Estimation of Genetic and Environmental Correlations between Age at First Calving and Production Traits with Reproduction Traits in Holstein Cows Using Bayesian Multi-Trait Model

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Summary

The aim of the present study was to estimate heritability as well as genetic and environmental correlations between age at first calving (AFC) and production traits, namely 305-day milk yield (MY305), 305-day fat and protein yield (Fat305 and Pro305, respectively) and fat and protein percentage (Fat% and Pro%, respectively) with reproduction traits including calving to first heat (DFH), calving to first service (DFS), interval from first to last insemination (IFL), calving to conception interval (ICC), interval between two calvings (CI), number of inseminations (NIS), and conception rate at first insemination (CR) in Iranian Holstein. Records of 33,851 Holstein cows collected in five large dairy herds were used. The estimation of parameters was implemented by the Bayesian multi-trait linear and threshold animal and sire models. Heritability estimates were moderate for production traits and low for reproduction traits suggesting that the improvement of environmental conditions is necessary for improving reproduction traits. Genetic correlations between production and reproduction traits ranged from -0.46 (between Fat305 and CR) to 0.48 (between Fat305 and ICC) in animal model and from -0.55 (between Pro305 and CR) to 0.64 (between Fat305 and DFH) in sire model. Accurate estimates of genetic parameters can be used in selection plans in order to optimally select parents of the next generation.

Key words

Bayesian multi-trait model, genetic correlation, age at first calving, days to first heat, calving interval, conception rate

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Introduction

Dairy farmers rely on milk production as their primary source of income. However, functional traits such as fertility traits also play a crucial role in reducing production costs. Health-related problems and reproductive failure burden a huge economic loss to dairy farmers (Hou et al., 2009; Chegini et al., 2019). High replacement costs have been imposed by high involuntary culling, an increase in the expense of reproductive treatments and repeated inseminations as a result of infertility problems (Hou et al., 2009; Dhakal et al., 2015). The profitability of a dairy herd is directly influenced by reproductive efficiency, and fertility has been categorized as the first important trait (Egyedy and Ametaj, 2022).

After calving, a well-fertilized cow is able to restart her reproductive cycle and conceive (Liu et al., 2017). The problem is that the increase in milk yield without considering reproductive performance has led to a big drop in reproductive performance over time (Gou et al., 2014; Rahbar et al., 2016; Liu et al., 2017). This is because female fertility and milk production are linked in a way that breeding for higher milk production would lead to a genetic decline in female fertility (Royal et al., 2002; Andersen-Ranberg et al., 2005; Sewalem et al., 2010). Several studies (Liu et al., 2008; Walsh et al., 2011; Tiezzi et al., 2012; Liu et al., 2017) reported significant decline in cows' reproduction efficiency over the past five decades, due to the antagonist genetic correlations between yield and female reproductive performance, which is one of the consequences of extensive selection for milk output. The rising cost of replacement heifers for commercial dairy farms is directly related to the rising cost of dairy cows' decreasing fertility (Gou et al., 2014). Despite having low heritabilities, reproductive traits exhibit significant genetic variations that allow for successful selection. (Gou et al., 2014; Liu et al., 2017).

Although genomic selection has become the principal method for genetic evaluation in the last decade, conventional breeding programs are still in practice in many countries. Updated genetic parameters are needed in order to construct selection plans. Therefore, the aim of this study was to estimate genetic and environmental correlations between age at first calving (AFC) and production traits with several reproduction traits in Iranian Holstein cattle population. It has been demonstrated that multi-trait analysis leads to more reliable and accurate estimates, especially when low heritable traits are analyzed with highly heritable traits (Schaeffer, 1984). One reason is the better connections in the data due to residual covariance between traits (Thompson and Meyer, 1986). Therefore, we implemented several Bayesian multi-traits animal and sire models to take advantage of this feature.

