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Bayesian Inference of (Co) Variance Components and Genetic Parameters for Economic Traits in Iranian Holsteins via Gibbs Sampling

Research Article

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ABSTRACT

The aim of this study was using Bayesian approach via Gibbs sampling (GS) for estimating genetic parameters of production, reproduction and health traits in Iranian Holstein cows. Data consisted of 320666 first-lactation records of Holstein cows from 7696 sires and 260302 dams collected by the animal breeding center of Iran from year 1991 to 2010. (Co) variance components were estimated using a multi-trait animal model analyzed via Gibbs sampling. After convergence, the highest posterior density region of heritability for milk (MY305), fat (FY305), protein (PY305), age at first calving (AFC), calving interval (CI) and somatic cell score (SCS) were 0.255-0.275, 0.195-0.215, 0.195-0.225, 0.260-0.275, 0.065-0.080 and 0.055-0.075, respectively. Genetic correlations ranged from -0.121 (between FY305 and AFC) to 0.914 (between MY305 and PY305) and for phonotypic correlations, it was from -0.083 (between MY305 and SCS) to 0.929 (between MY305 and PY305. The result of this study showed that production traits and AFC have enough genetic variation to develop breeding programs. The estimated genetic correlations suggest that milk production traits and CI would be affected if increasing milk production is the selection goal. The high genetic correlation between CI with SCS suggests that increasing calving interval trait result in an increased SCS.

KEY WORDS Bayesian inference, production traits, reproduction traits, somatic cell score.

INTRODUCTION

Estimation of (Co) variance components is important in animal breeding. Prediction error variances of predicted levels of random effects (e.g., breeding values) increase as differences between estimated and true values of variance component increase, thus, accurate estimates of (Co) variance are important (Henderson, 1975; Van Tassell and Van Vleck, 1996). Likelihood based methods, such as maximum likelihood (ML), restricted maximum likelihood (REML) and Bayesian methods became appropriate, since they can handle complex pedigrees and different breeding designs (Shaw, 1987; Blasco, 2001; Ovaskainen *et al.* 2008). Among these methods, there is an increasing interest towards Bayesian modeling (Beaumont and Rannala, 2004). The major benefit of Bayesian method was being the ability to quantify uncertainty in multivariate problems by determining the full joint posterior distribution of the model parameters (Gelman *et al.* 2004). Improvement through selection in traits associated with milk quality, milk yield and reproduction in dairy cattle depends on availability of credible genetic parameters for these traits. The accuracy of

an estimated genetic parameter is related to many factors, such as, the quantity and quality of information (records and pedigree), the statistical model and the methods of (Co) variance component estimation (Aspilcueta- Borquis *et al*. 2010a; Aspilcueta-Borquis *et al*. 2010b). Although REML methods have desirable properties, when applied to a large data set it requires a large memory space. With increasing the size of data an alternative approach to estimation with less computational burden in which, estimate has desirable properties, needs to be developed (Arakawa *et al*. 2009). The Bayesian analysis via Gibbs sampling (Gelfand and Smith, 1990) that has often been used in the field of animal breeding has certain benefits over REML, especially, regarding memory space required for estimating variance components (Van Tassell *et al*. 1995).

Bayesian methods have been used for estimation of genetic parameters in different traits, for example, milk flow (Ilahi and Kadarmideen, 2004), disease traits (Ghavi Hossein-Zadeh and Ardalan, 2011), production traits (Firat *et al*. 1997; Ben Gara *et al*. 2006; Paula *et al*. 2008; Lidauer *et al*. 2009; Aspilcueta-Borquis *et al*. 2010a; Aspilcueta-Borquis *et al*. 2010b; Penasa *et al*. 2010), reproduction traits (Ghiasi *et al*. 2011) and somatic cell score (Penasa *et al*. 2010). Until now, REML has been the method of estimation of genetic parameters for production and reproduction traits in Iranian. In this study a Bayesian approach to estimation of covariance components via Gibbs sampling was performed.

MATERIALS AND METHODS

A total of 320666 first lactation Holstein records from 7696 sire and 260302 dams belong to 1089 herds were used in this study. Records were collected by Animal Breeding Center of Iran from 1991 to 2010. The pedigree structure of records is showen in Table 1.

