AKADÉMIAI KIADÓ

Population genetic features of calving interval of the Limousin beef cattle breed in Hungary

SZABOLCS BENE[1]*, PÉTER J. POLGÁR[1], MÁRTON SZŰCS[2], JUDIT MÁRTON[3], ESZTER SZABÓ[4] and FERENC SZABÓ[5]

[1] Institute of Animal Sciences, Georgikon Faculty, Hungarian University of Agriculture and Life Sciences, Deák Ferenc str. 16, H-8360 Keszthely, Hungary

[2] Association of Hungarian Limousin and Blonde d'Aquitaine Breeders, Lőportár str. 16, H-1134 Budapest, Hungary

[3] Hungarian Hereford, Angus and Galloway Breeders Association, Dénesmajor 2, H-7400 Kaposvár, Hungary

[4] University of Szeged, Juhász Gyula Faculty of Education, Boldogasszony sgt 6, H-6725 Szeged, Hungary

[5] Department of Animal Sciences, Faculty of Agricultural and Food Sciences, Széchenyi István University, Vár place 2, H-9200 Mosonmagyaróvár, Hungary

Acta Veterinaria Hungarica

70 (2022) 2, 113–120

DOI:
10.1556/004.2022.00008

RESEARCH ARTICLE

Received: 19 January 2022 • Accepted: 19 April 2022

ABSTRACT

Variance, covariance components, heritability, breeding values (BV) and genetic trends in calving interval (CI) of the Limousin population in Hungary were evaluated. A total of 3,008 CI data of 779 cows from three herds in 1996–2016 were processed. For influencing effects GLM method, for population genetic parameters and BV estimation BLUP animal model, for trend analyses linear regression was applied. The average CI obtained was 378.8 ± 3.1 days. The variance distribution components of the phenotype were as follow: age of cow at calving 34.30%, season of calving 26.09%, year of calving 23.00%, sire 7.45%, herd 3.23%, sex of calf 0.33% and type of calving 0.30%. The heritability of CI proved to be low ($h^2_d = 0.04 \pm 0.02$ and 0.03 ± 0.02; $h^2_m = 0.01 \pm 0.02$). The repeatability was low ($R = 0.03 \pm 0.02$). Based on the phenotypic trend calculation, the CI of cows decreased by an average of 0.60 days per year ($R^2 = 0.19$; $P < 0.05$). In case of genetic trend calculation, the average BV of sires in CI increased 0.07 and 0.17 days per year ($R^2 = 0.23$ and 0.27; $P < 0.05$).

KEYWORDS

Limousin, calving interval, population genetic parameters, breeding value, phenotypic and genetic trend

INTRODUCTION

The calving interval (CI) of cows, that is the period between their two consecutive calvings, is an important trait as it reflects the reproductive performance of the population as well as the individual (Zöldág, 1980). The later the cow becomes pregnant after calving, the longer the CI will be. This is economically disadvantageous as the cow will have fewer calves during her lifetime, so the cost of raising one calf will increase (Zöldág and Gábor, 1980). For this reason, the breeding goal is for the cow to conceive as soon as possible after calving and for the CI to be as short as possible (Bourdon and Brinks, 1983; MacGregor and Casey, 1999).

Theoretically, the CI could be approximately one year (285 days gestation +80 days open). Lopez et al. (2019) reported that the average CI of Korean Hanwoo cows was 363 ± 29 days. However, several literature data for CI showed values over 12 months (365 days). In the report for dairy herds of Hare et al. (2006) the average CI was as follows: 390 days for Jersey, 398 days for Ayrshire, 404 days for Holstein-Friesian, 406 days for Guernsey,

---

*Corresponding author. Tel.: +36 (83) 545 398.
E-mail: Bene.Szabolcs.Albin@uni-mate.hu

AKJournals

and 407 days for Brown Swiss cows. In line with the above results, Slama et al. (1976) found the CI of Ayrshire, Guernsey, Holstein-Friesian, and Jersey cows to be between 396 and 414 days. Silveira et al. (2004) found that the CI of Nellore cows was 465 days. In a study by Kanuya and Greve (2000), in a Tanzanian Ayrshire herd, the average CI of cows was 435 days in the rainy season and 443 days in the dry season. Yagüe et al. (2009) reported 381–429 days for CI.

The heritability and repeatability of the CI are low based on data from most literature sources (Meacham and Notter, 1987). Vergara et al. (2009) showed that the heritability of this trait in a mixed-genotype beef herd was 0.11–0.18. In the Nellore herd Gressler et al. (2005) estimated the heritability of the CI between the first two calvings to be 0.03. Brzáková et al. (2020) reported that the heritability of the CI in Charolais and Angus herds was 0.08. The mean number of days open (DO) was 171 days, and the h^2 value of the trait was 0.06 in Cuban Charolais herds (Espinosa et al., 2016). Lopez et al. (2019) reported that the heritability of the CI of Hanwoo cows was 0.03 and the repeatability of the trait was 0.01. Berry and Evans (2014) reported data on repeatability of reproduction indices *R*, ranging from 0.02 to 0.06 based on Irish beef databases. In their work, similar repeatability values were found by Werth et al. (1996) and Yagüe et al. (2009) as well.

