

Bayesian inference of genetic parameters for reproductive traits in Sistani native cows using Gibbs sampling

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Abstract This study was undertaken to estimate the genetic parameters for some reproductive traits in Sistani beef cattle. The data set consisted of 1489 records of the number of insemination, calving, and insemination dates in different calving events. Reproductive traits, including the calving interval (CI), gestation length (GL), days open (DO), calving to first service (CTFS), first service to conception (FSTC), conception rate (CR), pregnancy rate (PR), and number of inseminations per conception (NSPC) were evaluated. Variance components for traits were estimated using different single-trait animal models analyzed by Gibbs sampling, and correlations between traits were estimated using the best multi-trait animal models. After convergence, the posterior mean of heritabilities for CI, GL, DO, CTFS, FSTC, CR, PR and NSPC in the best model were estimated as 0.032, 0.113, 0.096, 0.002, 0.012, 0.082, 0.023, and 0.123, respectively. The highest and lowest genetic correlations were found for CI×CR (-0.999) and CTFS×NSPC (0.001) interactions, respectively. The results showed that additive genetic for most reproductive traits in Sistani beef cattle was low; therefore, selection for these traits would make slow genetic progress. However, the estimated heritability of GL, DO, and NSPC, and the genetic correlations of these traits with CI, CR and PR suggested that selection for these traits in Sistani beef cattle may enhance genetic progress in fertility.

Keywords: calving interval, genetic correlation, fertility, conception rate

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Introduction

Cow fertility is an important trait in profitability of cattle enterprises, and is considered as the most important objective in cattle breeding (Cammack et al., 2009). Early indices for improving the cow reproduction were mainly calving interval (CI), days open (DO), and gestation length (GL) (Jansen, 1986). However, accessibility to data on insemination and calving date has allowed the use of other traits such as age at first service (AFS), age at first conception (AFC), interval from calving to first service (CTFS), first service to conception (FSTC), non-return rate (NRR), and number of inseminations per conception (NSPC) in breeding programs (Jamrozik et al., 2005).

Reproduction in domestic animals is a complex character with low heritability that is influenced by many environmental factors. However, it has been reported that the average heritability of reproductive traits for beef cattle are higher than those for dairy cattle suggesting that high genetic variation in reproductive traits of beef cattle may lead to better genetic improvement in these breeds (Koots et al., 1994). Cows that do not wean

a live calf cannot compensate the cost of several months rearing and management (Heaton et al., 2013). However, research on reproductive traits in beef cattle have been limited due to inaccessible of records (hard to measuring) and their low heritability (Buzanskas et al., 2013; Johnston, 2014). Low heritability, longer generation intervals, low selection intensity, and low numbers of correlated traits are amongst the factors that result in low level of reproductive performance and genetic progress in female fertility (Johnston et al., 2014). Accurate estimates of (co)variance components for economically important traits, such as reproductive ones, are pre-requisites for efficient designing of breeding strategies (Falconer and Mackey, 1996).

Iranian native breeds have valuable traits that differentiate from their Western counterparts (Mohammadbadi et al., 2011). Sistani cattle (*Bos indicus*), an important native meat type breed in Iran, are well adapted to the tropical region of Sistan (located in east of Iran). Such characteristic has become a biotype of great interest for meat production industry within the last few years.

One of the most distinctive features of Sistani cattle is its great capability to resist diseases which makes it a potential reservoir of germplasm useful for future crosses (Mohammadi et al., 2009). In recent years, the population of Sistani breed has been decreasing, therefore, effective strategies should be implemented to prevent the extinction of this breed. Identifying superior animals for the next generation requires the comprehensive knowledge on the variance-covariance components and genetic parameters of the traits. *Bos indicus* heifers have a higher age at puberty, indicating the importance of maturity in indigenous breeds and selection programs for reproductive traits under local systems in tropics (Carvalho et al., 1995; Buzanskas et al., 2013; Chud et al., 2014; Diskin and Kenny, 2014). The objective of this study was to estimate the genetic parameters for CI, GL, DO, CTFS, FSTC, CR, PR, and NSPC traits in Sistani cattle using Gibbs sampling.

Materials and methods

A total of 1489 insemination and calving dates of 346 Sistani cows, recorded from 1999 to 2013, were used to estimate the genetic parameters for the reproductive traits. Reproductive traits including the calving interval (CI), gestation length (GL), days open (DO), calving to first service (CTFS), first service to conception (FSTC), conception rate (CR), pregnancy rate (PR), and number of inseminations per conception (NSPC) were calculated. Calving interval was measured as the number of days between two consecutive calving (Berry and Evans, 2014). Gestation length was calculated as the interval between the last insemination and subsequent calving date, and ranged between 250 to 300 days (Eghbalsaied, 2011). An interval of calving date to last observed insemination date was considered as days open and outlier records (i.e., out of range of 15 to 390 days) were omitted (Eghbalsaied 2011). Conception rate was defined as the percentage of successful insemination, and calculated as: $CR = (1/NSPC) * 100$ (Zambrano

and Echeverri, 2014). The NSPC is the number of inseminations per conception. Pregnancy rate was the success rate for getting pregnant; 1 for successful pregnancy, and 0 for other cases (Rust and Groeneveld, 2001). Pregnancy rate was calculated as $PR = 0.25 \times (233 - DO)$ (Kuhn et al., 2004). A summary of the data is shown in Table 1.

The data were edited and the significance of fixed effects were checked using the R program. Variance components of traits were estimated via Gibbs sampling in a single- traits analysis using the following models:

$$y = \mathbf{X}b + \mathbf{Z}a + e \tag{1}$$

$$y = \mathbf{X}b + \mathbf{Z}a + \mathbf{W}pe + e \tag{2}$$

$$y = \mathbf{X}b + \mathbf{Z}_1a + \mathbf{Z}_2s + e \tag{3}$$

$$y = \mathbf{X}b + \mathbf{Z}_1a + \mathbf{Z}_2s + \mathbf{W}pe + e \tag{4}$$

where, y was the vector of observed traits, X was the incidence matrix associating data to the fixed effects (year- season of calving, lactation, sex, year – season of insemination, birth weight of calf, linear and quadratic effect of age at first calving), b was the vector of fixed effects, Z and Z₁ were the incidence matrices associating data to the additive genetic effects, Z₂ was the incidence matrix associating data to the sire effects (service sire), W was the incidence matrix associating data to the permanent environmental effects, and a, s, pe, and e were the vectors of additive genetic, service sire, permanent environmental, and residual random effects, respectively. The models were compared using the deviance information criteria (DIC) as follows:

$$DIC = PD + \bar{D} \tag{5}$$

where, PD was the effective number of parameters, and calculated as follows:

$$PD = \frac{1}{2} \hat{var}(D(\theta)) \tag{6}$$

and \bar{D} was the posterior expectation of the deviance $\bar{D} = E(D(\theta)), D(\theta) = -2\log(p(y| \theta)) + c$

