BLUPF90 software⁽²³⁾. Standard deviations of the estimated parameters were approximated based on their expectations using the REMLF90 software⁽²³⁾.

Analysis by periods (additive genetic variance and genetic values)

Taking into consideration that the import of germplasm from different countries worldwide, especially from the United States and Canada, has been increasing in recent years, representing almost 80 % of the bulls used in the population studied, as well as changes in the values of the reproductive parameters of these countries (due to the introduction of genomic information in the evaluation and selection processes since 2009), data were grouped into three periods, each of four years (P1: 2006-2009, P2: 2010-2013 and P3: 2014-2017). In the first period, selection was considered to be based on pedigree, which uses information from the records of cows and their relatives. In the second period, the incorporation of genomic information into the selection began. In the third period, it is considered that genomic selection is established, and with it the possibility of increasing the accuracy of evaluations of low heritability traits.

Results and discussion

Reproductive parameters

The average for CFI was 71.5 d, which could indicate that the first inseminations are being carried out between 10 and 30 d after the restoration of the estrous cycle (21 d) and the subsequent voluntary waiting period (usually 40 d). In comparison, measurements made in different countries reported averages ranging from 70 to 93 d (Table 1).

Table 1: Descriptive statistics of reproductive parameters in Holstein populations, including those of the present study

Author	Country	CFI	NSC	DO	IBC	AFC
		$\bar{x} \pm SD$				
29	USA	87.6 ± 26	-	109.2 ± 38	-	33.6 ± 12.1
6	USA	-	-	131.5	-	-
26	CAN	80.2	1.66	108.4	-	-
34	USA	-	-	-	-	27.2 ± 3.3
36	USA	70.5 ± 26	-	-	-	-
36	USA	91.5 ± 40	-	-	-	-
31	ITA	84.5 ± 37	1.7 ± 0.1	-	413.5 ± 82	-
12	ESP	81 ± 28	1.9 ± 1.2	117 ± 57.1	400 ± 60	-
33	MEX	-	-	-	406 ± 67	27.6 ± 2.9
33	USA	-	-	-	401 ± 62	27.1 ± 3.1
28	DNK	81.3 ± 40	2.2 ± 1.5	133.3 ± 76	413.1 ± 76	-
18	MEX	73 ± 45	2.0 ± 1.3	101 ± 54	389 ± 57	-
25	TUN	93.2 ± 80	2.6 ± 1.7	150.9 ± 76	444.2 ± 102	-
19	MEX	-	-	-	418.6 ± 89	-
30	IRN	72.9 ± 35	2.1 ± 1.4	117.7 ± 64	393.9 ± 63	-
27	COL	-	1.6 ± 1.0	127.2 ± 77	410.3 ± 78	-
32	CZE	-	-	-	400 ± 59	25.3 ± 2.5
Present study	MEX	71.5 ± 23	2.7 ± 1.9	131.6 ± 74	413.6 ± 85	24.2 ± 2.7

CFI = calving to first insemination interval in days, NSC= number of services per conception, DO = days open, IBC= interval between calvings in days, AFC= age at first calving in months, \bar{x} = average for the traits, SD= standard deviation

The results for NSC were 2.7 on average (Table 1), similar to the 2.55 reported in a population of this same breed (Holstein) from Tunisia⁽²⁵⁾. Lower averages from 1.58 and up to 2 services per conception have been reported in Holstein populations of Spain⁽¹²⁾, Mexico⁽¹⁸⁾, Canada⁽²⁶⁾ and Colombia⁽²⁷⁾. The difference can be caused by the upper limits of 7 services established by the aforementioned authors, with respect to the 10 services considered in the estimates of this work.

For DO, the results showed 131.6 d, in accordance with the 131.5 d reported in a population of the United States⁽⁶⁾, of Denmark with 133.3 d⁽²⁸⁾; or in Colombia with 127.2 d⁽²⁷⁾ (Table 1). While lower averages were obtained in other studies from 101 d to 117 d^(18,29,30). In contrast, a value of 150 d was reported in Tunisia⁽²⁵⁾. As in the traits discussed above, the differences between this study and those cited here could be due to the variation of the limits

used for each population, as well as to postpartum health problems specific to each population studied⁽²⁹⁾.

