

## ARTICLE

# ESTIMATION OF GENETIC PARAMETERS FOR MILK YIELD, SOMATIC CELL SCORE, AND FERTILITY TRAITS IN IRANIAN HOLSTEIN DAIRY CATTLE

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## ABSTRACT

This study was conducted to estimate genetic parameters for the lactation curve parameters, milk yield, somatic cell score (SCS), age at first calving (AFC), calving interval (CI) and lactation length (LL) in Iranian Holstein cows. The data originated from the national Animal Breeding Center of Iran, belonged to the first lactation dairy cows from 2001 to 20104. The genetic parameters were estimated using REML method by applying random regression model (RRM). To compare the models, different criterion LogL, AIC and BIC values were used for considered traits. Based on obtained results, RRM with legend repolynomial (3,3) were chosen as better model for milk yield and SCS traits. Based on obtained results, for milk yield and SCS traits the additive genetic variance was highest in the beginning and end lactation and permanent environmental variance was highest in beginning of lactation than other lactation period. Heritabilities estimate for milk yield and SCS traits, were found to be lowest during early lactation (0.48, and 0.04 respectively). Heritabilities estimated  $0.02 \pm 0.01$ ,  $0.04 \pm 0.01$  and  $0.10 \pm 0.01$  for AFC, CI and LL, respectively. Additive genetic correlation between adjacent test days was more than between distant test days. The was estimated negative genetic correlations between fertility traits and positive phenotypic correlations between them. The genetic trends of milk yield and SCS was showed an increasing phase during previous years.

## INTRODUCTION

Milk production is the most economically important trait in the dairy cattle breeding industry. However, in addition to milk yield, reproductive and health traits are among the major traits that should be improved genetically in dairy cattle. In recent years intensive selection for milk yield has depressed reproductive performance of cows [1]. One of the important breeding program processes is the estimation of genetic parameters using appropriate models. The TD Model has been described using various models, such as repeatability, fixed regression, multiple-trait and random regression model (RRM). Among the models that consider TD production, RRM has been widely observed to increase the accuracy of breeding value predictions [2]. Among these advantages are more precise adjustment for temporary environmental effects on the TD, avoidance of the use of extended records for culled cows and for records in progress, and the possibility of genetic evaluation for any part of lactation curve. Therefore, using TD measurements in an RRM could increase the accuracy of genetic evaluations. Schaeffer and Dekkers (1994) introduced the concept of the RRM for the analysis of TD records in dairy cattle as a means of accounting for the covariance structure of repeated records over time or age [2].

Deficient reproductive performance exhibited as longer calving intervals and increased involuntary culling, may result in less milk and fewer calves per cow per year, lower voluntary culling and consequently increased replacement costs and finally, reduced returns [3]. Before the 1990 most attention of dairy cattle breeding programs were focused on milk production. Since the negative genetic relationship exist between milk production and fertility this caused decline in fertility performance of Holstein dairy cow [4]. Therefore, in current decades in many breeding programs fertility traits have been included. But the heritabilities of fertility traits are low, ranging from 0.01 to 0.1, which leads to slow improvement in fertility performance [5,6]. Genetic analysis of fertility traits for various breed is studied in different countries, such as: Zebu cow in Mexico [7]; South African Holstein cows [8]; Spanish dairy cattle [9]. Although, some investigations have been carried out in Iranian Holstein dairy cows in regard to the estimation of genetic parameters of milk yield traits [10,11,12,13] but compare different order Legendre polynomial (LP) of fertility traits still needs further work.

Thus, the objectives of this study were 1) to compare different order LP of the RRM to determine the best fitting model to TD milk yield and SCS, and 2) to estimate genetic parameters milk yield, SCS, age at first calving (AFC), calving interval (CI) and lactation length (LL) in Iranian Holstein cows.