Table 1 Pedigree structure of records

Animals	Number
Animals in total	460801
Inbreeds in total	238700
Sires in total	7696
Dams in total	260302
Founders animal	49340
Non-founders animal	411461
Animals with known sire	19813
Animals with known dam	18461
Animals with known sire and dam	373187

The connectedness between herds was existed because of using artificial insemination. The seasons of calving for animals were defined by month of calving. Month of calving Dey, Bahman and Esfand (January, February and March), Farvardin, Ordibehesht and Khordad (April, May and June), Tir, Mordad and Shahrivar (July, August and September) and Mehr, Aban and Azar (October, November and December) were used for winter, spring, summer and autumn season, respectively. The traits were production traits (305 days milk, fat and protein yield), reproduction traits (age at first calving and calving interval) and hygiene trait (somatic cell score). Number of levels herd year season of calving effect was 13366. Minimum and maximum of animals in herd year season of calving levels were 6 and 591 animals, respectively. Edition of records were as: animals that had same number with sires and dams were omitted, age at first calving for edition of records was set to be 18 to 40 month (Penasa *et al*. 2010), calving interval was restricted to the range of 260 and 750 days as Ansari *et al*. (2009). To obtain an approximate normal distribution, somatic cell count (SCC) records were transformed into somatic cell score (SCS) and the lactation mean of the natural log of test day somatic cell count (LSCS) was determined as described in equation Schukken *et al*. (1992) and Odegard *et al*. (2003):

$$LSCS= 1 / n \sum_{n}^{1}(\log_e(SCC/1000cells/mL)+3)$$

Where:
n: number of test day records for animal i.

The data structure is presented in Table 2. The covariance components were estimated via Gibbs sampling in a multi-trait analysis using (DMU) software package (Madsen and Jensen, 2008). The models used for the analysis were:

$$y= Xb + Zu + e$$

Where:
y: vector of observed traits.
X: incidence matrix associating data to the fixed effects.
b: vector of fixed effects (herd year season and age at calving as linear and quadratic effects).
Z: incidence matrix associating data to the additive genetic effects.
u: vector of additive genetic random effects.
e: vector of random residuals.

For age at first calving trait, another analysis was performed by two random effects. In this analysis, herd- sire effect as well as additive genetic was fitted in model (model 2). Uniform, Gaussian and inverted Wishart prior distributions were specified for fixed effects (b) random effects and (Co) variance components, respectively (Van Tassel and Van Vleck, 1996).

β α constant

$\alpha \mid G \sim MVN\ [0, (G \otimes A)]$
$G \mid S_g, V_g \sim IW\ [S_g V_g, V_g]$
$R \mid S_r, V_r \sim IW\ [S_r V_r, V_r]$

Where:
A, G and R: matrices of additive genetic relationship, covariances of additive genetic effects among the traits, and residuals, respectively.
$\otimes$: Kronecker product.
S_g and V_g; S_r and V_r: prior values and degrees of freedom for additive genetic and residual covariances, respectively.

Gibbs chains with 120000 iterations were generated, with an initial discard of 20000 samples and a sampling interval of 100 iterations. Therefore, each analysis 1200 samples of (Co) variance components were obtained. The convergence checking of the chains generated by the Gibbs sampler was done using graphical analysis and diagnosis tests available in Bayesian output analysis program (BOA) (Smith, 2007). Credible intervals and high density regions for all the estimates of (Co) variance components and genetic parameters were determined at 95% level. Geweke method was used for diagnosis (Geweke, 1992). Diagnostic of Geweke (1992) is assessed by comparing the sample mean in early segment of the chain to the mean in later segment. Geweke originally suggested the comparison between the first n_1= 0.1 n and the last n_2= 0.5 n samples in the chain, although the diagnostic can be applied with other choices.