The average of IBC of 413 d coincides with other populations^(28,31) (Table 1), as well as reports ranging from 400 to 416 d^(19,27,32). On the other hand, lower averages of 389 d were reported in 2010 in a Holstein and Brown Swiss Mexican population under subtropical conditions⁽¹⁸⁾.

For AFC, the results were 24.15 mo (Table 1), similar to that reported in several studies, such as the 25.34 mo mentioned in the Czech Republic⁽³²⁾, 27.1 in populations of the United States^(33,34), as well as 27.6 mo in another Mexican population⁽³³⁾ of the Holstein association of Mexico that includes data from 1971 to 1995. In contrast, 33.6 mo were reported in a population of the United States⁽²⁹⁾. This parameter shows about the female calf's ability to grow and conceive at an early age⁽⁵⁾, which may be different for each population, since there is a cost-benefit ratio in achieving earlier ages at first calving⁽¹¹⁾. That is, it is a voluntary and economic decision of the administrators of each population, because the age at first insemination determines AFC and the first is almost always an administrative decision, since the cost associated with developing the female calf faster can be important in some environments (countries and production systems)^(11,35).

The differences obtained in the RPs evaluated and those mentioned above illustrate the difficulty in estimating them and the lack of consensus on acceptable biological limits in the measurements of these traits^(3,5), which generates possible biases to the estimates and difficulties for comparison. Other issues such as the dependence of these traits on the conditions of each country^(26,27,30), the economic purposes of each farm⁽¹²⁾, as well as the conditions and management that vary from one herd to another⁽³⁵⁾, may be generating the changes observed between countries.

Genetic parameters

Heritability ranged from 4 % to 9 % for the RPs studied, being higher for AFC (9 %), of 5 % for NSC, DO and IBC, and the lowest for CFI with 4 % (Table 2), similar to that previously reported for fertility traits^(12,26,27).

The lowest heritability obtained was for CFI, with 4 %, similar to the 3 % reported in populations of Tunisia⁽²⁵⁾ and Canada⁽²⁶⁾, as well as 5 % of a Spanish population⁽¹²⁾. However, the results of the present study were lower than the 6 % reported by Italy⁽³¹⁾ and Iran⁽³⁰⁾, as well as the 9 % estimated in Denmark⁽²⁸⁾.

Table 2: Narrow-sense heritability and repeatability in Holstein populations, including those of the present study

Author	Country	CFI		NSC		DO		IBC		AFC
		h ²	r	h ²						
6	USA	-	-	-	-	0.05	-	-	-	0.05
26	CAN	0.03	0.08	0.03	0.07	0.05	0.10	-	-	-
31	ITA	0.06	0.14	0.03	-	-	-	0.07	-	-
12	ESP	0.05	-	0.02	-	0.04	-	0.04	-	-
28	DNK	0.09	-	0.03	-	0.07	-	0.07	-	-
25	TUN	0.03	0.13	0.03	0.03	0.04	0.14	0.06	0.15	-
19	MEX	-	-	-	-	-	-	0.01	-	0.03
30	IRN	0.06	-	0.05	-	0.08	-	0.07	-	-
27	COL	-	-	0.04	0.07	0.08	0.1	0.09	0.09	-
32	CZE	-	-	-	-	-	-	0.03	0.09	0.03
PS	MEX	0.04 (0.003)	0.09 (0.003)	0.05 (0.004)	0.08 (0.003)	0.05 (0.004)	0.08 (0.003)	0.05 (0.004)	0.08 (0.003)	0.09 (0.007)

RP: reproductive parameter, CFI: calving to first insemination interval in days, NSC: number of services per conception, DO: days open, IBC: interval between calvings in days, AFC: age at first calving in months, h²: heritability, r: repeatability, standard error in parentheses, PS: present study.

The estimated heritability for NSC was 5 %, consistent with that reported in an Iranian population⁽³⁰⁾, in a Colombian⁽²⁷⁾ with 4 %, and the 3 % reported in populations of Spain⁽¹²⁾, Tunisia⁽²⁵⁾ and Canada⁽²⁶⁾.

Regarding DO, the heritability is consistent with that reported in Canada⁽²⁶⁾ and the United States⁽⁶⁾ of 5 %, as well as those estimated in Spain⁽¹²⁾ and Tunisia⁽²⁵⁾ with 4 %; on the other hand, 7 % was reported in Denmark⁽²⁸⁾ and 8 % estimated in populations of Colombia and Iran^(27,30).