Due to the low heritability and repeatability, the CI is influenced by or related to several environmental factors. In the study of Silveira et al. (2004) the CI of Nellore cows was significantly influenced by the age of the cow, the year and the month of fertilisation. Grossi et al. (2016) also found that herd, year and season had a significant effect on the CI of Nellore cows.

Numerous research results have been obtained examining the relationship between CI and other traits. Gutiérrez et al. (2002) found a week negative genetic correlation between the CI and the results of conformation scoring. Brzáková et al. (2020) reported a loose, negative genetic and phenotypic correlation between the age at first calving (AFC) and the CI between the first two calvings in Charolais herds. Veselá et al. (2013) also found a loose negative genetic correlation between the AFC and the period between two calvings ($r_g = –0.01$) and longevity ($r_g = –0.07$) during the analysis of the Czech beef database. According to López-Paredes et al. (2018), the AFC showed a positive correlation with CI (0.14) in a Blonde d'Aquitaine herd. In the study of Gutiérrez et al. (2007) a moderately strong genetic correlation ($r_g = +0.49$) was found between the CI and the calving difficulty in the Asturiana de los Valles herd. Brzáková et al. (2020) found that calving difficulty had a significant effect on the CI of Charolais cows. Yagüe et al. (2009) reported that the age of the cow at calving had a significant effect on CI of Rubia Gallega cows, namely the interval increased with increasing age of cows. Similarly, Hare et al. (2006) observed a small increase in the CI with increasing cow age in dairy breeds. Similar results were obtained by Nieuwhof et al. (1989). Nguyen et al. (2011) found a positive relationship between the days open (DO) and somatic cell count.

There is less information in the literature on the phenotypic and genetic trends of CI than on the magnitude of this trait. Magnabosco et al. (2016) observed a decreasing genetic trend of CI in the Brazilian Nellore herd. Vergara et al. (2009) also observed a decrease in the mentioned trait in a mixed genotype beef herd between 1989 and 2004. According to Bernardes et al. (2015), the genetic trends indicated small and increasing genetic changes for CI in the Tabapua breed in Brazil.

Since the interval between two calvings is generally longer than 365 days, and sometimes shows a decreasing tendency, breeders are looking for the possibility of reducing this period, besides improved management, by applying appropriate breeding and selection methods.

As we have found limited information on the population genetic features of CI for beef cows, the objective of this research was to evaluate: (1) The effect of sire, herd, age of cow, year, season, sex of the calf and type of calving on the CI of Limousin cows; (2) Variance components, heritability, repeatability of the trait at issue; (3) Breeding values (BV) and rank of Limousin breeding bulls based on this trait; (4) Phenotypic and genetic trends in CI.

MATERIALS AND METHODS

The present study is a continuation of our earlier works on Holstein-Friesian (Bene et al., 2013) and on Limousin (Bene et al., 2021) cows. Therefore some similarities of methods can be found in the previous and the current paper.

The database

For this research data were collected in the three largest Limousin herds in Hungary. CI was calculated as the difference between calving dates from succeeding parities. Data only from cows with a CI between 320 and 480 days were processed. In this work, values above 400 days were left in the database due to possible supplemental parity cycles. Lower and higher values were set as missing values. This was different from the study of Ansari-Lari et al. (2009) and Brzáková et al. (2020), who used wider boundaries (290–500 days and 260–750 days) for CI.

Thus, a total of 3,008 CI data from 779 cows between 1996 and 2016 were included in the evaluation. The studied cows were the offspring of 60 sires and 753 dams (Table 1).

The Kolmogorov–Smirnov and Levene's test were used to check the normal distribution and homogeneity of variances of the database.

Examining the effects of different factors

General Linear Model (GLM) univariate analysis of variance was used for studying the various effects on CI. The herd, the age of cow at calving, the year and season of calving, the sex of calf and the type of calving were handled as a fixed effect, while sire was a random effect. The fix effects concerned to the first of two calvings in CI. The used model was described as follows:

Table 1. The structure of the evaluated database for Limousin population

Starting parameters	Used database
Number of calving interval data (*N*)	3,008
Time period of examination	1996–2016
Number of herds	3
Number of cows	779
Birth date of cows	1992–2012
Breed of cows	Limousin
Average calving interval data per cow	3.9
Number of the examined sires (sire of cow)	60
Breed of sire	Limousin
Average number of female progeny (cow) per sire	13.0
Average calving interval data per sire	50.1
Number of the examined dams (dam of cow)	573

$$\hat{y}_{hijklmn} = \mu + S_h + H_i + A_j + Y_k + M_l + G_m + T_n + e_{hijklmn}$$

where: $\hat{y}_{hijklmn}$ = CI of cow born from sire 'h', in herd 'i', calved at 'j' age, in 'k' year, 'l' season, 'm' sex of the calf with 'n' type of calving; μ = mean of all observations; S_h = effect of sire; H_i = effect of herd; A_j = effect of age of dam at calving; Y_k = effect of calving year; M_l = effect of calving season; G_m = effect of sex of calf; T_n = effect of type of calving; $e_{hijklmn}$ = random error.