RESULTS AND DISCUSSION

Variance components and heritability

The two-side p-value obtained from Geweke method confirmed convergence for all chains. After confirming convergence, 1200 samples used for the estimation of posterior means and highest posterior densities (HPD) of (Co) variance components and genetic parameters. Table 3 presents the posterior means and HPD of variance components and heritability for different traits. Posterior means of heritability for production traits (milk, fat and protein production) and age at first calving were moderate but it was low for calving interval and somatic cell score. The range of heritabilities varied from 0.063 (SCS) to 0.268 (AFC). This result suggests that a greater part of phenotypic variance in MY305, FY305, PY305 and AFC is due to additive action of genes. Thus selection for these traits would result in considerable genetic gain. Figures 1 and 2 shows the trace plots and marginal posterior densities of heritability for MY305, FY305, PY305, AFC, CI and SCS. The plots indicate that the algorithm mixed well, despite of differences among traits. In particular, the mixing of the Gibbs sampler was slightly worse for CI and SCS, compared to the other traits.

Distributions for the traits other than CI and SCS were closed to the normal distribution. The skewed densities for CI and SCS reflect the scant statistical information in the sample. The heritability for MY305, FY305 and PY305 were 0.264, 0.206 and 0.211, respectively. These estimates were similar to the estimates from other studies in Iranian Holstein (Ghasemi, 2012; Toghiani, 2012; Nafez *et al.* 2012).

Reports of the heritability of milk yield in Iranian Holstein have been based on REML and a subset of the data. In agreement to this result, Paula *et al.* (2008) reported a heritability of 0.27 in Paraná state, Brazil. The estimates of heritability using Bayesian approach for Burlina (0.18) and Tunisian (0.17) (Ben Gara *et al.* 2006; Penasa *et al.* 2010) were lower than our estimates, but for Nordic Red cattle (0.35-0.48) (Madsen, 2008) it was higher.

The REML estimates of heritability in Iranian Holstein for fat and protein yield has been 0.149-0.19 and 0.23, respectively (Toghiani, 2012; Ghasemi, 2012; Nafez *et al.* 2012). The posterior means of heritability for PY305 and FY305 in Burlina, Paraná state and Nordic Red Holstein (Penasa *et al.* 2010; Paula *et al.* 2008; Madsen, 2008) were larger than our results for PY305 (0.211) and FY305 (0.206). The estimate of heritability for AFC was moderate (0.268; Table 3). Posterior mean of heritability for AFC with model 2 (additive genetic of animal and herd-sire random effect) was 0.262. Herd sire variance for AFC was estimated 0.634 (Table 3). Results of AFC with model that included of herd sire as well as additive genetic don't have difference, significantly. It was larger than the heritability observed for Serbian Simmentals (0.093) (Pantelic *et al.* 2011) or for Brazilian (0.19) and Colombian (0.13) Holsteins (Ceron-Munoz *et al.* 2004). Our estimate of AFC heritability was similar to that of 0.28 reported by Montaldo *et al.* (2010) but was smaller than the estimated heritability of Kenyan Holstein (0.38; Ojango and Pollott, 2001). Estimates of heritability for AFC in Holstein cattle using REML were 0.19 (Faraji-Arough *et al.* 2011) and 0.1 (Nafez *et al.* 2012) that were smaller than 0.268 in this study.

Heritability estimates for CI were small (0.072; Table 3). Small estimates (i.e., <0.10) are common for many fertility traits in dairy cows. In a review paper regarding genetic evaluation for fertility traits worldwide, Van Raden *et al.* (2004) argued that fertility traits in dairy cattle populations have heritability of 0.04 or less. The corresponding estimates in the current study are similar to those reported by Toghiani (2012) and Ghiasi *et al.* (2011) in Iranian Holstein (0.07 and 0.074, respectively) and larger than that of Haile-Mariam *et al.* (2008) in Australia (0.02-0.04) and Faraji-Arough *et al.* (2011) in Iran (0.04). HPD of heritability for SCS were between 0.055 and 0.0.075 (Table 3).