Table 1. Descriptive statistics for reproductive traits

Trait ¹	Mean	SD ²	Min	Max
CI (day)	425.87	92.52	301	800
GL (day)	285.52	8.20	250	300
DO (day)	131.53	78.98	18	389
CTFS (day)	115.91	73.52	20	395
FSTC (day)	26.08	59.82	0	396
CR (%)	83.77	25.98	16	100
PR (%)	40.50	17.54	0	59
NSPC	1.42	0.76	1	6

¹CI: calving interval, GL: gestation length, DO: days open, CTFS: calving to first service, FSTC: first service to conception, CR: conception rate, PR: pregnancy rate, NSPC: number of inseminations per conception

²SD: standard deviation

y and θ were the data and unknown parameters of the model, respectively, $p(y|\theta)$ was the likelihood function, and C was a constant that was deleted in all calculations that compare different models (Berg et al. 2004; Gelman et al., 2013).

Genetic and environmental correlations between traits were estimated by Gibbs sampling in a multi-traits analysis and best model for each trait. The matrix model used was:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} SS_1 & 0 \\ 0 & SS_2 \end{bmatrix} \begin{bmatrix} s_1 \\ s_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix} \begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \quad (7)$$

in which, y_i = vector of observations for i^{th} trait; b_i = vector of fixed effects (year- season of calving, lactation, sex, year – season of insemination, birth weight of calf, linear and quadratic effect of age at first calving) for i^{th} trait; a_i = vector of random animal effects i^{th} trait; s_i = vector of random effects of service sire for i^{th} trait; pe_i = vector of random permanent environmental effects i^{th} trait (only considered for CI, FSTC, CR and NSPC); e_i = vector of random residual effects for a_i = vector of random animal effects i^{th} trait; X_i , Z_i , SS_i and W_i are incidence matrices which relate the data to the fixed and random effects, respectively. The expectations of the vectors and (co)variances of random effects for models are as follows:

$$\mathbf{E} \begin{bmatrix} Xb \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \text{var} \begin{bmatrix} a \\ s \\ pe \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 & 0 \\ 0 & I_s\sigma_s^2 & 0 & 0 \\ 0 & 0 & I_w\sigma_{pe}^2 & 0 \\ 0 & 0 & 0 & I_R\sigma_e^2 \end{bmatrix} \quad (8)$$

Direct genetic, service sire, permanent environment, and residual variances are represented by σ_a^2 , σ_s^2 , σ_{pe}^2 and σ_e^2 , respectively. A is the numerator relationship matrix of all animals, I is an identity matrix equal to the number of observations.

Gibbs chains for single-trait analysis were generated with 300000 iterations, an initial discard of 30000 samples, and a sampling interval of 100 iterations. The same chains for multi- trait analysis were generated with 1000000 Gibbs chain, 100000 samples as burn in and sampling interval of 50. The convergence checking of the chains generated by the Gibbs sampler was done using graphical analysis and diagnosis tests (Geweke algorithm) available in Bayesian output analysis program (BOA) (Smith, 2007). Credible intervals and high density regions for all estimates of covariance components and genetic parameters were determined at 95% level. Geweke method was used for diagnosis (Geweke, 1992),

which was assessed by comparing the sample mean in early segment of the chain and the mean in subsequent segments.

Results

The P-value obtained from Geweke algorithm supported convergence for all chains. After convergence, 3000 and 20000 samples were used for the estimation of posterior means of genetic parameters in single-trait and multi-trait analyses, respectively. Figures 1 and 2 show the trace plots and marginal posterior densities of heritability for reproductive traits in the best models for single- traits. The plots indicated that the algorithm mixed well, despite of differences among traits. Variance components, heritability, and DIC of different models are shown in Table 2. According to DIC of the models, the best model for CI, FSTC, CR, and NSPC was model 4 whereas the best model for GL, DO, CTFS, and PR was model 3. The posterior mean of heritability for GL and NSPC was higher than those for other traits (> 0.1). The lowest heritability was for FSTC and CTFS (< 0.01) and the range of heritabilities for DO, CI, CR, PR was 0.012 to 0.096. For comparison of the service sire and permanent environmental variance with the additive genetic variance of each trait, the ratio of these effects (service sire and permanent environmental variance) to additive genetic variance was calculated. The ratios of service sire variance to additive genetic variance for CI, GL, DO, CTFS, FSTC, CR, PR, and NSPC were 0.43, 0.57, 0.64, 0.21, 0.22, 0.39, 0.13, and 0.41, respectively. The ratios of permanent environmental variance to additive variance in the best models for CI, FSTC, CR, and NSPC were 0.13, 0.88, 0.19, and 1.01, respectively. The proportions of permanent environmental variance were noticeably high for FSTC and NSPC.

Table 3 shows the posterior mean of genetic and environmental correlations between reproductive traits. The genetic correlation between CI with DO and NSPC was close to 1, thus the effected genes for these traits are the same as expected. High negative associations were observed for CI×CR, DO×CR, DO×PR, and CTFS×CR indicating that selection for one of these traits could lead to decrease in others. Genetic correlations for CI×CTFS, CI×FSTC, GL×DO, GL×CTFS, GL×FSTC, GL×CR, GL×NSPC, DO×PR, CTFS×FSTC, and CTFS×PR were moderate. Low genetic correlations were found for CI×GL, CI×PR, GL×PR, DO×CTFS, DO×FSTC, DO×NSPC, FSTC×PR, CR×PR, and CR×NSPC (Table 3). The genetic correlations for CTFS×NSPC, FSTC×CR, FSTC×NSPC, and PR×NSPC were less than 0.1. The highest environmental correlations were