The GLM method was based on to Harvey's (1990) 'Least Square Maximum Likelihood' procedure using the 'Harvey' program (Bene, 2013).

Estimation of population genetic parameters and breeding values

To estimate the population genetic parameters and breeding values of CI, two methods – GLM (Bene et al., 2021) and repeatability BLUP (Best Linear Unbiased Prediction) animal model (Mrode, 1996) – were applied in the study. The estimation of variance components was based on the instructions of Henderson (1975), Szőke and Komlósi (2000) and Lengyel et al. (2004).

Using the repeatability BLUP model, two matrices were created. One of these was the database matrix and the other was the pedigree matrix. In the BLUP animal model the same fixed effects were taken into account as in the case of the GLM method. A random effect was the individual and the maternal genetic effect. The matrix of relatives included pedigree data for sires, dams, full sibs, half sibs and grandparents. Because a cow can have more calving interval data, the permanent environmental effect (as random effect) was also included in the model (Rudiné Mezei et al., 2015). As in the study of Nagy et al. (2011), the used basic repeatability model was as follows:

$$y = Xb + Za + Wpe + e$$

where: 'y' is the vector of observations; 'b' is the vector of fixed effects; 'a' is the vector of random animal effects; 'pe' is the random vector of permanent environmental effects; 'e' is the vector of random residual effects; X, Z and W are the incidence matrices relating records to fixed, animal and random permanent environmental effects, respectively.)

The total heritability (h^2_T) was calculated using the following formula (Willham, 1972):

$$h^2_T = \left(\sigma^2_d + 0,5\sigma^2_m + 1,5\sigma_{dm}\right) \Big/ \sigma^2_p$$

where: σ^2_d = additive direct genetic variance; σ^2_m = maternal genetic variance; σ_{dm} = direct maternal genetic covariance; σ^2_p = phenotypic variance.

The repeatability value (*R*) was calculated according to the work of Rastogi et al. (2000) and Rudiné Mezei (2015). The formula was as follows:

$$R = \left(\sigma^2_d + \sigma^2_{pe}\right) \Big/ \left(\sigma^2_d + \sigma^2_{pe} + \sigma^2_e\right)$$

where: σ^2_d = additive direct genetic variance; σ^2_{pe} = maternal permanent environmental effect; σ^2_e = residual variance.

Rank of sires was estimated using Spearman's rank correlation (Spearman, 1904; Núnez-Dominguez et al., 1995; Lengyel et al., 2004).

Population genetic parameters were estimated using the DFREML (Meyer, 1998) and MTDFREML (Boldman et al., 1993) programs, based on the guidelines of Lengyel et al. (2004).

Calculating phenotypic and genetic trends

Phenotypic trend was shown by annual phenotypic average of CI. The calculation method was the same as described previously (Bene et al., 2021).

The genetic trend of CI was determined in several ways: on the one hand, from the GLM breeding value of sires born in the same year; on the other hand, from the BLUP direct and maternal breeding value of sires born in the same year; thirdly, from the BLUP direct and maternal breeding value of each animal born in the same year. The genetic trend of CI was evaluated using a weighted linear regression method. BV of sires as well as BV of each animal in the total population obtained was averaged annually. The annual mean values were the dependent value, the appropriate year was the independent value and the numbers of animals were the weight in the used regression method.

RESULTS

Effect of environmental factors

The arithmetic mean (±SE) of the CI of Limousin cows was 375.6 ± 0.7 days (Table 2). Subtracting the average gestation length (285 days) of cattle from the CI revealed that the average DO of Limousin cows in this work was 90 days.

Among the examined factors, the effect of the sire, the age of cow at calving, the year of calving and the season of

Table 2. Descriptive statistics of calving interval trait of Limousin cows

Parameters	Calving interval
N	3,008
Mean (days)	375.6
Standard error (SE) (days)	0.7
Standard deviation (SD) (days)	38.9
Coefficient of variation (cv%)	10.4
Median (days)	368.0
Range (days)	160
Minimum (days)	320
Maximum (days)	480
Kolmogorov–Smirnov test† (P)	0.000

† if $P > 0.05$, the normal distribution is confirmed.

calving on the CI were significant ($P < 0.01$) (Table 3). The effect of the herd, the sex of calf and the type of calving were not found to be significant. The proportion of evaluated factors in phenotype was as follows: age of cow at calving 34.30%, season of calving 26.09%, year of calving 23.00%, sire 7.45%, herd 3.23%, sex of calf 0.33% and type of calving 0.30%. The residual was 5.30%.