Table 2 Descriptive statistics for production, reproduction and somatic cell score

Description	MY305 (kg)	FY305 (kg)	PY305 (kg)	AFC (month)	CI (day)	SCS
No. animal	320666	320666	320666	320666	320666	320666
No. observation	320666	275872	164467	320666	227709	131996
Mean	7144.98	224.82	231.34	26.69	414.2	7.78
SD	1599.27	57.67	43.87	3.01	83.98	1.20
Min	2222.75	49.87	97.13	18.01	301	3.92
Max	12088.91	402.96	366.98	39.97	699	11.60
CV (%)	22.38	25.65	18.96	11.55	20.28	15.46

MY305: 305 days milk yield; FY305: 305 days fat yield; PY305: 305 days protein yield; AFC: age at first calving; CI: calving interval; SCS: somatic cell score; SD: standard deviation and CV: coefficient of variation.

Table 3 Posterior means and highest posterior density (HDP) region of variance components and genetic parameters for MY305, FY305, PY305, AFC, CI and SCS

Traits	Parameter[1]	Mean	SD	HPD	
				Low limit	High limit
MY305	σ_a^2	387310.3	5420.571	376699.177	397599.44
	σ_r^2	1078968	4235.756	107826.486	1087583.53
	σ_p^2	1466278	3214.677	1459631	1472080
	h^2	0.264	0.003	0.255	0.275
FY305	σ_a^2	290.949	4.870	281.265	300.442
	σ_r^2	1121.227	3.786	1113.611	1128.402
	σ_p^2	1412.176	2.644	1407.076	1417.369
	h^2	0.206	0.003	0.195	0.215
PY305	σ_a^2	249.126	4.792	240.399	258.203
	σ_r^2	933.037	3.553	926.105	939.854
	σ_p^2	1182.163	2.514	1177.131	1186.740
	h^2	0.211	0.004	0.195	0.225
AFC	σ_a^2	1.720	0.016	1.689	1.750
	σ_r^2	4.707	0.013	4.679	4.730
	σ_p^2	6.426	0.011	6.405	6.448
	h^2	0.268	0.002	0.260	0.275
CI	σ_a^2	471.227	17.337	441.180	506.462
	σ_r^2	6053.429	16.307	6023.713	6085.277
	σ_p^2	6524.656	12.636	6499.702	6548.803
	h^2	0.072	0.002	0.065	0.080
SCS	σ_a^2	0.061	0.003	0.054	0.068
	σ_r^2	0.915	0.004	0.907	0.921
	σ_p^2	0.971	0.003	0.971	0.982
	h^2	0.063	0.003	0.055	0.075
AFC[2]	σ_a^2	1.754	0.026	1.706	1.804
	σ_r^2	4.30	0.021	4.260	4.340
	σ_p^2	6.867	0.022	6.644	6.728
	σ_{hs}^2	0.634	0.017	0.600	0.665
	h^2	0.262	0.004	0.255	0.269

[1] σ_a^2= additive genetic variance; σ_r^2= residual variance; σ_p^2=phenotypic variance; σ_{hs}^2= herd sire variance and h^2= heritability.
[2] Parameters for AFC with two random effects in model (animal and herd-sire effects).
MY305: 305 days milk yield; FY305: 305 days fat yield; PY305: 305 days protein yield; AFC: age at first calving; CI: calving interval; SCS: somatic cell score and SD: standard deviation.