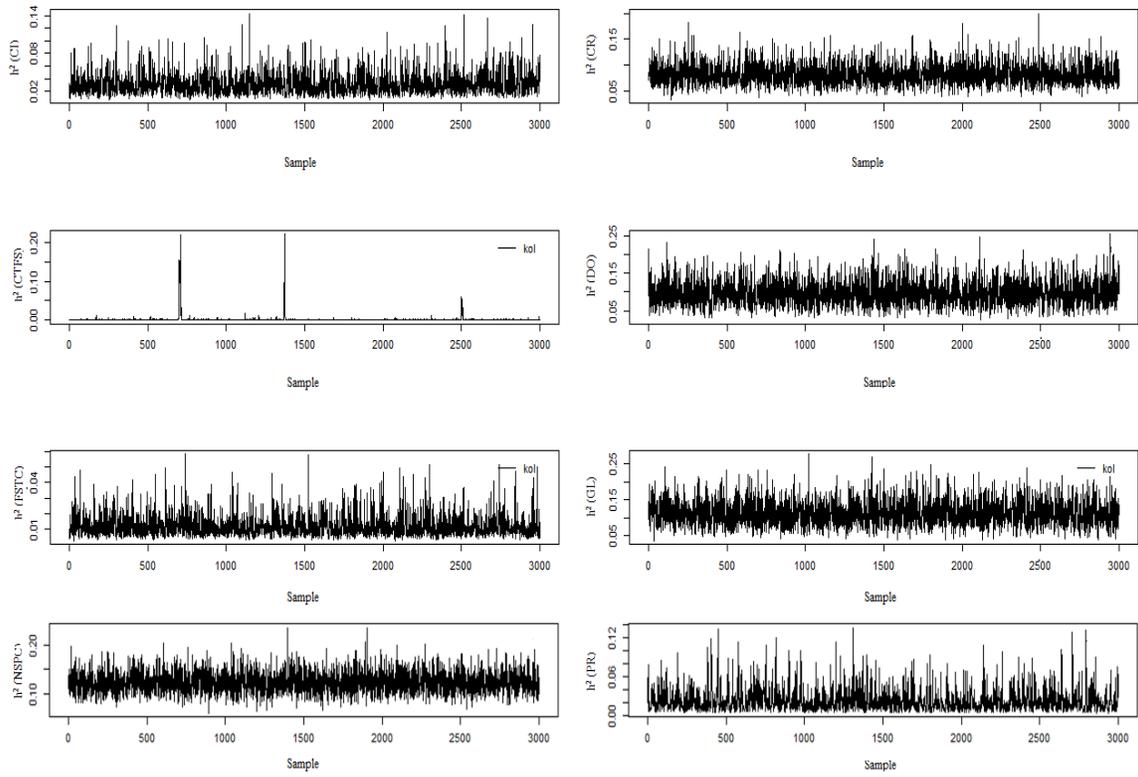


Figure 1. Trace plot of heritability for reproductive traits in best models by single- trait analysis

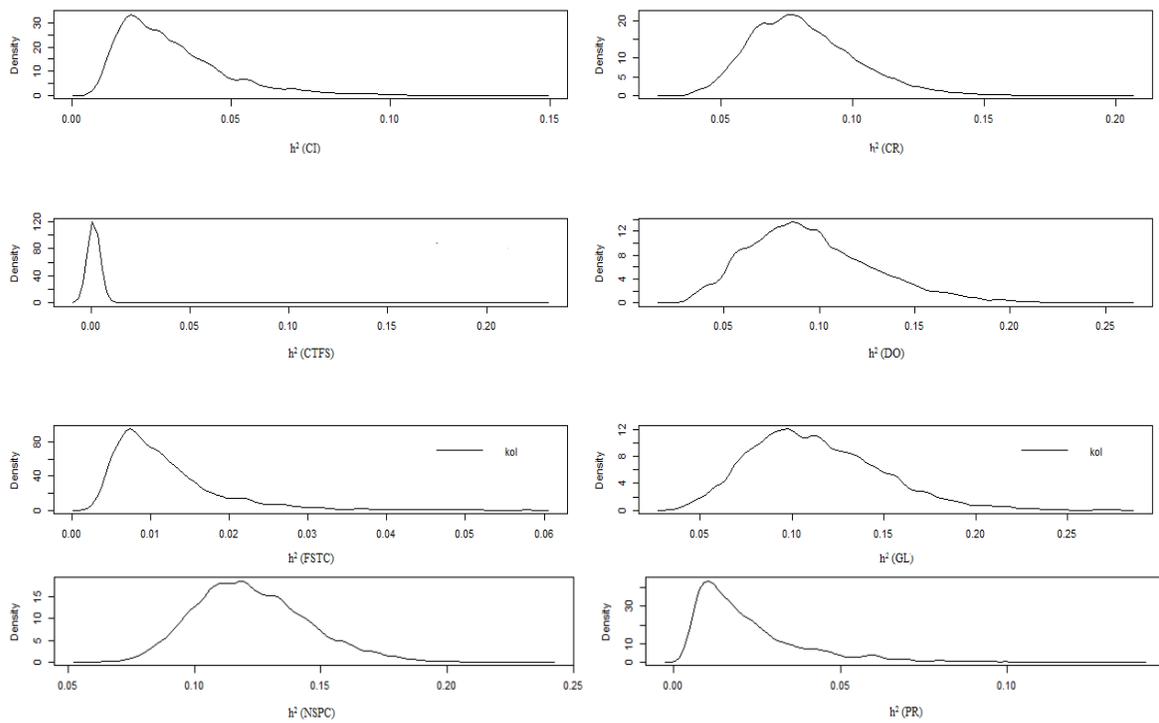


Figure 2. Posterior densities for reproductive traits in best models by single- trait analysis

Table 2. Variance components, heritability, and DIC of different models for reproductive traits