## MATERIALS AND METHODS

The test day (TD) milk yield records obtained from national Animal Breeding Center of Iran, belonged to the first lactation dairy cow from 2001 to 2014. Edited data included the following: The TD data were excluded before 5<sup>th</sup> day and after the 305<sup>th</sup> day of lactation. In addition, irregular data for milk yield (<2 and >70 kg) were excluded. Cows had also, only cows with more than 5 TD records, and herds with more than 5 cows per herd in year of calving and cows with at least one known parent and age at first calving between 18 to 45 months were kept. The data of cows with the first TD at least 60 days after parturition and TD intervals less than 15 days were discarded. Finally edited data included 795724 and 278230 for milk yield and SCS traits, respectively. The fertility records were: AFC, CI and LL. The RRM fitted for the genetic analysis was used as following:

## KEY WORDS

Genetic evaluation, Dairy cow, Random regression model, Fertility traits

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$$y_{ijltmno} = F_{ijl} + \sum b_{ijn} z_{tp} + \sum a_{ijmp} z_{tp} + \sum p_{ijmp} z_{tp} + e_{ijltmno}$$

Where  $y_{ijltmno}$  is the  $o^{th}$  TD record (Milk yield and SCS) of  $m^{th}$  cow in  $t^{th}$  DIM, in  $l^{th}$  herd-test-date (HTD) effect;  $F_{ijl}$  is fixed effects in the model (including herd-test date, interaction between year-season of calving and DIM and dam age (linear and quadratic).  $Z_{tp}$  is  $p^{th}$  LP for  $t^{th}$  DIM.  $b_{ijn}$  is the  $n^{th}$  fixed regression coefficients  $p^{th}$  class of cows calving age-season.  $a_{ijmp}$  and  $p_{ijmp}$  are regression coefficients for additive genetic and permanent environment effects respectively;  $e_{ijltmno}$  random residual effect associated with  $y_{ijltmno}$ . The traits descriptive statistics are summarized in Table 1 and 2.

**Table 1:** Descriptive statistics of data sets for milk yield (kg) and SCS

	Milk (kg)	SCS
Number of TD records	795724	278230
Number of total animals	277400	278230
Number of animals with record	65100	65320
Number of dam with progeny	2100	2210
Number of sire with progeny	8840	8922
Number of HTD	16973	16989

**Table 2:** Descriptive statistics of data sets

DIM	5	35	65	95	125	155	185	215	245	275	305
Mean of Milk yield (kg)	29.24	34.80	33.76	33.41	34.08	33.5	32.75	31.96	31.00	29.89	28.91
Maximum Milk yield	59.43	70.35	65.21	60.27	56.86	56.65	59.51	58.70	57.54	56.67	54.76
Minimum Milk yield	9.13	13.45	11.51	9.17	8.09	8.41	9.17	9.20	8.81	7.75	7.42
Mean of SCS	4.33	4.31	4.03	4.03	4.06	4.11	4.14	4.19	4.23	4.27	4.30
Maximum SCS	2.30	2.30	2.30	2.30	2.30	2.30	2.30	2.30	2.30	2.30	2.30
Minimum SCS	9.9	9.9	9.8	9.9	9.8	9.8	9.8	9.7	9.6	9.8	9.7

Mean of AFC, CI and LL was 840.2 days (28 month), 494.70 and 335.45 respectively. To calculate the standard DIM ( $d^*$ ), the following equation was used:

$$d_i^* = -1 + 2 \left( \frac{d_i - d_{min}}{d_{max} - d_{min}} \right)$$

Where  $d_{min}$  and  $d_{max}$  are minimum and maximum, and  $d_i$ ,  $t^{th}$  DIM. For the  $t^{th}$  standardized DIM, the  $n^{th}$  polynomial is given as [14].

$$P_n(d_i^*) = \sum_{i=0}^n (-1)^i \binom{n}{i} \left( \frac{d_i^* - d_{min}}{d_{max} - d_{min}} \right)^i c_i^*$$

Where  $d_i^*$ , is the  $i^{th}$  DIM; and  $i$ , is order LP function;  $m$ , index number needed to determine the  $k^{th}$  polynomial.