Materials and Methods

Data

The dataset utilized in this study consisted of observations from 33,851 Holstein cows from five large herds located in hot and dry regions in Iran. It contained information such as progeny ID number, sire ID number and dam ID number, parity number, dates of births and calvings, milk yield, fat and protein contents, as well as their percentage values. Furthermore, heat dates and insemination dates were utilized in the calculation of various reproductive parameters such as calving to first heat (DFH), calving to first service (DFS), interval from first to last insemination (IFL), calving to conception interval (ICC), interval between two calvings (CI), number of inseminations (NIS), and conception rate at first insemination (CR). The data was edited using MS Excel (version 2019). Observations from animals with an AFC between 540 to 1,200 days and a CI between 290 to 700 days were included for this study. The months of calving were grouped into four categories: April to June as spring; July to September as summer; October to December as fall, and January to March as winter. After editing the initial dataset, 27,714 records of first lactation cows remained and were used for the further analysis. Pedigree construction, which involved renumbering animal IDs and calculating inbreeding, was carried out using CFC software (Sargolzaei et al., 2006). Table 1 presents a summary of the pedigree information.

Table 1. Summary of pedigree information

Description	Number
Total number of animals	35662
Animals with record	27714
Animals without progeny	16370
Animals with progeny	19292
Base animals	7948
Sires	1536
Dams	17756
Average inbreeding coefficient*	0.0136 (%)
Number of herd-year-season	240

Note: * On average, animals had well-known ancestors for 2.71 generations and animals with records had ancestors for 3.20 generations

Statistical Analysis

Model selection was done using the GLM procedure of SAS 9.4 software. A significance level of $P < 0.05$ was considered in order to make it eligible to be included in the model. The following model was fitted to the data to estimate the genetic and environmental parameters:

$$Y_{ijkl} = \mu + HYS_i + AFC_j + A_k + e_{ijkl}$$

where Y_{ijkl} is the response variable which was AFC and for production traits was 305-day milk yield (MY305), 305-day fat and protein yield (Fat305 and Pro305, respectively) and fat and protein percentage (Fat% and Pro%, respectively), and for reproduction traits was DFH, DFS, IFL, ICC, CI, NIS, and CR. μ is the mean of the trait; HYS_i is the fixed effect of herd-year-season of calving (i = 1, …, 240); AFC_j is the fixed effect of age at first calving (j = 1, …, 12); A_k is the random additive genetic effect of the kth cow; and e_{ijkl} is the random residual effect. The model for AFC was similar to the above-mentioned model, with the exception that the fixed effect of AFC was excluded. Since CR was a threshold trait, TM software was used which is able to consider the threshold nature of the trait. Bayesian multi-trait animal and sire models were performed to estimate heritabilities, genetic and environmental correlations between studied traits. The number of iterations was set to 450,000 rounds and first 90,000 rounds were discarded as burn-in period. Regarding the number and nature of traits as well as amount of data, to make the analyses computationally feasible and less demanding, five different runs were performed. To take full advantage of multi-trait analysis, traits were grouped to be analyzed together so that low heritable traits were analyzed with high heritable traits. The combinations of traits in the analyzes were as follows:

two 7-trait analyses:

a) Fat305 – Pro305 – Pro% – AFC – IFL – CI – NIS and

b) Fat305 – Pro305 – Pro% – DFH – DFS – ICC – CR);

two 6-trait analyses:

c) MY305 – Fat% – AFC – IFL – CI – NIS and

d) MY305 – Fat% – DFH – DFS – ICC – CR);

one 8-trait analysis:

e) AFC – DFH – DFS – IFL – ICC – CI – NIS – CR).

Results and Discussion

Descriptive Statistics and Heritabilities

Descriptive statistics of studied traits are presented in Table 2. The means of MY305, Fat305 and Pro305 for the whole dataset were 8,785.6 kg, 307.40 kg and 291.11 kg, respectively. In addition, the mean of Fat% and Pro% were 3.24% and 3.06%, respectively. The mean of AFC and CI for cows in this study were 782.58 and 417.80 days, respectively. More than 2.7 inseminations were needed to conceive a cow and 0.346 of first inseminations resulted in pregnancy. The range of coefficient of variation for milk production traits was between 8.13% to 27.25%. Reproductive traits had significantly higher coefficient of variation (between 21.23% to 137.51%) than milk production traits.