Trait ¹	Model	$\sigma_a^2 \pm SE$	$\sigma_e^2 \pm SE$	$\sigma_{pe}^2 \pm SE$	$\sigma_s^2 \pm SE$	$h^2 \pm SE$	DIC ²
CI	1	376.32±2.9138	6289.76±5.9299	-	-	0.056±0.0004	3914.05
	2	269.15±2.5856	6322.86±5.8742	37.38±0.8864	-	0.040±0.0004	3890.28
	3	249.45±2.6959	7227.15±8.1268	-	102.74±1.1903	0.033±0.0003	2616.04
	4	238.64±2.4713	7192.28±8.0830	28.64±0.4789	102.48±1.2053	0.032±0.0003	2598.00
GL	1	6.16±0.0279	48.34±0.0438	-	-	0.113±0.0005	4573.85
	2	5.69±0.0263	47.98±0.0436	1.03±0.0105	-	0.104±0.0005	4628.32
	3	6.34±0.0384	46.04±0.0511	-	3.62±0.0280	0.113±0.0006	3201.64
	4	5.91±0.0365	45.51±0.0517	1.20±0.0141	3.55±0.0270	0.105±0.0006	3240.70
DO	1	421.42±2.5802	4246.52±4.1794	-	-	0.090±0.0005	3680.11
	2	211.12±1.7306	4142.20±4.2622	286.44±2.2616	-	0.045±0.0004	3685.22
	3	480.12±3.2192	4194.96±5.1140	-	310.26±2.2298	0.096±0.0006	2536.71
	4	241.07±2.1985	4137.16±4.9286	269.99±2.3200	308.56±2.1282	0.049±0.0004	2549.08
CTFS	1	4.15±0.0914	3661.70±3.2180	-	-	0.001±0.00003	3672.59
	2	4.65±0.2080	3641.81±3.4442	9.85±1.1544	-	0.001±0.00006	3683.52
	3	6.87±0.6581	3542.68±3.9335	-	1.46±0.0361	0.002±0.0002	2551.71
	4	12.77±1.1615	3539.56±4.0091	1.64±0.0277	1.47±0.0316	0.004±0.0003	2563.28
FSTC	1	14.60±0.1347	1599.10±1.2171	-	-	0.01±0.00008	5141.20
	2	14.21±0.1297	1590.56±1.2086	13.59±0.1329	-	0.009±0.00007	5067.32
	3	16.83±0.1739	1423.72±1.3793	-	3.72±0.0465	0.012±0.0001	3550.11
	4	17.07±0.1835	1411.31±1.3398	15.13±0.1590	3.78±0.0490	0.012±0.0001	3549.21
CR	1	28.06±0.1187	395.65±0.3122	-	-	0.066±0.0003	5146.02
	2	27.66±0.1158	393.61±0.3182	5.67±0.0478	-	0.065±0.0003	5135.72
	3	34.29±0.1660	361.38±0.3682	-	13.16±0.0983	0.084±0.0004	3569.62
	4	33.73±0.1620	358.92±0.3588	6.57±0.0607	13.22±0.1023	0.082±0.0004	3542.72
PR	1	6.59±0.0790	260.89±0.2112	-	-	0.025±0.0003	4984.53
	2	3.79±0.0441	251.43±0.2010	15.20±0.0911	-	0.014±0.0002	4991.31
	3	6.15±0.0881	263.29±0.2637	-	0.823±0.0109	0.023±0.0003	3210.4
	4	3.95±0.0494	249.95±0.2559	18.68±0.1241	0.827±0.0123	0.014±0.0002	3281.27
NSPC	1	0.014±0.00006	0.282±0.0002	-	-	0.047±0.0002	5201.95
	2	0.006±0.00002	0.047±0.00004	0.005±0.00002	-	0.097±0.0002	5029.03
	3	0.017±0.00009	0.246±0.0002	-	0.0022±0.00004	0.064±0.0003	3625.84
	4	0.008±0.00003	0.043±0.00004	0.008±0.00003	0.0031±0.00002	0.123±0.0004	3376.42

¹CI: calving interval, GL: gestation length, DO: days open, CTFS: calving to first service, FSTC: first service to conception, CR: conception rate, PR: pregnancy rate, NSPC: number of inseminations per conception.

² σ_a^2 : Additive variance, σ_e^2 : error variance, σ_{pe}^2 : permanent environmental variance, h^2 : heritability, DIC: deviance information criteria, SE: standard error.

recorded for CI×DO, CI×PR, DO×PR, and CTFS×PR (>0.88); however, most reproductive traits had environmental correlations of less than 0.1. The high positive and negative genetic correlations between traits indicate that improving the additive genetic level in one trait may lead to either partial genetic improvement or genetic suppression in other traits, respectively (Pantelić et al., 2011).

Discussion

In this study, several important indices of reproductive performance in Sistani cattle were analyzed. The model

consisting of the additive, sire, and permanent environment parameters (i.e., model 4) was the most appropriate model for CI, FSTC, CR, and NSPC, indicating that sire and environment effects should be considered together in the model for accurate estimation of the genetic parameters. On the other hand, model 3 was the most suitable model for other traits so that including sire effect in the additive effect as random effect produced unbiased estimation. In reported studies, comparisons of model had not been done for estimation of genetic parameters of reproductive traits and most studies used model 1 (additive and residual) or model 2 (additive, permanent environmental and residual). The model 1 was

Table 3. Genetic and environmental correlation between reproductive traits

Trait 1 ¹	Trait 2	$r_g \pm SE$	$r_e \pm SE$ ²
CI	GL	-0.235±0.0033	-0.073±0.0005
	DO	0.974±0.0001	0.990±0
	CTFS	0.512±0.0019	0.737±0.0001
	FSTC	-0.590±0.0020	-0.052±0.0003
	CR	-0.999±0	0.014±0.0003
	PR	0.250±0.0024	-0.919±0
	NSPC	0.900±0.005	0.014±0.0003
GL	DO	-0.552±0.0015	-0.078±0.0004
	CTFS	-0.446±0.0016	-0.095±0.0004
	FSTC	-0.529±0.0019	-0.172±0.0030
	CR	-0.405±0.0018	0.164±0.0003
	PR	0.177±0.0025	-0.028±0.0003
	NSPC	0.446±0.0019	-0.119±0.0003
DO	CTFS	0.215±0.0022	0.795±0.0001
	FSTC	0.223±0.0025	-0.043±0.0003
	CR	-0.986±0.0001	0.029±0.0004
	PR	-0.794±0.0009	-0.994±0
	NSPC	0.162±0.0018	0.019±0.0003
CTFS	FSTC	-0.488±0.0024	0.015±0.0003
	CR	-0.947±0.0003	0.036±0.0003
	PR	-0.457±0.0020	-0.883±0
	NSPC	0.001±0.0001	0.0005±0.0003
FSTC	CR	-0.028±0.0021	-0.516±0.0002
	PR	-0.180±0.0028	0.075±0.0003
	NSPC	-0.007±0.0018	0.435±0.0002
CR	PR	0.262±0.0020	-0.045±0.0003
	NSPC	-0.250±0.0018	-0.648±0.0002
PR	NSPC	-0.056±0.0019	0.042±0.0003

¹CI: calving interval; GL: gestation length; DO: days open; CTFS: calving to first service; FSTC: first service to conception; CR: conception rate; PR: pregnancy rate; NSPC: number of inseminations per conception

² r_g : Genetic correlation; r_e : environmental correlation; SE: standard error

used for CI (Van der Westhuizen et al., 2001; Gutiérrez et al., 2002; Bernardes et al., 2015; Do Amaral Grossi et al., 2016; Martínez et al., 2016), PR (Bormann et al., 2006; Johnston et al., 2014), CR (Johnston et al., 2014) and DO (González-Peña et al., 2010). Eghbalsaied (2011) used simple animal model for estimation of 13 reproductive traits in Iranian Holstein cattle. The animal model with additive and permanent environmental random effect was used for estimation of genetic parameters of the reproductive traits in UK Holstein-Friesian (Kadarmideen et al., 2000), Spanish dairy cattle (González-Recio and Alenda, 2005), Chinese Holstein (Guo et al., 2014), Holstein and Jersey (Zambrano and Echeverri, 2014), Brahman cattle (Cavani et al., 2015), Mexican Brown Swiss (Colli et al., 2015), Nellore cattle (Ulhoa Magnabosco et al., 2016), Canadian Holstein (Jamrozik and Kistemaker, 2016), and Tunisian Holstein (Zaabza et al., 2016). Fitting of service sire effect in the model as random effect was reported for CTFS traits (Andersen-Ranberg et al., 2005) and GL (Jamrozik and Kistemaker, 2016). In this study, three models

as well as combination of three models (model 4) were compared and the best model was selected for each trait.