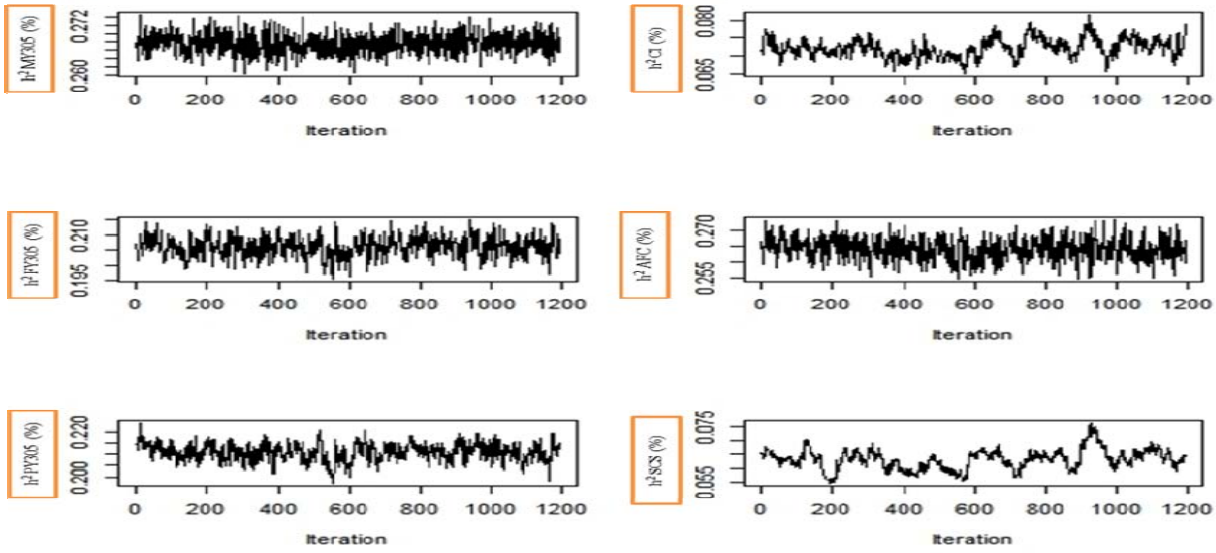

Figure 1 Trace plot of heritability for MY305, FY305, PY305, AFC, CI and SCS

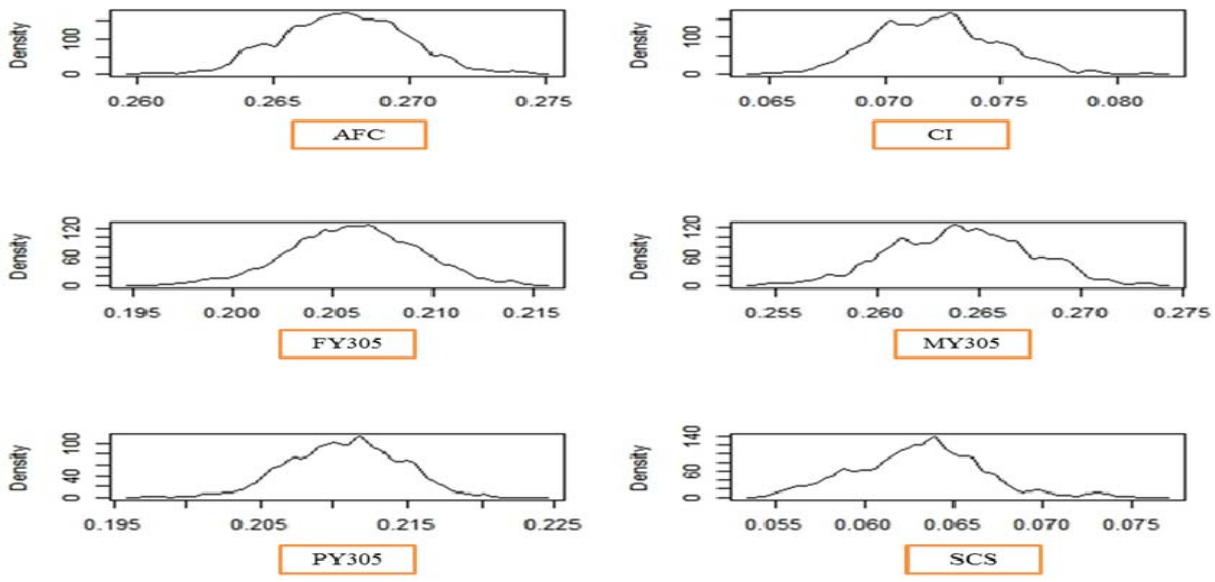

Figure 2 Marginal posterior densities for the heritabilities of MY305, FY305, PY305, AFC, CI and SCS

For Iranian Holstein, heritability was reported in the range of 0.05 to 0.082 (Ghasemi, 2012; Faraji-Arough *et al.* 2011), similar to the result in this research. Several authors have reported estimates as large as 0.1-0.25 (Montaldo *et al.* 2010; Aspilcueta-Borquis *et al.* 2010b). Cassandro *et al.* (2008) reported a heritability of 0.07 in Italian Holstein Friesian cows and The posterior mean of heritability for Burlina cows was 0.05 that is in agreement with the result of this study (Penasa *et al.* 2010).