For IBC, a heritability of 5 % was estimated, which was also similar to previous works done in Tunisia (6 %)⁽²⁵⁾, Spain (4 %)⁽¹²⁾, Czech Republic (3 %)⁽³²⁾ and lower than the 7 % in Italy⁽³¹⁾, Denmark⁽²⁸⁾ and Iran⁽³⁰⁾. The maximum heritability value reported for this reproductive parameter is 9 % in Colombia⁽²⁷⁾, and the lowest value reported is 1 %, in the same study population over a period of time from 1998 to 2003⁽¹⁹⁾.

The highest heritability obtained in the present study was for AFC, with 9 %, higher than the 5 % reported in one population of the United States⁽⁶⁾, or the 3 % reported in another Mexican population⁽¹⁹⁾ and in the Czech Republic⁽³²⁾. Therefore, it would be expected that, in our population, the response to selection for this trait would have a better result, due to differences in heritabilities.

The repeatability estimate for NSC and DO was the same, slightly higher for CFI and IBC with 9 % (Table 2). Other values reported for the Holstein breed are similar to those obtained in the present study^(26,27,32).

The genetic parameters of the reproductive traits included in this study have relatively low values (heritability < 10 % and repeatability < 15 %)^(12,19,26), so, in addition to genetics, the environment has an important effect as a source of variation⁽³⁶⁾. That is, other factors such as health^(29,36), nutritional aspects⁽³⁶⁾, as well as administrative management issues (voluntary waiting period) by producers impact these traits^(6,26,29).

It is important to highlight that, although the heritabilities found in this study are low, genetic improvement can allow positive, permanent and cumulative benefits to be obtained in populations^(11,16,17).

The estimated phenotypic and genetic correlations were positive for almost all reproductive parameters (Table 3). The highest genetic correlations were found between DO and IBC (0.99), as well as high values of 0.84 and 0.88 for NSC with DO and IBC, respectively. For CFI with DO and IBC, an intermediate correlation (0.55 and 0.51) was found. For the other combinations of fertility traits, low correlations (from 0.09 to 0.22) were found.

Table 3: Genetic correlations above the diagonal (standard error), phenotypic correlations below the diagonal (number of records for each pair of traits)

	CFI	NSC	DO	IBC	AFC
CFI	-	0.13 (0.06)	0.55 (0.05)	0.51 (0.06)	0.09 (0.07)
NSC	-0.05 (202,545)	-	0.84 (0.02)	0.88 (0.02)	0.22 (0.08)
DO	0.26 (192,527)	0.77 (194,816)	-	0.99 (0.002)	0.09 (0.08)
IBC	0.23 (138,277)	0.78 (139,901)	0.98 (137,158)	-	0.12 (0.11)
AFC	0.08 (103,467)	0.01 (84,675)	0.06 (80,467)	0.07 (62,999)	-

CFI = calving to first insemination interval-in days; NSC= number of services per conception; DO = days open; IBC= interval between calvings in days; AFC= age at first calving in months.

All phenotypic correlations had a $P < 0.001$.

In particular, the lowest estimated genetic correlation was for the association between CFI and NSC (0.13), similar to the 0.12 reported for these parameters in an Italian population⁽³⁰⁾, and it was also the lowest estimated for another Mexican population⁽¹⁸⁾ with a value of 0.25. CFI and DO had a positive and moderate genetic association of 0.55, in contrast, in another population of Spain⁽¹²⁾ and Mexico⁽¹⁸⁾, a value of 0.82 was obtained for this association. The correlation estimator for CFI and IBC indicates that these two reproductive traits show a

positive and moderate genetic association (0.51), and lower than another Mexican population (0.89)⁽¹⁸⁾.

The correlation between NSC and DO was positive and high (0.84), although lower than that reported in Spain⁽¹²⁾, Mexico⁽¹⁸⁾ and Colombia⁽²⁷⁾ (0.94, 0.97, 0.98, respectively). A similar correlation value of 0.88 was found between NSC and IBC, close to the 0.89 reported in Spain⁽¹²⁾, lower than the 0.95 and 0.97 in Colombia⁽²⁷⁾ and Mexico⁽¹⁸⁾, respectively; unlike the 0.61 reported in Italy⁽³⁰⁾. High values of genetic correlation indicate the possibility of selecting for a trait, because as one can be decreased or increased, the same effect on the other is expected. In addition, the close relationship and dependence of the estrus detection rate and pregnancy between these measurements may explain these results, as well as the fact that the same genetic regions are encoding these traits^(29,37).