The very low heritability for CI (0.032, Table 2) is in agreement with other reports (Olori et al., 2002; Berry et al., 2013; Berry and Evans, 2014; Colli et al., 2015, Cavani et al., 2015). The reported heritability of CI in beef and dairy cattle ranged from 0.04 to 0.39 (Roughsedge et al., 2005; Veselá et al., 2013; Bernardes et al., 2015; Do Amaral Grossi et al., 2016; Martínez et al., 2016). Gestation length certainly varies among individual cows which is reflected in CI. The estimated heritability for GL (>0.1) in our study was close to the values reported in the Nellore cattle (Azevêdo et al., 2006; Ulhoa Magnabosco et al., 2016) but smaller than in other studies (Crews, 2006; Mujibi and Crews, 2009; Johanson et al., 2011; Chud et al., 2014). Selection for this trait might result in genetic improvement and indirectly result in genetic gain for CI. The discrepancy between our findings and other reports could be due to differences in genetic variation among the populations, statistical models used for genetic analysis, or environmen-

tal conditions.

Days open (DO) and CI are usually influenced by the same factors because GL is a fixed interval (Jainudeen and Hafez, 2000). Estimated heritability of 0.096 for DO in the present study was close to the values in Australian beef cattle (0.11; Berry et al., 2014), Colombia Jersey (0.09; Zambrano and Echeverri, 2014) and Australian beef cattle (0.09; Goyache et al., 2005) but higher than reported range of 0.03- 0.07 in other studies (Demeke et al., 2004; Oseni et al., 2004; Goodling et al., 2005; Chang et al., 2006; Ulh a Magnabosco et al., 2016). The reported heritability value of 0.01 to 0.136 for CTFS (Kadarmideen et al., 2000; Morris et al., 2000; Biffani et al., 2005; Guo et al., 2014; Zaabza et al., 2016) was higher than our estimate (0.002). The estimated heritability for FSTC in the present study (0.01) was higher than for Iranian Holstein (0.003; Eghbalsaied, 2011). The reported heritability of FSTC for Spanish (0.02; Gonz alez-Recio and Alenda, 2005), Canadian dairy cattle (0.03- 0.055; Koeck et al., 2014; Jamrozik and Kistemaker, 2016), and Tunisian Holstein (0.024; Zaabza et al., 2016) were higher than findings in the present study.

The heritability of CR for Sistani cattle in the present study (0.084) was higher than that for Australian composite breed and Colombia Holstein (0.01 and 0.03, respectively) but smaller than that for Australian Brahman and Colombia Jersey (0.11 and 0.147, respectively) (Johnston, 2014; Zambrano and Echeverri, 2014). The heritability of PR was estimated at 0.023 that was close to (0.02) in composite cows as reported by Johnson et al. (2014), and smaller than those (0.03 to 0.33) reported in other studies (Evans et al., 1999; Bormann et al., 2006; MacNeil et al., 2006; Cushman and Perry, 2012).

The NSPC is an indirect measure of reproductive cycle showing large variations between animals. This trait requires the record of each service, which is rarely available under natural service conditions. The heritability of NSPC was estimated at 0.12. NSPC is related to FSTC and CTFS and any improvement in NSPC could indirectly influence the latter traits. The estimate of heritability value of NSPC was higher than the recorded heritabilities (0.009- 0.093) in other breeds (Kadarmideen et al., 2000; Demeke et al., 2004; Azev do et al., 2006; Guo et al., 2014; Koeck et al., 2014). Because of the low heritability and repeatability of the reproductive traits, their improvement through mass selection may be slow; however, it is essential because of economic value of these traits. The heritability of fertility traits in hot climates was reported to be smaller than in temperate climates (Zaabza et al., 2016). Hansen et al. (2011) also reported that the major cause of the decrease in reproductive performances was heat stress that occurred through

physiological adaptations ensuring a better thermoregulatory potential. Improvement in NSPC could impact on CR due to its inverse relationship with NSPC. On the other hand, lower NSPC could decrease DO and increase PR.

Genetic correlation between reproductive traits varied from 0.001 (between CTFS and NSPC) to - 0.999 (between CI and CR). Genetic correlation between CI and other traits was very high, except for PR and GL. Residual correlations of CI with DO and CTFS were highly positive, and highly negative for CI \times PR. Genetic correlation between GL and other traits was moderate (<0.56) and residual correlation between GL and other traits was low. High negative genetic correlation of DO with CR and PR indicated that increases in DO may result in decreases in CR and PR. The same trend was found for CTFS and CR.

The estimated genetic correlation of -0.23 between CI and GL in Sistani cattle was higher than 0.12 for Iranian Holstein (Eghbalsaied, 2011). The genetic correlation of 0.97 between CI and DO was within the range of values (0.58- 99) in previous reports (Gonz alez-Recio and Alenda, 2005; Guo et al., 2014; Zambrano and Echeverri, 2014; Zaabza et al., 2016). Selection for fewer days open would contribute towards shorter calving intervals because the genes that act on one trait also act on the other. The recorded genetic correlation of 0.51 between CI and CTFS was close to 0.55 reported by Guo et al. (2014), higher than 0.33 found by Eghbalsaied (2011), and smaller than (range 0.67 to 0.80) in other reports (Biffani et al., 2005; Berry et al., 2014; Zaabza et al., 2016). According to Gonz alez-Recio and Alenda (2005), Berry et al. (2014) and Zaabza et al. (2016), genetic correlation between CI and FSTC was within the range of 0.79- 0.98, which is higher than our estimate (- 0.59). Genetic correlation (0.25) for CI \times PR in the present study was smaller than that (0.94) found by Gonz alez-Recio and Alenda, (2005). The estimated genetic correlation between CI and NSPC (0.90) was close to the reported values (0.96- 1) for several cattle populations (Gonz alez-Recio and Alenda, 2005; Eghbalsaied, 2011; Zambrano and Echeverri, 2014), but higher than the heritabilities in Chinese (0.49), Italian (0.61), and Tunisian (0.77) Holstein (Biffani et al., 2005; Guo et al., 2014; Zaabza et al., 2016), and in beef cattle (0.50; Berry et al., 2013).