Differences between the estimates of heritability obtained in this study and estimates from other countries are most likely caused by management and climate differences affecting genetic and environmental variances and the difference in the methodology applied to estimate the (Co) variance components and size and structure of data sets. The inclusion of traits with small estimates of heritability in progeny testing programs of sires such as CI and SCS is possible, but to reach a minimum reliability for PTA, more daughter records would be necessary for the evaluation of a sire for an index involving SCS and CI than for MY305, FY305, PY305 and AFC alone.

Posterior means and HPD regions for the genetic and residual covariances between the traits are displayed in Tables 4 and 5, respectively.

Table 4 Posterior means and highest posterior density (HPD) region of genetic covariances between traits

Traits	Mean	SD	HPD	
			Low limit	High limit
MY305/FY305	7286.499	230.821	6856.967	7747.3445
MY305/PY305	9203.139	227.496	8809.780	9669.556
MY305/AFC	-73.186	16.049	-105.038	-39.350
MY305/CI	6067.828	344.561	5428.071	6744.519
MY305/SCS	18.437	5.620	8.343	29.323
FY305/PY305	199.197	6.573	187.358	211.941
FY305/AFC	-2.645	0.0355	-3.300	-1.9496
FY305/CI	391.939	9.886	371.152	409.135
FY305/SCS	0.318	0.018	0.011	0.680
PY305/AFC	-1.646	0.395	-2.397	-0.898
PY305/CI	167.958	11.269	144.209	189.223
PY305/SCS	0.638	0.153	0.328	0.919
AFC/CI	0.034	0.020	0.976	1.037
AFC/SCS	-0.011	0.001	-0.014	0.013
CI/SCS	6.228	0.033	5.563	6.854

MY305: 305 days milk yield; FY305: 305 days fat yield; PY305: 305 days protein yield; AFC: age at first calving; CI: calving interval; SCS: somatic cell score and SD: standard deviation.

Table 5 Posterior means and highest posterior density (HPD) region of residual covariances between traits

Traits	Mean	SD	HPD	
			Low limit	High limit
MY305/FY305	26982.74	175.734	26669.742	27338.265
MY305/PY305	29464.70	169.429	29134.721	29772.243
MY305/AFC	143.472	44.923	38.198	220.860
MY305/CI	13136.20	313.089	12524.214	13738.353
MY305/SCS	-117.891	4.566	-127.200	-109.405
FY305/PY305	743.910	5.044	733.4822	753.04
FY305/AFC	0.214	0.200	-0.318	0.683
FY305/CI	78.504	6.541	65.824	90.753
FY305/SCS	-2.015	0.151	-2.317	-1.728
PY305/AFC	3.550	0.878	1.670	5.068
PY305/CI	422.340	10.940	400.203	442.541
PY305/SCS	-2.498	0.14	-2.761	-2.227
AFC/CI	0.011	0.010	-1.011	0.955
AFC/SCS	- 0.050	0.033	-0.013	-0.113
CI/SCS	0.938	0.232	0.449	1.347

MY305: 305 days milk yield; FY305: 305 days fat yield; PY305: 305 days protein yield; AFC: age at first calving; CI: calving interval; SCS: somatic cell score and SD: standard deviation.

The means of genetic covariances between traits were positive except for the genetic covariances between milk, fat and protein with AFC and AFC with SCS. The residual covariance between traits except for the residual covariance between milk, fat and protein with SCS and AFC/SCS were positive.

Genetic and phenotypic correlations

Posterior means and HPD regions for the genetic and phenotypic correlations between the traits are displayed in Tables 6 and 7, respectively. The range of genetic correlations between the traits varied from -0.121 (between FY305 and AFC) to 0.914 (between MY305 and PY305). Genetic correlation between MY305 and FY305; PY3O5 and AFC and AFC and SCS were low and negative. The negative genetic correlations between these traits suggest that decreasing AFC in Holstein result in an increased MY305, FY305, PY305 and SCS. The genetic correlations between production traits (MY305, FY305 and PY305) were high, especially for MY305 and PY305. The genetic correlations between production traits with CI; CI and SCS were high. Therefore, selecting animals for higher MY305 could lead to increasing FY305, PY3O5, but it can also result in increased calving interval. Increasing in CI resulted in increasing in SCS (positive correlation between CI and SCS). Therefore, animal would be sensitive to mastitis disease. The genetic correlation between AFC and SCS; AFC and CI were close to zero. When the genetic correlations are positive, improving the additive genetic level in one trait causes a partial genetic improvement in the other trait. Negative genetic correlation presents inverse changes of additive effects two traits (Pantelic *et al.* 2011).