The effect of the examined environmental factors on the CI is summarised in Tables 4a and 4b. The estimated adjusted mean of the CI by the GLM method proved to be 378.8 ± 3.1 days. Examining the effect of the calving age of the cows, it can be stated that the shortest CI (370–376 days) was reached by the cows aged 5–8 years. For both younger and older cows, a longer period (380–390 days) was calculated. Examined by years the shortest CI (367.1 ± 9.9 days) was observed in 2016 and the longest (396.1 ± 9.6 days) in 1996. The difference in CI between these two years was 29 days. The CI of autumn-calved cows (374.2 ± 3.5 days) was on average 8.8 days shorter than that of their winter-calved counterparts (383.0 ± 3.3 days).

Table 3. The effect of different factors on the calving interval trait of Limousin cows

Trait		Calving interval		
		The effect and rate of factors in phenotype		Levene-test*
Factor	Classes	P	%	P_L
Sire of cow	60	<0.05	7.45	–
Herd	3	NS	3.23	0.00
Age of cow at calving	13	<0.01	34.30	0.00
Year of calving	21	<0.01	23.00	0.00
Season of calving	4	<0.05	26.09	0.00
Sex of calf	2	NS	0.33	0.52
Type of calving	2	NS	0.30	0.01
Residual	–	–	5.30	–
Total	–	–	100.00	–

* if $P_L > 0.05$, the homogeneity is confirmed.

Table 4a. The effect of the environmental factors on the calving interval trait of Limousin cows 1

Trait	N	Calving interval (days)	
Corrected overall mean (±SE)		378.8 ± 3.1	
Environmental factors	3,008	Mean ± SE	Deviation from overall mean
Herd (code)			
- 1	1,870	378.5 ± 3.9	−0.3
- 2	1,028	374.9 ± 5.7	−3.9
- 3	110	383.0 ± 5.4	+4.2
Age of cow at calving (year)			
- 2	155	381.3 ± 5.5	+2.5
- 3	434	389.7 ± 4.5	+10.9
- 4	400	380.4 ± 4.2	+1.6
- 5	425	370.0 ± 3.8	−8.8
- 6	389	370.5 ± 3.7	−8.3
- 7	336	376.0 ± 3.7	−2.8
- 8	265	371.3 ± 3.7	−7.6
- 9	210	379.1 ± 4.0	+0.3
- 10	151	380.0 ± 4.5	+1.2
- 11	108	378.7 ± 5.0	−0.1
- 12	64	373.0 ± 6.1	−5.8
- 13	47	384.5 ± 6.9	+5.7
- 14≤	24	390.2 ± 9.1	+11.3
Year of calving			
- 1996	28	396.1 ± 9.6	+17.3
- 1997	54	391.8 ± 8.0	+12.9
- 1998	79	370.1 ± 7.0	−8.7
- 1999	136	384.2 ± 6.1	+5.4
- 2000	148	380.5 ± 5.7	+1.7
- 2001	209	375.1 ± 5.1	−3.7
- 2002	204	379.1 ± 4.8	+0.3
- 2003	223	373.0 ± 4.4	−5.8
- 2004	244	378.5 ± 4.1	−0.3
- 2005	242	377.1 ± 3.9	−1.8
- 2006	251	383.8 ± 3.7	+5.0
- 2007	204	371.5 ± 4.1	−7.3
- 2008	123	395.3 ± 4.6	+16.4
- 2009	153	374.3 ± 4.7	−4.5
- 2010	93	391.1 ± 5.3	+12.3
- 2011	104	373.8 ± 5.6	−5.0
- 2012	154	368.4 ± 5.3	−10.4
- 2013	155	371.0 ± 5.9	−7.8
- 2014	120	376.3 ± 6.5	−2.5
- 2015	56	377.0 ± 7.9	−1.8
- 2016	28	367.1 ± 9.9	−11.7

Population genetic parameters

The heritability of the CI trait proved to be very small in the examined Limousin population (Table 5). Values of $h^2 = 0.04 \pm 0.02$ were estimated by the GLM method and $h^2 = 0.03 \pm 0.02$ by the BLUP animal model.

The maternal effect on the studied trait proved to be very small. The value of maternal heritability (h^2_m) was 0.01 ±0.02, and the value of maternal permanent environmental impact (c^2) was 0.00 ± 0.02. Therefore, the repeatability of CI was also estimated to be very small ($R = 0.03 \pm 0.02$).

Table 4b. The effect of the environmental factors on the calving interval trait of Limousin cows 2

Trait	N	Calving interval (days)	
Corrected overall mean (±SE)		378.8 ± 3.1	
Environmental factors	3,008	Mean ± SE	Deviation from overall mean
Season of calving			
- winter	759	383.0 ± 3.3	+4.2
- spring	1,161	380.5 ± 3.2	+1.7
- summer	486	377.5 ± 3.5	–1.3
- autumn	602	374.2 ± 3.5	–4.6
Sex of calf			
- bull	1,468	378.6 ± 3.3	–0.2
- heifer	1,540	379.0 ± 3.1	+0.2
Type of calving			
- single	2,738	378.5 ± 2.9	–0.3
- twin	270	379.1 ± 3.8	+0.3

Breeding values (the effect of sire)

Between the mean values of CI of the progeny groups of different sires considerable differences were found with the GLM method (Table 6). The shortest CI (374.9 ± 3.0 days) was observed for the female progeny group of the sire with registration number 12946, and the longest (381.0 ± 3.4) in the progeny group of sire number 12485.