Estimates of genetic and residual variances as well as mean and highest posterior density of heritabilities at 95% for the studied traits estimated by multi-trait animal models are presented in Table 3. Heritability estimates for milk production traits were generally moderate and varied from 0.17 (Fat305) to 0.32 (Pro%). This is in agreement with the results obtained by Toghiani (2012) who reported the heritability of milk production traits from 0.149 (for Fat305) to 0.26 (for MY305) in Holstein dairy cows. A recent meta-analysis study by Khanzadeh et al. (2022) reported the heritabilities of milk yield, fat and protein percentage in Holsteins cows to be 0.253, 0.290 and 0.378, respectively, which are slightly higher than the estimates of the present study.

Heritability of AFC was relatively low (0.11). Heritability of interval reproductive traits (i.e., DFH, DFS, IFL, ICC and CI) ranged from 0.07 for DFS and IFL to 0.15 for CI. NIS and CR had relatively similar heritability of about 0.08. The low heritabilities of reproductive traits imply that improvements in reproductive managements such as managing of insemination and feeding programs, or employing cooling systems during hot seasons could improve reproductive performance (Rahbar et al., 2016).

Table 2. Descriptive statistics for the phenotypic values of the studied traits

Trait*	n	Mean	S.D.	CV (%)
MY305 (kg)	27714	8785.6	2161.42	24.60
Fat305 (kg)	13972	307.40	83.77	27.25
Pro305 (kg)	13789	291.11	55.64	19.11
Fat (%)	13972	3.24	0.4958	15.29
Pro (%)	13789	3.06	0.2489	8.13
AFC (day)	27714	782.58	93.23	11.91
DFH (day)	8087	46.85	44.62	95.24
DFS (day)	22269	70.49	40.21	57.04
IFL (day)	22269	69.20	84.77	122.5
ICC (day)	22269	140.11	91.83	65.54
CI (day)	22269	417.80	88.71	21.23
NIS	22269	2.738	2.0335	74.27
CR	22269	0.346	0.4758	137.51

Note:* MY305: 305-day milk yield; Fat305: 305-day fat yield; Pro305: 305-day protein yield; Fat%: Fat percent; Pro%: Protein percent; AFC: Age at first calving; DFH: Calving to first heat; DFS: Calving to first service; IFL: Interval from first to last insemination; ICC: Calving to conception Interval; CI: Interval between two calvings; NIS: Number of inseminations; CR: Conception rate at first insemination.

Table 3. Estimates of animal genetic (V_g) and residual (V_e) variance as well as heritabilities (h^2) for age at first calving, milk production traits and measures of reproductive traits using Bayesian animal model.

Trait*	Vg	Ve	h^2
Milk305	510919.91	1592365.30	**0.24,0.25 (0.24)**
Fat305	499.16	2473.38	**0.16,0.17 (0.17)**
Pro305	463.01	1411.27	**0.21,0.29 (0.25)**
Fat%	0.04183151	0.11005121	**0.27,0.28 (0.28)**
Pro%	0.01417892	0.02996411	**0.32,0.33 (0.32)**
AFC	0.565735	4.586581	**0.09,0.13 (0.11)**
DFH	128.39	1488.06	**0.08,0.08 (0.08)**
DFS	105.99	1330.54	**0.07,0.08 (0.07)**
IFL	578.18	7399.34	**0.06,0.09 (0.07)**
ICC	864.08	8258.59	**0.09,0.10 (0.10)**
CI	1356.60	7621.22	**0.15,0.16 (0.15)**
NIS	0.2927705	3.553844	**0.07,0.08 (0.09)**
CR	0.0849031	1.00	**0.05,0.10 (0.08)**

Note: V_g = Genetic variance; V_e = Residual variance; h^2 = Highest posterior density at 95% for the heritabilities is shown (heritabilities in parentheses).
* For traits, see Table 2.