Table 6 Posterior and highest posterior density (HPD) region of genetic correlations between traits

Traits	Mean	SD	HPD	
			Low limit	High limit
MY305/FY305	0.695	0.009	0.677	0.711
MY305/PY305	0.914	0.003	0.908	0.920
MY305/AFC	-0.09	0.019	-0.128	-0.049
MY305/CI	0.517	0.027	0.465	0.569
MY305/SCS	0.132	0.041	0.054	0.214
FY305/PY305	0.774	0.010	0.754	0.793
FY305/AFC	-0.121	0.016	-0.149	-0.088
FY305/CI	0.818	0.013	0.792	0.842
FY305/SCS	0.085	0.049	-0.010	0.183
PY305/AFC	-0.080	0.019	-0.115	-0.043
PY305/CI	0.573	0.034	0.505	0.636
PY305/SCS	0.179	0.043	0.098	0.126
AFC/CI	0.001	0.021	-0.039	0.041
AFC/SCS	-0.004	0.023	-0.049	0.042
CI/SCS	0.786	0.022	0.745	0.829

MY305: 305 days milk yield; FY305: 305 days fat yield; PY305: 305 days protein yield; AFC: age at first calving; CI: calving interval; SCS: somatic cell score and SD: standard deviation.

Table 7 Posterior and highest posterior density (HPD) region of phenotypic correlations between traits

Traits	Mean	SD	HPD	
			Low limit	High limit
MY305/FY305	0.753	0.002	0.748	0.757
MY305/PY305	0.929	0.003	0.924	0.934
MY305/AFC	0.023	0.018	-0.021	0.052
MY305/CI	0.196	0.002	0.191	0.200
MY305/SCS	-0.083	0.003	-0.088	-0.078
FY305/PY305	0.73	0.003	0.725	0.735
FY305/AFC	-0.026	0.005	-0.035	-0.017
FY305/CI	0.155	0.003	0.149	0.161
FY305/SCS	0.054	0	0.054	0.054
PY305/AFC	0.022	0.012	-0.004	0.042
PY305/CI	0.213	0.003	0.206	0.218
PY305/SCS	-0.055	0.003	-0.061	-0.049
AFC/CI	0	0	-0.008	0.007
AFC/SCS	-0.02	0.014	-0.009	0.045
CI/SCS	0.09	0.004	0.081	0.098

MY305: 305 days milk yield; FY305: 305 days fat yield; PY305: 305 days protein yield; AFC: age at first calving; CI: calving interval; SCS: somatic cell score and SD: standard deviation.

Phenotypic correlation between production traits had the same trend of genetic correlation. Phenotypic correlation between production traits were high and positive phenotypic correlation (0.73-0.929). Phenotypic correlation between MY305, FY305, PY305 and CI was positive. Phenotypic correlations between other traits were lower than 0.10 and close to zero.

The posterior means of genetic correlations between MY305/FY305, MY305/PY305 and FY305/PY305 were 0.695, 0.914 and 0.774, respectively.

These estimates were higher than those reported for Iranian Holsteins by Toghiani (2012) (0.81, 0.7 and 0.705, respectively). Montaldo *et al.* (2010) reported values of 0.49, 0.83 and 0.59 for genetic correlations of MY305/FY305, MY305/PY305 and FY305/PY305, respectively, that is smaller than the corresponding estimates in this study.