Estimated by the GLM method, the lowest BV in CI (–7.8 days) was found in case of sire of registration number 12946. The highest BV in CI (+4.4 days) was shown by the sires of registration number 12015 and 12485. The difference between these two extremes was rather small, 12.2 days.

Table 5. Population genetic parameters of the calving interval trait of Limousin cows

Parameters	Calving interval	
	GLM method	BLUP animal model
- additive direct genetic variance (σ_d^2)	53.20	43.19
- maternal genetic variance (σ_m^2)	–	–7.28
- direct maternal genetic covariance (σ_{dm})	–	11.53
- maternal permanent environmental effect (σ_{pe}^2)	–	0.00
- residual variance (σ_e^2)	1,404.63	1,371.93
- phenotypic variance (σ_p^2)	1,457.83	1,419.38
- direct heritability (h_d^2)	0.04 ± 0.02	0.03 ± 0.02
- maternal heritability (h_m^2)	–	0.01 ± 0.02
- direct-maternal genetic correlation (r_{dm})	–	–0.33 ± 0.77
- the ratio of the permanent environmental variance to the phenotypic variance (c^2)	–	0.00 ± 0.02
- the ratio of the residual variance to the phenotypic variance (e^2)	–	0.97 ± 0.01
- $h^2{}_m + c^2$	–	0.01
- total heritability (h_T^2)	–	0.03
- repeatability (R)		0.03 ± 0.02

The direct BV's obtained with the animal model were very similar to the data estimated by the GLM method. In the case of animal models, the lowest (–8.5 days) BV was found in the case of sire number 12946, while the highest (+4.7 days) for sire number 12485. Regarding the maternal breeding values, we did not find any significant difference between the tested breeding bulls.

Between the rankings of sires set up in the GLM method and BLUP animal model (direct BV) a very strong, positive rank correlation ($r_{rank} = +0.98$; $P < 0.01$) value was found. Between the rankings of sires set up in direct and maternal BV a moderate close, negative rank correlation ($r_{rank} = -0.74$; $P < 0.01$) value was obtained.

Phenotypic and genetic trends

Based on the phenotypic trend calculation (Table 7), the CI of Limousin cows decreased on average 0.60 days per year ($b = -0.60 \pm 0.29$; $P < 0.05$). The fit of the phenotypic trend ($R^2 = 0.19$; $P < 0.05$) was low and significant.

Genetic trend by the GLM method showed 0.07 days increase per year ($b = +0.07 \pm 0.03$; $P < 0.05$). Based on the estimated direct BV of sires by the BLUP animal model, the slope ($b = +0.17 \pm 0.07$; $P < 0.05$) and the fitting ($R^2 = 0.27$; $P < 0.05$) values were very similar to the GLM method. For the maternal BV of sires the results were not significant.

Based on the estimated direct BV of all animals, the genetic trend was almost stagnant ($b = -0.03 \pm 0.01$; $P < 0.05$), but it was statistically proven ($R^2 = 0.18$; $P < 0.05$).

DISCUSSION

In this study, the average CI of Limousin cows was slightly longer than 365 days. The CI of Limousin cows in our study was shorter than that reported by Slama et al. (1976), Silveira et al. (2004) and Hare et al. (2006). In contrast, in work of Lopez et al. (2019) the CI for Hanwoo cows was shorter than CI of Limousin cows in present work.

Results for the environmental effects on the CI of Limousin cows were similar to the studies of Silveira et al. (2004) and Grossi et al. (2016). Our results partly differed from those of Nieuwhof et al. (1989), Hare et al. (2006) and Yagüe et al. (2009) who observed an increase in the CI with increasing maternal age. The effect of the season in our study was similar to that observed by Kanuya and Greve (2000).

There are few research results in the literature on the BV of beef cattle breeding for the CI. In the case of Limousin sires, no such published data were found.