Liu et al. (2017) reported heritabilities of NIS, CR, and IFL in Chinese Holstein population to be 0.026, 0.012, and 0.027, respectively, which are lower than our estimates. Employing a Bayesian approach, Mokhtari et al. (2015) estimated heritabilities of NIS and ICC for Holstein cows 0.029 and 0.049, respectively, using a linear model and heritability of CR 0.039 using a threshold model. In another study using repeatability model, Ghiasi et al. (2011) reported heritabilities of CR, ICC and NIS to be 0.029, 0.076 and 0.046, respectively. In general, our estimates are slightly higher than reports of the previous studies.

Correlations

Estimates of genetic and environmental correlations between AFC and milk production traits with reproduction traits using multi-trait animal and sire models are shown in Table 4 and Table 5, respectively. Genetic correlation between AFC and Milk305 was estimated -0.18 using animal model and the corresponding value estimated by sire model was -0.26. This indicates that animals with a higher (unfavorable) breeding value for AFC have a lower genetic merit for Milk305; in other words, the selection for increasing Milk305 would result in a decrease in AFC. However, environmental correlation of 0.11 between these two traits shows that an increase in AFC would slightly increase Milk305, which is in agreement with previous studies (Eastham et al., 2018; Ferrari et al., 2024). A recent study employing a large dataset (Ferrari et al., 2024), showed an increase of 735 kg in Milk305 in first lactation cows with AFC of 36 months compared with that of 18-21 months. Genetic correlations between Fat% and Pro% with AFC were relatively high, implying that focusing on increasing Fat% and Pro%, probably through delaying maturation, could lead to an increase in AFC. This is in agreement with the positive genetic correlations found between Fat% and Pro% with DFH (0.23 and 0.20 using animal model and 0.45 and 0.14 using sire model). The high environmental correlations between Fat% and Pro% with AFC suggest that any environmental and managemental factor that increases AFC would also increase milk compositions. A previous study reported a positive correlation between AFC with Fat% (Atashi et al., 2021). In other studies it was found that increase in AFC was associated with an increase in milk, fat and protein yield at first calving (Eastham et al., 2018; Ferrari et al., 2024).

In general, genetic correlations between AFC and reproductive traits were low. Animals with higher (unfavorable) breeding value for AFC had shorter DFH and DFS; however, by having longer IFL and ICC they will consequently have longer CI. This is consistent with the negative genetic correlation between AFC and CR (-0.15 and -0.48 using animal and sire model, respectively), indicating that despite an earlier commencement of luteal activity in animals with higher AFC, they are difficult to conceive and require higher NIS for each conception (genetic correlation of 0.21 between AFC and NIS).

Table 4. Estimates of genetic (above diagonal) and environmental correlations (below diagonal) between age at first calving and milk production traits with measures of reproductive traits using Bayesian multi-trait animal model