The genetic correlations of GL \times DO, GL \times FSTC, GL \times NSPC, GL \times CTFS were estimated at -0.55, -0.53, 0.44 and -0.44, and higher than 0.02 (GL \times DO), -0.19 (-0.28) (GL \times FSTC), -0.22- (0.23) (GL \times NSPC) and 0.14 (GL \times CTFS) for Iranian (Eghbalsaied 2011) and Canadian Holstein (Jamrozik and Kistemaker, 2016) cattle. Genetic correlation between DO and CR was almost id-

entical to the value reported by González-Recio and Alenda (2005). Genetic correlations of DO with CTFS (0.22), FSTC (0.22), PR (-0.79), NSPC (0.16) in the present study were higher than those reported in other studies (González-Recio and Alenda, 2005; Berry et al., 2014; Guo et al., 2014; Zaabza et al., 2016). The genetic correlation of CTFS×FSTC (-0.49) was in line with the values (-0.40 to -0.50) reported by others (González-Recio and Alenda, 2005; Eghbalsaied, 2011; Berry et al., 2014), whereas lower values were reported for Canadian Holstein (-0.26) and Tunisian Holstein (-0.13) (Zaabza et al., 2016; Jamrozik and Kistemaker, 2016). The estimated genetic correlations of CTFS with PR (-0.46) and NSPC (0.001) in the present study were lower than other reports (Kadarmideen et al., 2000; Biffani et al., 2005; Zaabza et al., 2016; Jamrozik and Kistemaker, 2016). However, the reported genetic correlations of FSTC×PR, FSTC×NSPC, CR×PR, CR×NSPC (González-Recio and Alenda, 2005; Eghbalsaied, 2011; Johnston et al., 2014; Zambrano and Echeverri, 2014) were higher than those recorded in the current study.

In general, differences between our results with other reports could be related to the management and climatic variations that may affect both the genetic and environmental variances, using of different methodology to estimate of variance- covariance components, size and structure of data sets and breed differences.

Conclusions

Genetic parameters for 8 reproductive traits were estimated by Gibbs sampling. The results showed that the sire effect as the second random effect should be included in analysis of all traits, and the effect of permanent environment should be used in the models for CI, FSTC, CR, and NSPC along with additive and sire effects. The estimates of heritability for all traits were smaller than 0.1, except for GL and NSPC. Strong genetic correlations were observed for CI×DO, CI×CR, CI×NSPC, DO×CR, DO×PR, and CTFS × CR suggesting that these traits have the same genetic structure with the same gene controls. Therefore, CI, CR and PR could be improved by selecting for GL, DO and NSPC. The results showed that Sistani cows had genetic variations for some reproductive traits in their natural habitat (warm and dry climate with diet shortage) and these traits may be included in their breeding programs.

References

Andersen-Ranberg, I.M., Heringstad, B., Gianola, D., Chang, Y.M., Klemetsdal, G., 2005. Comparison between bivariate models for 56-day nonreturn and interval from calving to first insemination in Norwegian Red. *Journal of Dairy Science* 88, 2190-2198.

Azevêdo, D.M.M.R., Martins Filho, R., Lôbo, R.N.B., Malhado, C.H.M., Lôbo, R.B., Moura, A.A.A., Pimenta Filho, E.C., 2006. Reproductive performance of Nelore cows in the North and Northeast regions of Brazil. *Revista Brasileira Zootecnia* 35, 988-996.

Berg, A., Meyer, R., Yu, J., 2004. Deviance information criterion for comparing stochastic volatility models. *Journal of Business and Economic Statistics* 22, 107-120.

Bernardes, P.A., Grossi, D.A., Savegnago, R.P., Buzanskas, M.E., Urbinati, I., Bezerra, L.A.F., Lôbo, R.B., Munari, D.P., 2015. Estimates of genetic parameters and genetic trends for reproductive traits and weaning weight in Tabapuã cattle. *Journal of Animal Science* 93, 5175-5185.

Berry, D.P., Evans, R.D., 2014. Genetics of reproductive performance in seasonal calving beef cows and its association with performance traits. *Journal of Animal Science* 92, 1412-1422.

Berry, D.P., Kearney, J.F., Twomey, K., Evans, R.D., 2013. Genetics of reproductive performance in seasonal calving dairy cattle production systems. *Irish Journal of Agricultural and Food Research*, 1-16.

Berry, D.P., Wall, E., Pryce, J.E., 2014. Genetics and genomics of reproductive performance in dairy and beef cattle. *Animal* 8, 105-121.

Biffani, S., Canavesi, A., Samore, A.B., 2005. Estimates of genetic parameters for fertility traits of Italian Holstein-Friesian cattle. *Stočarstvo* 59, 145-153.

Bormann, J.M., Totir, L.R., Kachman, S.D., Fernando, R.L., Wilson, D.E., 2006. Pregnancy rate and first-service conception rate in Angus heifers. *Journal of Animal Science* 84, 2022-2025.

Buzanskas, M.E., Savegnago, R.P., Grossi, D.A., Venturini, G.C., Queiroz, S.A., Silva, L.O.C., Júnior, R.A.A.T., Munari, D.P., Alencar, M.M., 2013. Genetic parameter estimates and principal component analysis of breeding values of reproduction and growth traits in female Canchim cattle. *Reproduction, Fertility and Development* 25, 775-781.

Cammack, K.M., Thomas, M.G., Enns, R.M., 2009. Review: Reproductive traits and their heritabilities in beef cattle. *The Professional Animal Scientist* 25, 517-528.

Carvalho, J.G., Blake, R.W., Pollak, E.J., Van Soest, P.J., 1995. Comparison of Landim and Africander cattle in southern Mozambique: II. female fertility, reproduction, and beef offtake. *Journal of Animal Science* 73, 3527-3533.

Cavani, L., Garcia, D.A., Carreño, L.O.D., Ono, R.K., Pires, M.P., Farah, M.M., Ventura, H.T., Millen, D.D., Fonseca, R., 2015. Estimates of genetic parameters for reproductive traits in Brahman cattle breed. *Journal of Animal Science* 93, 3287-3291.