In our study, the heritability of the CI of Limousin cows was similar to that described by Gressler et al. (2005) for Nellore and by Lopez et al. (2019) for Hanwoo cows. In

Table 6. The effect of sire and breeding values on the calving interval of Limousin cows

Trait	*N*	Calving interval (days)				
Corrected overall mean (±SE)		378.8 ± 3.1				
		GLM method			BLUP animal model	
					BV	
Sire of cow (registration number)	3,008	Mean of progeny (mean ± SE)	EPD	BV	Direct	Maternal
- 12015	246	381.0 ± 2.8	+2.2	+4.4	+3.6	−1.0
- 12470	89	378.7 ± 3.2	−0.1	−0.2	−0.2	−0.4
- 12481	109	378.7 ± 3.1	−0.1	−0.2	+0.9	+0.2
- 12482	91	379.6 ± 3.2	+0.8	+1.6	+2.3	+0.0
- 12483	133	378.5 ± 3.1	−0.3	−0.6	−0.1	+0.2
- 12484	104	379.4 ± 3.2	+0.6	+1.2	+1.1	−0.9
- 12485	58	381.0 ± 3.4	+2.2	+4.4	+4.7	−1.0
- 12946	159	374.9 ± 3.0	−3.9	−7.8	−8.5	+0.8
- 13098	344	377.9 ± 2.4	−0.9	−1.8	−3.4	−2.5
- 14474	68	379.7 ± 3.4	+0.9	+1.8	+2.0	−0.7
- 14476	75	378.2 ± 3.4	−0.6	−1.2	−0.6	+0.2
- 14684	316	376.8 ± 2.8	−2.0	−4.0	−3.0	+1.3
- 15250	230	376.1 ± 2.8	−2.7	−5.4	−4.9	+0.5
- 16444	120	376.6 ± 3.1	−2.2	−4.4	−3.2	+1.6
- 18750	101	380.5 ± 3.3	+1.7	+3.4	+4.4	−0.2
Spearman rank-correlation value (r_{rank})		BV_{GLM} – BV_{BlupD}		+0.98 ($P < 0.01$)		
		BV_{GLM} – BV_{BlupM}		−0.83 ($P < 0.01$)		
		BV_{BlupD} – BV_{BlupM}		−0.74 ($P < 0.01$)		

EPD = estimated progeny difference; BV = breeding value; BV_{GLM} = breeding value with GLM method; BV_{BlupD} = direct breeding value with BLUP model; BV_{BlupM} = maternal breeding value with BLUP model.

Table 7. Phenotypic and genetic trends in the calving interval trait of Limousin cows

		Slope			Intercept				
		bX			a			Fitting	
Trend	Y	b	SE	*P*	a	SE	*P*	R^2	*P*
Phenotypic	ACI	−0.60	0.29	<0.05	1,590.50	575.87	<0.05	0.19	<0.05
Genetic									
- BV_{GLM} of sires	ACI^{BV}	+0.07	0.03	<0.05	−142.38	61.81	<0.05	0.23	<0.05
- BV_{BlupD} of sires	ACI^{BV}	+0.17	0.07	<0.05	−344.38	133.14	<0.05	0.27	<0.05
- BV_{BlupM} of sires	ACI^{BV}	−0.01	0.01	NS	20.08	25.59	NS	0.03	NS
- BV_{BlupD} of all	ACI^{BV}	−0.03	0.01	<0.05	65.30	26.47	<0.05	0.18	<0.05
- BV_{BlupM} of all	ACI^{BV}	−0.00	0.00	NS	2.59	7.16	NS	0.01	NS

X = birth year; ACI = average calving interval (days); ACI^{BV} = average breeding value in calving interval (days); BV_{Anova} = breeding value with GLM method; BV_{BlupD} = direct breeding value with BLUP model; BV_{BlupM} = maternal breeding value with BLUP model.

contrast, Vergara et al. (2009), Espinosa et al. (2016) and Brzáková et al. (2020) published slightly higher h^2 values than we estimated. The extremely low repeatability value observed in our work was similar to that found in most literature sources (Werth et al., 1996; Berry and Evans, 2014; Lopez et al., 2019).

The results on the phenotypic trend obtained in our study indicate a small decrease in the CI in the studied Limousin population. A similar trend was reported for the AFC trait in Limousin population in our previous work (Bene et al., 2021).

In line with the results of Bernardes et al. (2015), we observed a small increase in the genetic trend of the CI. In contrast, most relevant literature sources (Vergara et al., 2009; Magnabosco et al., 2016) reported a decreasing genetic trend for CI.

In conclusion, based on our numerical results it seems that there were no considerable genetic changes in the CI of the Limousin population during the evaluated period.

ACKNOWLEDGEMENTS

The publication is supported by the EFOP-3.6.3-VEKOP-16-2017-00008 project. The project is co-financed by the European Union and the European Social Fund.

REFERENCES

Ansari-Lari, M., Rezagholi, M. and Reiszadeh, M. (2009): Trends in calving ages and calving intervals for Iranian Holsteins in Fars province, southern Iran. Trop. Anim. Health Prod. **41,** 1283–1288.

Bene, Sz. (2013): Performance test results of stallions of different breeds between 1998–2010 in Hungary. 6th paper: Population genetics parameters, breeding values [in Hungarian, with English abstract]. Állattenyésztés és Takarmányozás [Hung. J. Anim. Prod.] **62,** 21–36.

Bene, Sz., Polgár, J. P. and Szabó, F. (2013): Effect of milk production and somatic cell count of milk on calving interval of Holstein-Friesian cows. [in Hungarian, with English abstract]. Magy. Allatorvosok [Hung. Vet. J.] **135,** 725–736.