The matrices notation of the model can be written as:  $y = Xb + Q\alpha + Zpe + e$ ; where  $y$  is the a vector of observations,  $b$  is the a vector of fixed effects,  $a$  and  $pe$  were vectors of additive genetic and permanent environment effects respectively,  $e$  is the vector of residual effects and  $X$ ,  $Q$  and  $Z$  are the incidence matrices. The (co)variance structure for random parts of the model was defined as:

$$\text{Var} \begin{bmatrix} \alpha \\ pe \\ e \end{bmatrix} = \begin{bmatrix} G \otimes A & 0 & 0 \\ 0 & I \sigma_p^2 & 0 \\ 0 & 0 & R \end{bmatrix}$$

$G$  is the genetic covariance matrix of the random regression coefficients,  $\otimes$  is the kronecker product function,  $A$  is the additive genetic relationship matrix coefficients among animals,  $\sigma_p^2$  is the variance of the permanent environment effects,  $I$  is the identity matrix, and  $R$  is the diagonal matrices of residual variance. For estimated heritability for  $i^{th}$  DIM was calculated as:

$$h_i^2 = \frac{\sigma_{a(i)}^2}{\sigma_{a(i)}^2 + \sigma_{pe(i)}^2 + \sigma_e^2}$$

Where  $\sigma_{a(i)}^2 = qGq'$ ,  $\sigma_{pe(i)}^2 = qPq'$ , where  $q$  is the vector of the associated polynomial function;  $G$  and  $P$ , are the (co)variance matrices for additive genetic and permanent environmental RR coefficients, respectively; and  $\sigma_{a(i)}^2$ ,  $\sigma_{pe(i)}^2$  and  $\sigma_e^2$  are additive genetic, permanent environmental and residual variances for  $i^{th}$  days in milk, respectively.

Additive genetic correlation for 305-days production between LP were calculated as:

$$r_{g(i,j)} = \frac{\text{Cov}_{g(i,j)}}{\sqrt{\text{Var}_{g(i,i)} \times \text{Var}_{g(j,j)}}$$

Where  $\text{Cov}_{g(i,j)}$ , is genetic covariance between  $i$  and  $j$  day,  $\text{Var}_{g(i,i)}$  and  $\text{Var}_{g(j,j)}$  are additive genetic variance  $i$  and  $j$  day, respectively. Goodness of fit for the models was examined using likelihood based criteria as LogL, AIC (Akaike's information criterion.) and BIC (Bayesian information criterion). AIC and BIC criteria are:

$$\begin{aligned} AIC &= -2 \log L + 2 \times k \\ BIC &= -2 \log L + k \times \log(N - r(x)) \end{aligned}$$

Where,  $k$  is the number of parameters estimated,  $N$  is the sample size and  $r(x)$  is the rank of the coefficient matrices for fixed effects in the model. The model giving the lowest  $-2 \log L$ , AIC and BIC values is chosen as

the better approximating model. Residual variance were considered homogeneous along the lactations, since the use of homogeneous residual variance in the literature is cited as a good assumption for use in data analysis of dairy cattle [15]. Estimation of genetic parameters with REML methodology was done by WOMBAT program [16]. The significance of fixed effects was examined using GLM procedure of SAS software [17].

## RESULTS

Fig. 1 shows changes of the milk yield and SCS traits along lactation month and indicates that the high amount of milk yield in 2 and 3 month (Peak of lactation), however, low amount of SCS During this time.