Correlation	Trait*	AFC	DFH	DFS	IFL	ICC	CI	NIS	CR
Genetic	Milk305	-0.33, -0.02 (-0.18)	0.20, 0.22 (0.21)	0.28, 0.30 (0.29)	0.04, 0.41 (0.24)	0.37, 0.39 (0.38)	0.30, 0.32 (0.31)	0.20, 0.23 (0.21)	-0.48, -0.15 (-0.31)
	Fat305	-0.13, 0.33 (0.15)	0.33, 0.35 (0.34)	0.43, 0.45 (0.44)	0.11, 0.42 (0.26)	0.47, 0.49 (0.48)	0.27, 0.29 (0.28)	0.22, 0.24 (0.23)	-0.74, -0.15 (-0.46)
	Pro305	-0.45, -0.05 (-0.21)	0.19, 0.45 (0.34)	0.06, 0.31 (0.20)	0.02, 0.54 (0.17)	0.16, 0.37 (0.28)	0.13, 0.35 (0.26)	0.18, 0.41 (0.29)	-0.54, -0.02 (-0.31)
	Fat%	0.28, 0.59 (0.44)	0.22, 0.24 (0.23)	0.12, 0.14 (0.13)	-0.01, 0.07 (0.03)	0.02, 0.05 (0.03)	-0.03, -0.01 (-0.02)	0.01, 0.03 (0.02)	-0.35, 0.09 (-0.15)
	Pro%	0.20, 0.44 (0.34)	0.18, 0.21 (0.20)	-0.06, -0.03 (-0.04)	0.04, 0.28 (0.17)	-0.09, -0.07 (-0.08)	-0.11, -0.08 (-0.09)	0.02, 0.06 (0.04)	-0.34, -0.23 (-0.29)
	AFC	---	-0.42, 0.15 (-0.13)	-0.32, 0.12 (-0.09)	0.28, 0.72 (0.53)	0.10, 0.23 (0.16)	0.08, 0.42 (0.26)	0.02, 0.33 (0.21)	-0.40, 0.10 (-0.15)
Environmental	Milk305	0.06, 0.17 (0.11)	0.00, 0.04 (0.04)	-0.03, -0.01 (-0.02)	0.06, 0.11 (0.08)	0.05, 0.07 (0.06)	0.05, 0.08 (0.06)	0.09, 0.12 (0.10)	-0.01, -0.05 (-0.04)
	Fat305	0.24, 0.34 (0.29)	-0.02, 0.03 (0.01)	-0.04, -0.01 (-0.03)	0.09, 0.15 (0.12)	0.03, 0.06 (0.04)	0.05, 0.08 (0.06)	0.05, 0.09 (0.07)	-0.15, -0.07 (-0.11)
	Pro305	0.01, 0.15 (0.08)	-0.03, 0.05 (0.01)	-0.03, 0.02 (0.00)	0.14, 0.22 (0.18)	0.08, 0.13 (0.11)	0.09, 0.15 (0.12)	0.10, 0.15 (0.13)	-0.23, -0.14 (-0.18)
	Fat%	0.44, 0.53 (0.49)	-0.04, 0.01 (-0.02)	-0.03, 0.01 (-0.01)	0.00, 0.04 (0.02)	0.01, 0.05 (0.03)	0.01, 0.05 (0.03)	0.00, 0.05 (0.02)	-0.02, 0.05 (0.01)
	Pro%	0.56, 0.63 (0.60)	-0.06, -0.01 (-0.03)	-0.03, 0.01 (-0.02)	-0.03, 0.04 (0.00)	0.02, 0.06 (0.04)	0.03, 0.07 (0.05)	0.00, 0.04 (0.02)	0.00, 0.04 (0.02)
	AFC	---	-0.59, -0.49 (-0.54)	-0.33, -0.19 (-0.26)	-0.04, 0.09 (0.03)	0.00, 0.03 (0.02)	-0.12, -0.03 (-0.08)	-0.07, 0.00 (-0.03)	0.01, 0.13 (0.07)

Note: Highest posterior density at 95% for the correlations is shown (correlations in parentheses).

* For traits, see Table 2.

Table 5. Estimates of genetic (above diagonal) and environmental correlations (below diagonal) between age at first calving and milk production traits with measures of reproductive traits using Bayesian multi-trait sire model