- Chang, Y.M., Andersen-Ranberg, I.M., Heringstad, B., Gianola, D., Klemetsdal, G., 2006. Bivariate analysis of number of services to conception and days open in Norwegian Red using a censored threshold-linear model. *Journal of Dairy Science* 89, 772-778.
- Chud, T.C.S., Caetano, S.L., Buzanskas, M.E., Grossi, D.A., Guidolin, D.G.F., Nascimento, G.B., Rosa, J.O., Lôbo, R.B., Munari, D.P., 2014. Genetic analysis for gestation length, birth weight, weaning weight, and accumulated productivity in Nellore beef cattle. *Livestock Science* 170, 16-21.
- Colli, R.D.C.C., Estrada-León, R., Magaña-Monforte, J., Segura-Correa, J.C., Núñez-Domínguez, R., 2015. Genetic parameters for growth and reproductive traits of Brown Swiss cattle from Mexico. *Ecosistemas y Recursos Agropecuarios* 3, 11-20.
- Crews, D.H.J., 2006. Age of dam and sex of calf adjustments and genetic parameters for gestation length in Charolais cattle. *Journal of Animal Science* 84, 25-31.
- Cushman, R.A., Perry, G.A., 2012. What we know about the genetics of reproduction. Proceedings of the Applied Reproductive Strategies in Beef Cattle, Sioux Falls, South Dakota, U.S.A.
- Demeke, S., Naser, F.W.C., Schoeman, S.J., 2004. Estimates of genetic parameters for Boran, Friesian and crosses of Friesian and Jersey with the Boran cattle in the tropical highlands of Ethiopia: reproduction traits. *Journal of Animal Breeding and Genetics* 121, 57-65.
- Diskin, M.G., Kenny, D.A., 2014. Optimising reproductive performance of beef cows and replacement heifers. *Animal* 8, 27-39.
- Do Amaral Grossi, D., Berton, M.P., Buzanskas, M.E., Chud, T.C.S., Grupioni, N.V., De Paz, C.C.P., Lôbo, R.B., Munari, D.P., 2016. Genetic analysis on accumulated productivity and calving intervals in Nellore cattle. *Tropical Animal Health and Production* 48, 207-210.
- Eghbalsaid, S., 2011. Estimation of genetic parameters for 13 female fertility indices in Holstein dairy cows. *Tropical Animal Health and Production* 43, 811-816.
- Evans, J.L., Golden, B.L., Bourdon, R.M., Long, K.L., 1999. Additive genetic relationships between heifer pregnancy and scrotal circumference in Hereford cattle. *Journal of Animal Science* 77, 2621-2628.
- Falconer, D.S., Mackay, T.F.C., 1996. Introduction to quantitative genetics. 4th Ed. Longman, Harlow, UK.
- Gelman, A., Carlin, J.B., Stern, H.S., Rubin, D.B., 2013. Bayesian data analysis. 3rd Ed. Chapman and Hall/CRC, London, UK.
- Geweke, J., 1992. Evaluating the accuracy of sampling based approaches to the calculation of posterior moments. Available at: <http://citeseer.ist.psu.edu/viewdoc/summary?doi=10.1.1.27.2952> [verified 10 March 2016].
- González-Peña, D., Espinoza-Villavicencio, J.L., Guerra, D., Palacios, A., Évora, J.C., Portales, A., 2010. Components of (co) variance of the days open in Siboney dairy cows. *Arquivo Brasileiro de Medicina Veterinária e Zootecnia* 62, 136-143.
- González-Recio, O., Alenda, R., 2005. Genetic parameters for female fertility traits and a fertility index in Spanish dairy cattle. *Journal of Dairy Science* 88, 3282-3289.
- Goodling, R.C., Shook, G.E., Weigel, K.A., Zwald, N.R., 2005. The effect of synchronization on genetic parameters of reproductive traits in dairy cattle. *Journal of Dairy Science* 88, 2217-2225.
- Goyache, F., Gutiérrez, J.P., Fernández, I., Royo, L.J., Álvarez, I., 2005. Genetic analysis of days open in beef cattle. *Livestock Production Science* 93, 283-289.
- Guo, G., Guo, X., Wang, Y., Zhang, X., Zhang, S., Li, X., Liu, L., Shi, W., Usman, T., Wang, X., Du, L., Zhang, Q., 2014. Estimation of genetic parameters of fertility traits in Chinese Holstein cattle. *Canadian Journal of Animal Science* 94, 281-285.
- Gutiérrez, J.P., Álvarez, I., Fernández, I., Royo, L.J., Díez, J., Goyache, F., 2002. Genetic relationships between calving date, calving interval, age at first calving and type traits in beef cattle. *Livestock Production Science* 78, 215-222.
- Hansen, P.J., 2011. Heat stress and climate change. In: Moo-Young, M. (Ed.), *Comprehensive Biotechnology*. Elsevier, Amsterdam, pp. 477-485.
- Heaton, K., Wilde, T., Nelson, M., ZoBell, D., 2013. Practical reproduction strategies for Utah beef Ranches. Available at: http://extension.usu.edu/files/publications/publication/AG_Beef_2013-01pr.pdf [Verified 10 March 2016].
- Jainudeen, M.R., Hafez, E.S.E., 2000. Cattle and buffalo. In: Hafez, B., Hafez, E.S.E. (Eds.), *Reproduction in Farm Animals*. Wiley-Blackwell, New Jersey, pp. 157-171.
- Jamrozik, J., Kistemaker, G.J., 2016. Updated genetic parameters for Holstein reproductive traits using more recent data. Available at: http://www.cdn.ca/Articles/GEBAPR2016/3_New%20RP%20Parameter%20-%20Janusz.pdf. [Verified 1 July 2016].
- Jamrozik, J., Fatehi, J., Kistemaker, G.J., Schaeffer, L.R., 2005. Estimates of genetic parameters for Canadian Holstein female reproduction traits. *Journal of Dairy Science* 88, 2199-2208.
- Jansen, J., 1986. Direct and maternal genetic parameters of fertility traits in Friesian cattle. *Livestock Production Science* 15, 153-164.
- Johanson, J.M., Berger, P.J., Tsuruta, S., Misztal, I., 2011. A bayesian threshold-linear model evaluation of perinatal mortality, dystocia, birth weight, and gestation length in a holstein herd. *Journal of Dairy Science* 94, 450-460.