Between DO and IBC, high genetic correlation values (0.99) were found, identical to those reported in Spain⁽¹²⁾ and Iran⁽³⁰⁾ and similar to the 0.98 reported in Colombia⁽²⁷⁾. The results found are to be expected, because the IBC includes DO and the length of gestation⁽²⁹⁾, as a consequence, any variation of days open should result in changes in the interval between calvings. Additionally, these two traits, being almost equivalent, suggest that they are controlled by the same genes or genetic regions, which is known as the pleiotropic effect⁽³⁷⁾.

The age at first calving is influenced by the environment and management practices common to female calves and heifers born in the same period (year or year-season)⁽⁶⁾, which was corroborated by the low correlations found between it and the other RPs (Table 3), so these results suggest genetic and phenotypic independence among them.

Analysis by periods

Additive genetic variance

The results of the estimates of variances by period can be divided into two groups of comparisons P1 vs P2 and P2 vs P3 (Table 4). In P1 vs P2, for additive genetic variances, was observed similar values in CFI (12.48-11.17), NSC (0.15-0.16), DO (229.8-214.6) and IBC (478-466.7), except for AFC (1.23-0.19) which showed a significant decrease, possibly due to the selection on milk production during this period, because as a cow becomes pregnant, it will begin its productive life.

Table 4: Additive genetic variance and heritability for five reproductive parameters in three periods of time (P1: 2006-2009, P2: 2010-2013 and P3: 2014-2017)

Reproductive parameter	Period	Number of records	$\sigma^2_a \pm SE$	h^2
CFI	P1:06-09	71,667	12.48 \pm 2.2	0.03
	P2:10-13	63,952	11.17 \pm 2.0	0.03
	P3:14-17	43,233	19.88 \pm 3.0	0.06
NSC	P1:06-09	71,667	0.15 \pm 0.02	0.05
	P2:10-13	63,952	0.16 \pm 0.02	0.05
	P3:14-17	43,233	0.10 \pm 0.02	0.04
DO	P1:06-09	69,417	229.8 \pm 35.32	0.04
	P2:10-13	62,783	214.6 \pm 33.87	0.04
	P3:14-17	42,790	194.8 \pm 25.66	0.05
IBC	P1:06-09	54,005	478.0 \pm 51.1	0.07
	P2:10-13	48,388	466.7 \pm 52.5	0.07
	P3:14-17	25,801	266.8 \pm 53.9	0.05
AFC	P1:06-09	31,542	1.23 \pm 0.12	0.22
	P2:10-13	34,094	0.19 \pm 0.04	0.04
	P3:14-17	31,222	0.15 \pm 0.03	0.04