Correlation	Trait*	AFC	DFH	DFS	IFL	ICC	CI	NIS	CR
Genetic	Milk305	-0.41, -0.09 (-0.26)	0.29, 0.48 (0.38)	0.31, 0.50 (0.40)	0.22, 0.58 (0.41)	0.10, 0.48 (0.30)	0.11, 0.47 (0.29)	0.05, 0.41 (0.24)	-0.54, -0.16 (-0.33)
	Fat305	-0.28, 0.17 (-0.07)	0.47, 0.74 (0.64)	0.12, 0.56 (0.41)	0.01, 0.68 (0.38)	0.04, 0.53 (0.29)	0.06, 0.50 (0.29)	-0.07, 0.35 (0.12)	-0.77, 0.09 (-0.29)
	Pro305	-0.44, -0.02 (-0.23)	0.17, 0.40 (0.29)	0.05, 0.31 (0.17)	0.11, 0.80 (0.43)	0.12, 0.58 (0.37)	0.09, 0.53 (0.30)	0.20, 0.56 (0.37)	-0.82, -0.22 (-0.55)
	Fat%	0.47, 0.75 (0.62)	0.18, 0.64 (0.45)	0.05, 0.46 (0.30)	0.00, 0.46 (0.25)	-0.13, 0.35 (0.10)	-0.14, 0.31 (0.09)	-0.31, 0.14 (-0.09)	-0.26, 0.31 (-0.01)
	Pro%	0.21, 0.55 (0.38)	-0.13, 0.39 (0.14)	-0.17, 0.30 (0.07)	0.02, 0.72 (0.33)	0.05, 0.53 (0.29)	-0.07, 0.41 (0.17)	0.04, 0.48 (0.27)	-0.21, 0.03 (-0.09)
	AFC	---	-0.31, 0.33 (-0.04)	-0.42, 0.19 (-0.10)	-0.06, 0.52 (0.20)	-0.24, 0.21 (0.01)	0.03, 0.43 (0.16)	0.08, 0.47 (0.20)	-0.84, -0.16 (-0.48)
Environmental	Milk305	-0.08, 0.02 (-0.03)	0.02, 0.06 (0.04)	-0.01, 0.02 (0.01)	0.07, 0.10 (0.09)	0.08, 0.11 (0.09)	0.09, 0.12 (0.10)	0.10, 0.13 (0.11)	-0.11, -0.08 (-0.10)
	Fat305	0.05, 0.11 (0.08)	0.02, 0.08 (0.05)	0.00, 0.04 (0.02)	0.08, 0.11 (0.10)	0.08, 0.12 (0.10)	0.09, 0.12 (0.11)	0.09, 0.12 (0.10)	-0.18, -0.11 (-0.14)
	Pro305	-0.02, 0.06 (0.02)	0.03, 0.08 (0.06)	0.00, 0.04 (0.02)	0.10, 0.14 (0.12)	0.10, 0.13 (0.12)	0.11, 0.15 (0.13)	0.11, 0.14 (0.13)	-0.22, -0.15 (-0.19)
	Fat%	0.44, 0.51 (0.47)	-0.03, 0.03 (0.00)	-0.02, 0.02 (0.00)	-0.02, 0.04 (0.01)	0.00, 0.04 (0.02)	0.00, 0.04 (0.02)	-0.01, 0.03 (0.01)	-0.03, 0.02 (-0.01)
	Pro%	0.60, 0.64 (0.62)	-0.03, 0.02 (-0.01)	-0.04, 0.00 (-0.02)	-0.01, 0.03 (0.01)	-0.02, 0.02 (0.00)	-0.01, 0.03 (0.01)	-0.01, 0.03 (0.01)	-0.02, 0.01 (-0.01)
	AFC	---	0.41, 0.51 (0.46)	-0.17, 0.04 (-0.06)	-0.09, 0.04 (-0.03)	-0.12, -0.01 (-0.07)	-0.01, 0.08 (0.04)	0.04, 0.10 (0.07)	-0.05, 0.07 (0.01)

Note: Highest posterior density at 95% for the correlations is shown (correlations in parentheses).

* For traits, see Table 2.

Moderate positive genetic correlation was found between AFC and CI using both animal and sire models, suggesting that animals with younger age at first calving would have a shorter CI. Environmental correlations between AFC and reproductive traits were generally low, except with DFH and DFS. Strong environmental correlations between AFC with DFH and DFS (-0.54 and -0.26) imply that animals having their first calving at an older age, start their luteal activity earlier after calving, probably due to more body reserves and subsequently better management of negative energy balance. Looking into the estimates from animal model, higher AFC is environmentally associated with slightly shorter CI and higher CR. It seems that favorability of AFC is not linear, so that extremely low and high AFC are unfavorable, which by intensifying negative energy balance and deposition of extra fat tissues in proximity to reproductive organs, respectively, causes inefficiency in reproductive performance of animal.