Bene, Sz., Polgár, J. P., Szűcs, M., Márton, J., Szabó, E. and Szabó, F. (2021): Environmental effects, population genetic parameters, breeding value, phenotypic and genetic trend for age at first calving of Limousin cows. J. Cent. Eur. Agric. **22**, 240–249.

Bernardes, P. A., Grossi, D. A., Savegnago, R. P., Buzanskas, M. E., Urbinati, I., Bezerra, L. A. F., Lôbo, R. B. and Munari, D. P. (2015): Estimates of genetic parameters and genetic trends for reproductive traits and weaning weight in Tabapuã cattle. J. Anim. Sci. **93,** 5175–5185.

Berry, D. P. and Evans, R. D. (2014): Genetics of reproductive performance in seasonal calving beef cows and its association with performance traits. J. Anim. Sci. **92,** 1412–1422.

Boldman, K. G., Kriese, L. A., Van Vleck, L. D. and Kachman, S. D. (1993): A manual for use of MTDFREML. A Set of Programs to Obtain Estimates of Variances and Covariances. USDA-ARS, Clay Center, NE.

Bourdon, R. M. and Brinks, J. S. (1983): Calving date versus calving interval as a reproductive measure in beef cattle. J. Anim. Sci. **57,** 1412–1417.

Brzáková, M., Cítek, J., Svitáková, A., Veselá, Z. and Vostrý, L. (2020): Genetic parameters for age at first calving and first calving interval of beef cattle. Animals **10,** 2122.

Espinosa, J. L., González Peña, D., Palacios Espinoza, A., Ortega, R. and Guillén, A. (2016): Genetic parameters of days open in Charolais cattle of Cuba [in Spanish with English abstract]. Revista Colombiana de Ciencias Pecuarias [Col. J. Vet. Anim. Sci.] **29,** 16–24.

Gressler, M. G. M., Pereira, J. C. C., Bergmann, J. A. G., Andrade, V. J., Paulino, M. F. and Gressler, S. L. (2005): Genetic aspects of weaning weight and some reproductive traits in Nellore cattle [in Portuguese with English abstract]. Arquivo Brasileiro de Medicina Veterinária e Zootecnia [Bras. J. Vet. Anim. Sci.] **57,** 533–538.

Grossi, D. D. A., Berton, M. P., Buzanskas, M. E., Chud, T. C. S., Grupioni, N. V., Pero de Paz, C. C., Lobo, R. B. and Munari, D. P. (2016): Genetic analysis on accumulated productivity and calving intervals in Nelore cattle. Trop. Anim. Health. Prod. **48,** 207–210.

Gutiérrez, J. P., Alvarez, I., Fernández, I., Royo, L. J., Díaz, J. and Goyache, F. (2002): Genetic relationships between calving date, calving interval, age at first calving and type traits in beef cattle. Liv. Prod. Sci. **78,** 215–222.

Gutiérrez, J. P., Goyache, F., Fernández, I., Alvarez, I. and Royo, L. J. (2007): Genetic relationships among calving ease, calving interval, birth weight, and weaning weight in the Asturiana de los Valles beef cattle breed. J. Anim. Sci. **85,** 69–75.

Hare, E., Norman, H. D. and Wright, J. R. (2006): Trends in calving ages and calving intervals for dairy cattle breeds in the United States. J. Dairy Sci. **89,** 365–370.

Harvey, W. R. (1990): User's Guide for LSLMW and MIXMDL PC-2 Version Mixed Model Least-Squares and Maximum Likelihood Computer Program. The Ohio State University, Columbus, OH.

Henderson, C. R. (1975): Best linear unbiased estimation and prediction under a selection model. Biometrics **31,** 423–447.

Kanuya, N. and Greve, T. (2000): Effect of parity, season and FSH treatment on the calving interval of Ayrshire cows in the tropics. Trop. Anim. Health Prod. **32,** 197–204.

Lengyel, Z., Balika, S., Polgár, J. P. and Szabó, F. (2004): Examination of reproduction and weaning results in Hungarian Limousin population. 2nd paper: Sire- and animal model comparison [in Hungarian, with English abstract]. Állattenyésztés és Takarmányozás [Hung. J. Anim. Prod.] **53,** 199–211.

Lopez, B. I., Son, J. H., Seo, K. and Lim, D. (2019): Estimation of genetic parameters for reproductive traits in Hanwoo (Korean cattle). Animals **9,** 715.

López-Paredes, J., Pérez-Cabal, M. A., Jiménez-Montero, J. A. and Alenda, R. (2018): Influence of age at first calving in a continuous calving season on productive, functional, and economic performance in a Blonde d'Aquitaine beef population. J. Anim. Sci. **96,** 4015–4027.

MacGregor, R. G. and Casey, N. H. (1999): Evaluation of calving interval and calving date as measures of reproductive performance in a beef herd. Liv. Prod. Sci. **57,** 181–191.