- Johnston, D.J., 2014. Genetic improvement of reproduction in beef cattle. Proceedings of the 10th World Congress on Genetics Applied to Livestock Production, Vancouver, Canada.
- Johnston, D.J., Barwick, S.A., Fordyce, G., Holroyd, R.G., Williams, P.J., Corbet, N.J., Grant, T., 2014. Genetics of early and lifetime annual reproductive performance in cows of two tropical beef genotypes in northern Australia. *Animal Production Science* 54, 1-15.
- Kadarmideen, H.N., Thompson, R., Simm, G., 2000. Linear and threshold model genetic parameters for disease, fertility and milk production in dairy cattle. *Animal Science* 71, 411-419.
- Koeck, A., Miglior, F., Jamrozik, J., Kelton, D.F., Schenkel, F.S., 2014. Genetic relationships of fertility disorders with reproductive traits in Canadian Holsteins. Proceedings of the 10th World Congress on Genetics Applied to Livestock Production, Vancouver, Canada.
- Koots, K.R., Gibson, J.P., Smith, C., Wilton, J.W., 1994. Analyses of published genetic parameter estimates for beef production traits. 1. Heritability. *Animal Breeding Abstracts* 62, 309-388.
- Kuhn, M.D., VanRaden, P.M., Hutchison, J.L., 2004. Use of early lactation days open records for genetic evaluation of cow fertility. *Journal of Dairy Science* 87, 2277-2284.
- MacNeil, M.D., Geary, T.W., Perry, G.A., Roberts, A.J., Alexander, L.J., 2006. Genetic partitioning of variation in ovulatory follicle size and probability of pregnancy in beef cattle. *Journal of Animal Science* 84, 1646-1650.
- Martínez, R.A., Dasseville, R., Bejarano, D., Jimenez, A., Even, G., Mészáros, G., Sölkner, J., 2016. Direct and maternal genetic effects on growth, reproduction, and ultrasound traits in Zebu Brahman cattle in Colombia. *Journal of Animal Science* 49, 1-9.
- Mohammadabadi, M.R., Soflaei, M., Mostafavi, H., Honarmand, M., 2011. Using PCR for early diagnosis of bovine leukemia virus infection in some native cattle. *Genetics and Molecular Research* 10, 2658-2663.
- Mohammadi, A., Nassiry M.R., Mosafer, J., Mohammadabadi, M.R., Sulimova, G.E., 2009. Distribution of BoLA-DRB3 allelic frequencies and identification of a new allele in the Iranian cattle breed Sistani (*Bos indicus*). *Russian Journal of Genetics* 45, 198-202.
- Morris, C.A., Wilson, J.A., Bennett, G.L., Cullen, N.G., Hickey, S.M., Hunter, J.C., 2000. Genetic parameters for growth, puberty, and beef cow reproductive traits in a puberty selection experiment. *New Zealand Journal of Agriculture Research* 43, 83-91.
- Mujibi, F.D.N., Crews, D.H., 2009. Genetic parameters for calving ease, gestation length, and birth weight in Charolais cattle. *Journal of Animal Science* 87, 2759-2766.
- Olori, V.E., Meuwissen, T.H.E., Veerkamp, R.F., 2002. Calving interval and survival breeding values as measure of cow fertility in a pasture-based production system with seasonal calving. *Journal of Dairy Science* 85, 689-696.
- Oseni, S., Tsuruta, S., Misztal, I., Rekaya, R., 2004. Genetic parameters for days open and pregnancy rates in US Holsteins using different editing criteria. *Journal of Dairy Science* 87, 4327-4333.
- Pantelić, V., Sretenović, L., Ostojić-Andrić, D., Trivunović, S., Petrović, M.M., Aleksić, S., Ružić-Muslić, D., 2011. Heritability and genetic correlation of production and reproduction traits of Simmental cows. *African Journal of Biotechnology* 10, 7117-7121.
- Roughsedge, T., Amer, P.R., Thompson, R., Simm, G., 2005. Genetic parameters for a maternal breeding goal in beef production. *Journal of Animal Science* 83, 2319-2329.
- Rust, T., Groeneveld, E., 2001. Variance component estimation on female fertility traits in beef cattle. *South African Journal of Animal Science* 31, 131-141.
- Smith, B.J., 2007. Boa: an R package for MCMC output convergence assessment and posterior inference. *Journal of Statistical Software* 21, 1-37.
- Ulhoa Magnabosco, C., Brito Lopes, F., De Magalhaes Rosa, G.J., 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 (Colombian Journal of Animal Science and Veterinary Medicine)* 29, 119-129.
- Van der Westhuizen, R.R., Schoeman, S.J., Jordaan, G.F., Van Wyk, J.B., 2001. Genetic parameters for reproductive traits in a beef cattle herd estimated using multitrait analysis. *South African Journal of Animal Science* 31, 41-48.
- Veselá, Z., Vostrý, L., Svitáková, A., 2013. Genetic analysis of female fertility traits in beef cattle in the Czech Republic. *Interbull Bulletin* 47, 172-175.
- Zaabza, H.B., Ben Gara, A., Hammami, H., Jemmali, B., Ferchichi, M.A., Rekik, B., 2016. Genetic parameters of reproductive traits in Tunisian Holsteins. *Archives Animal Breeding (Archiv Tierzucht)* 59, 209-213.
- Zambrano, J.C., Echeverri, J., 2014. Genetic and environmental variance and covariance parameters for some reproductive traits of Holstein and Jersey cattle in Antioquia (Colombia). *Revista Brasileira Zootecnia* 43, 132-139.

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استنباط بیزی پارامترهای ژنتیکی صفات تولیدمثلی در گاوهای بومی سیستانی با استفاده از نمونه‌گیری گیبس

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چکیده این مطالعه به منظور برآورد پارامترهای ژنتیکی برخی صفات تولیدمثلی گله‌های گوشتی سیستانی انجام شد. داده‌ها شامل ۱۴۸۹ رکورد تعداد تلقیح، گوساله‌زایی و تاریخ‌های تلقیح در زایش‌های مختلف بود. صفات تولیدمثلی از جمله فاصله گوساله‌زایی (CI)، طول دوره آبستنی (GL)، روزهای باز (DO)، فاصله زایش تا اولین تلقیح (CTFS)، فاصله اولین تلقیح تا آبستنی (FSTC)، نرخ گیرایی (CR)، نرخ آبستنی (PR) و تعداد تلقیح به ازای هر آبستنی (NSPC) مورد بررسی قرار گرفتند. مولفه‌های واریانس صفات با استفاده از مدل‌های مختلف تک‌صفتی به روش نمونه‌گیری گیبس برآورد شدند و همبستگی بین صفات با استفاده از بهترین مدل برای هر صفت توسط مدل چندصفتی بدست آمد. پس از به هم‌گرایی رسیدن، میانگین پسین وراثت‌پذیری‌ها برای CI، GL، DO، CTFS، FSTC، CR، PR و NSPC در بهترین مدل به ترتیب ۰/۰۳۲، ۰/۱۱۳، ۰/۰۹۶، ۰/۰۰۲، ۰/۰۱۲، ۰/۰۸۲، ۰/۰۲۳ و ۰/۱۲۳ برآورد شد. بالاترین و پایین‌ترین همبستگی ژنتیکی به ترتیب برای CI×CR (۰/۹۹۹-) و CTFS×NSPC (۰/۰۰۱) بدست آمد. نتایج نشان داد که ژنتیک افزایشی برای بیشتر صفات تولیدمثلی در گله‌های گوشتی سیستانی پایین بود، بنابراین انتخاب برای این صفات باعث پیشرفت ژنتیکی کمتری می‌شود. با این حال وراثت‌پذیری برآورد شده برای DO، GL و NSPC و همبستگی ژنتیکی این صفات با CI، CR و PR پیشنهاد می‌کند که انتخاب برای این صفات در گله‌های سیستانی ممکن است پیشرفت ژنتیکی در باروری را افزایش دهد.