Genetic correlations between Milk305 and interval reproductive traits were in the range of 0.21 (with DFH) to 0.38 (with ICC) using animal model and from 0.29 (with CI) to 0.41 (with IFL) using sire model. Kadarmideen et al. (2003) estimated genetic correlations between Milk305 with CI, DFS, ICC and NIS as 0.40, 0.28, 0.27 and 0.25, respectively. Relatively similar genetic correlations of 0.49, 0.39 and 0.44 were estimated between Milk305 with CI, DFS and NIS by Pritchard et al. (2013). Reports of correlation between DFH and production traits are scarce in literature. Royal et al. (2002) estimated genetic correlation of peak milk yield and start of luteal activity as 0.36, which is consistent to the obtained values of 0.21 and 0.38 between Milk305 and DFH using animal and sire model, respectively. Veerkamp et al. (2000) reported high and unfavorable genetic correlations between calving to first luteal activity interval with milk, fat and protein yields as 0.51, 0.65, and 0.48. Among milk production traits, Fat305 had the highest genetic correlation with the reproductive traits, ranging from -0.46 with CR to 0.48 with ICC. It has been stated that cows with higher milk yield mobilize larger amount of their body reserves to cover energy requirements for their high production levels (Pryce et al., 2004). There were moderate to high unfavorable genetic correlations between NIS and CR with production traits. Dematawewa and Berger (1998) reported higher correlation between NIS and milk compositions than with Milk305, which agrees with the present study. NIS had the highest genetic correlation with Pro305 amongst the production traits. Generally, obtained results are indicative of an unfavorable genetic correlation between production and reproduction traits. Therefore, genetically improving milk production traits would increase ICC, CI and NIS and decrease CR.

Corresponding environmental correlations were in agreement with the genetic correlations, which implies that, for instance, improving Fat305 and Pro305 even through better management practices would deteriorate NIS and CR. Previous studies reported similar values as genetic and environmental correlations between milk production traits and reproduction traits (Kadarmideen et al., 2003; Sewalem et al., 2010; Toghiani, 2012; Mokhtari et al., 2015).

In sire models, genetic correlations of AFC with production traits followed similar trend as animal model, although their absolute values were slightly higher. Also, a similar pattern in genetic correlations between AFC and reproductive traits was observed using sire models. Moreover, the genetic correlations between production and reproduction traits obtained using sire model were similar to those of animal models, with the exception that in the sire model, Pro305 showed the highest antagonist correlations with reproduction traits, while in the animal model, Fat305 had the highest antagonist correlations with reproduction traits. Similarly, in sire model, NIS and CR had unfavorable genetic correlations with production traits. The magnitude of genetic correlations between NIS with production traits varied from -0.09 to 0.37 using sire model. Also, genetic correlations between CR with production traits ranged from -0.01 to -0.55. Estimates of environmental correlations between production and reproduction traits were generally low. According to the results of this study, allocating accurate and appropriate weights to productive and reproductive traits in an index is necessary in order to optimize selection decisions and to avoid the selection of inferior individuals to produce the next generations.

Conclusion

This study evaluated the genetic and environmental relationship between age at first calving and production traits with reproduction traits using data from herds located in hot and dry areas in Iran. Different animal and sire as well as linear and threshold, if appropriate, models were implemented for the estimations. Production traits had moderate heritability. Reproduction traits exhibited low heritability; however, due to the existence of genetic variability, considerable response to selection could be expected. Genetic correlations between production and reproduction traits were unfavorable, implying that selection to maximize yield traits without allocating weights to reproduction traits would impair reproductive performance. Therefore, considering the relationship between production and reproduction traits in the selection indices is recommended for the optimal selection of individuals and also to maximize the economic gains in the dairy industry.

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CRediT Authorship Contribution Explanation

Arash Chegini: Conceptualization, Methodology, Formal analysis, Writing – original draft, Supervision, Performed most of the experiments. **Abbas Safari:** Writing – original draft. **Misagh Moridi:** Writing – review & editing.

Declaration of Competing Interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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