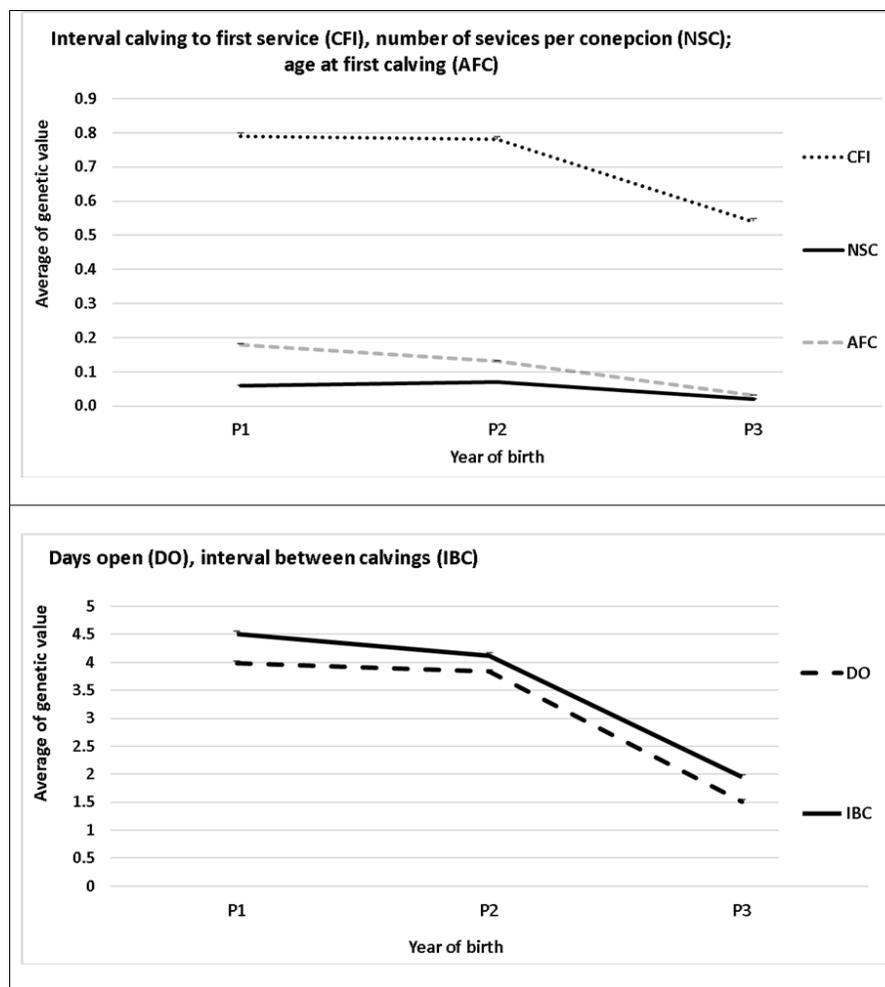
CFI = calving to first insemination interval-in days, NSC= number of services per conception, DO = days open, IBC= interval between calving in days, AFC= age at first calving in months, σ^2_a = additive genetic variance, SE= standard error, h^2 = narrow-sense heritability.

In P2 vs P3, an increase in CFI (11.17-19.88) was observed in additive genetic variance, which suggests genetic diversity and the larger it is, the greater the opportunity for response to selection⁽³⁸⁾. In contrast, decreases were observed for NSC (0.16-0.10), DO (214.6-194.8) and IBC (466.7-266.8), while AFC was similar to the previous period (0.19-0.15). The decrease in the additive genetic variances of NSC, DO and IBC may be due to a selective pressure of these traits.

Genetic values

The changes over time between groups P1 vs P2, and P2 vs P3 are shown in Figures 1a and 1b, where it can be seen how, in general, genetic trends were similar between P1 and P2, decreasing in P3. These results are in line with the farmers' criteria for choosing semen, who, during the first two periods, emphasized the volume of milk, which decreased in P3, while in case of reproductive traits, there were no changes in P1 and P2, but a positive change was observed in P3 [Durán C., 2022, unpublished data].

Figure 1: Genetic trends for CFI (=IPPS), NSC and AFC (=EPP) (a) and for DO (=DAB) and IBC (=IEP) (b) in three periods of time (P1: 2006-2009, P2: 2010-2013 and P3: 2014-2017)



For group II (P2 vs P3), a decrease in average genetic values can be observed for CFI, DO, IBC and AFC, but not for NSC. This reduction in genetic values is desirable because what is sought in these fertility traits studied is the decrease.

These changes in fertility traits could possibly be attributed to the import and use of germplasm from the United States since 1950⁽³⁹⁾, which has improved fertility traits since 2003⁽¹⁷⁾ and uses genomic selection since 2009⁽¹⁶⁾.

For NSC, no changes were observed in genetic values, probably because this characteristic depends significantly on insemination techniques, which do not depend on the population of origin of the germplasm.

The results of this study show how the incorporation of genomic information in the selection processes of the countries of origin of imported germplasm has apparently had a positive effect on the population (Figures 1a and 1b), regardless of the low heritability and difficulty of measuring fertility traits^(16,17).

Conclusions and implications

The estimates of heritability and repeatability of the reproductive parameters obtained in the present study were low and similar to previous reports in the breed. However, the existing additive genetic variation is sufficient to expect favorable and cumulative (although slow) results in the selection of these traits. The estimated correlations between the PRs were positive, highlighting that they were high between NSC, DO and IBC, in particular the correlation between DO and IBC, with a correlation of 0.99, which suggests that it would be advisable to select only for one parameter, since it could be considered that its effects are controlled by the same genetic regions. The results of the estimates of additive genetic variances and genetic values in different periods show the existence of changes in the population over time, possibly derived from the implementation of genomic selection in germplasm supplier countries, such as Canada and the United States.

Acknowledgements and conflict of interest

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