The results of this study are close to reports for milk production traits in Brazilian buffaloes (Aspilcueta-Borquis *et al.* 2010b) that were 0.753, 0.942 and 0.779 for the same pairs of traits. Posterior means for genetic correlation between MY305/FY305, MY305/PY305 and FY305/PY305 for Nordic Red cattle were 0.48, 0.87 and 0.65, respectively, that are smaller than the results of this study. The estimates for genetic correlation between production traits were larger than reports for Paraná state Holsteins and small number of Holstein herds in the US (Paula *et al.* 2008; Dechow *et al.* 2007). Estimates for genetic correlations between MY305, FY305, PY305 traits with AFC were -0.090, -0.121 and -0.080, respectively. These estimates were different from the reports by Montaldo *et al.* (2010) (-0.005, -0.031 and 0.144, respectively). These estimates are closer to zero than those previously reported in studies of Holstein cattle, which ranged from -0.44 to -0.20

(Cienfuegos-Rivas *et al.* 2006; Ruiz-Sánchez *et al*. 2007). The estimate of the genetic correlation between SCS and AFC (-0.004) was smaller than -0.06 for Mexican Holstein (Montaldo *et al*. 2010).

Posterior means of genetic correlation between production traits and CI; CI and SCS were in range of 0.517 to 0.818. The estimated genetic correlation between CI and FY305 was strong (0.818) and suggested that possibly heifers or dairy cows that have longer CI would seem to yield more fat or the opposite. The largest genetic correlation between reproductive performance and production traits belongs to CI and FY305 (0.818). This result demonstrates that focusing on fat yield lead to increasing the calving interval, which causes increased insemination and veterinary costs, higher culling rates and increased replacement costs. Increasing the difference between two calving can lead to reduce the number of calves born during the economic period of cows being in the herds.

Similar genetic correlations have been reported between CI and milk in the literature, ranging from 0.23 to 0.96 (Veerkamp *et al*. 2001; Kadarmideen *et al*. 2003; Toghiani, 2012). Correlation between milk production and CI; SCS and CI for Mexican Holstein were in range of (0.3) to (-0.449) and -0.051 that different from our results (Montaldo *et al*. 2010).

Milk production and reproductive performance are effective factors in profitability of a dairy herd. Prolonged calving intervals, increased forced culling, less milk production and fewer calves per cow per year, less directional culling and therefore increased replacement cost and ultimately, lower net returns could be seen in herds with inappropriate reproductive performance (Toghiani, 2012).

Genetic correlation between AFC and CI was close to zero that is similar to reports for Iranian Holstein (-0.049) and Mexican (0.048) (Montaldo *et al*. 2010; Faraji-Arough *et al*. 2011). Estimates of genetic correlation between MY305 and SCS, FY305 and SCS and PY305 and SCS were 0.132, 0.085 and 0.179, respectively, which is in agreement with result of Ghasemi (2012). Reports for correlation between milk, fat. Protein yield and SCS for Burlina Holstein were 0.12, -0.39 and -0.29, respectively, that are different from these results (Penasa *et al*. 2010). Result for the same pairs of traits in Brazilian buffaloes were -0.062, -0.02 and -0.104, respectively (Aspilcueta-Borquis *et al*. 2010b). Estimates of phenotypic correlation between production traits were positive and high in range of (0.53-0.929) that is higher than the result of Toghiani (2012) for Iranian Holstein. For Mexican Holstein and Brazilian buffaloes, similar trend were reported (Aspilcueta-Borquis *et al.* 2010b; Montaldo *et al.* 2010).

Phenotypic correlations for SCS with production and reproduction traits were small and close to zero. Reports for phenotypic correlation between SCS and production and reproduction traits in Mexican Cattle were different in magnitude and sign (Montaldo *et al*. 2010).

CONCLUSION

The results of this study suggest that the genetic variability in production traits and AFC in Iranian Holstein is high, whereas, it is notably lower for CI and SCS. These estimates indicate that response to selection would be feasible in production traits and AFC, but it will have lower selection response for CI and SCS. In general, fertility traits have low heritability; nevertheless, the estimated heritability can differ depending on the statistical methods and the models for their assessment, size and the structure of the data used for estimation of the heritability. The genetic correlations were large and favorable between production traits. In this study, unfavorable genetic correlations were found between CI/SCS or SCS with production traits, or between AFC and other traits. These parameters can be used to improve current breeding programs for the Iranian Holstein population. Accordingly, the genetic correlations between production traits with CI and CI/SCS must be noted in the breeding programs.

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