Magnabosco, C. U., Lopes, F. B., Rosa, G. J. M. and Sainz, R. D. (2016): Bayesian estimates of genetic parameters for reproductive traits in Nellore cows raised on pasture in tropical regions. Revista Colombiana de Ciencias Pecuarias [Col. J. Vet. Anim. Sci.] **29,** 119–129.

Meacham, N. S. and Notter, D. R. (1987): Heritability estimates for calving date in Simmental cattle. J. Anim. Sci. **64,** 701–705.

Meyer, K. (1998): DFREML. Version 3.0. User Notes.

Mrode, R. A. (1996): Linear Models for the Prediction of Animal Breeding Values. CAB International, 208.

Nagy, I., Radnai, I., Nagyné Kiszlinger, H., Farkas, J. and Szendrő, Zs. (2011): Genetic parameters and genetic trends of reproduction traits in synthetic Pannon rabbits using repeatability and multi-trait animal models. Arch. Tierz. **54,** 297–307.

Nguyen, T. C., Nakao, T., Gautam, G., Su, L. T., Ranasinghe, R. M. S. B. K. and Yusuf, M. (2011): Relationship between milk somatic cell count and postpartum ovarian cyclicity and fertility in dairy cows. Acta Vet. Hung. **59,** 349–362.

Nieuwhof, G. J., Powell, R. L. and Norman, H. D. (1989): Ages at calving and calving interval for dairy cattle in the United States. J. Dairy Sci. **72,** 685–692.

Núnez-Dominguez, R., Van Vleck, L. D. and Cundiff, L. V. (1995): Prediction of genetic values of sires for growth traits of crossbred cattle using a multivariate animal model with heterogeneous variances. J. Anim. Sci. **73,** 2940–2950.

Rastogi, R. K., Lukefahr, S. D. and Lauckner, F. B. (2000): Maternal heritability and repeatability for litter traits in rabbits in a humid tropical environment. Livest. Prod. Sci. **67,** 123–128.

Rudiné Mezei, A. (2015): Breeding Value Estimation of Sport Horses Based on Their Show Jumping Performance [in Hungarian, with English Abstract]. PhD Dissertation, University of Debrecen. pp. 48–49.

Rudiné Mezei, A., Posta, J. and Mihók, S. (2015): Comparison of different measurement variables based on Hungarian show jumping results. Ann. Anim. Sci. **15,** 177–183.

Silveira, J. C., McManus, C., Mascioli, A., Silva, L. O. C., da Silveira, A. C., Garcia, J. A. S. and Louvandini, H. (2004): Study of genetic and environmental factors on production and reproduction traits in a Nellore herd in Mato Grosso do Sul State [in Portuguese, with English abstract]. Revista Brasileira de Zootecnia [Bras. J. Anim. Sci.] **33,** 1432–1444.

Slama, H., Wells, M. E., Adams, G. D. and Morrison, R. D. (1976): Factors affecting calving interval in dairy herds. J. Dairy Sci. **59,** 1334–1339.

Spearman, C. (1904): The proof of measurement of association between two things. Am. J. Psychol. **15,** 72–101.

Szőke, Sz. and Komlósi, I. (2000): Comparison of BLUP models [in Hungarian, with English abstract]. Állattenyésztés és Takarmányozás [Hung. J. Anim. Prod.] **49,** 231–246.

Vergara, O. D., Elzo, M. A. and Cerón-Munoz, M. F. (2009): Genetic parameters and genetic trends for age at first calving and calving interval in an Angus-Blanco Orejinegro-Zebu multibreed cattle population in Colombia. Livest. Sci. **126,** 318–322.

Veselá, Z., Vostrý, L. and Svitáková, A. (2013): Genetic analysis of female fertility traits in beef cattle in the Czech Republic. Interbull Bull. **47,** 172–175.

Werth, L. A., Azzam, S. M. and Kinder, J. E. (1996): Calving intervals in beef cows at 2, 3, and 4 years of age when breeding is not restricted after calving. J. Anim. Sci. **74,** 593–596.

Willham, R. L. (1972): The role of maternal effects in animal breeding: III. Biometrical aspects of maternal effects in animals. J. Anim. Sci. **35,** 1288–1293.

Yagüe, G., Goyache, F., Becerra, J., Moreno, C., Sánchez, L. and Altarriba, J. (2009): Bayesian estimates of genetic parameters for pre-conception traits, gestation length and calving interval in beef cattle. Anim. Reprod. Sci. **114,** 72–80.

Zöldág, L. (1980): Data collection aspects for evaluating the reproductive performance of cattle herds [in Hungarian, with English abstract]. Magy. Allatorvosok [Hung. Vet. J.] **35,** 400–402.

Zöldág, L. and Gábor, Gy. (1980): Development of reproductive performance and the course of parturitions in a feedlot cattle farm [in Hungarian with English abstract]. Magyar Állatorvosok Lapja [Hung. Vet. J.] **35,** 738–741.