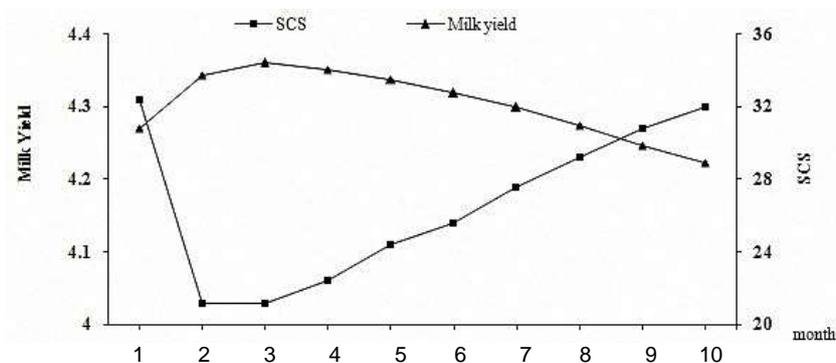


Fig. 1: Average of milk yield, and SCS along months

The values of comparison criteria (logL, AIC, BIC) for the different LP of milk yield, SCS traits were given in Tables 3, and 4 respectively. Selection of a bestmodel depends partly on the criteria that were used. For milk yield and SCS the LP (3,3) model had the lowestLogL, AIC and BIC values. Therefore, among models, for milk yield and SCS traits the LP (3,3) model was selected as the best model (LP (3,3) is 3 and 3 order for additive genetic and permanent environmental effects respectively).

**Table 3:** Criteria used for comparison of the models and their levels for the milk yield (best model in bold)

Model	K	logL	AIC	BIC
LP (2,2)	7	-915.327	-922.327	-940.059
<b>LP (3,3)</b>	<b>13</b>	<b>-906.304</b>	<b>-919.304</b>	<b>-952.225</b>
LP (4,4)	21	-1007.456	-1028.456	-1081.618
LP (5,5)	31	-960.737	-991.737	-1070.188
LP (6,6)	43	-963.850	-1006.850	-1115.631

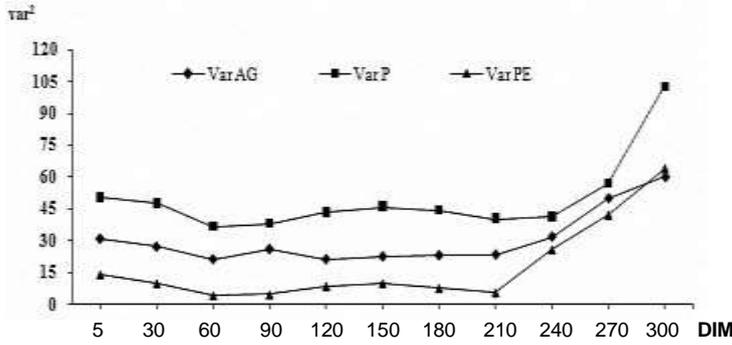
LP (i,j) is i and j order for additive genetic and permanent environmental effects respectively;

BIC: Bayesian information criterion and AIC: Akaike’s information criterion

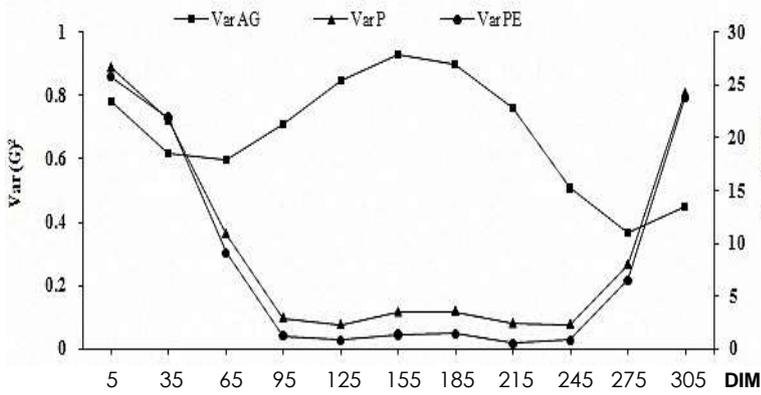
**Table 4:** Criteria used for comparison of the models and their levels for the SCS (best model in bold)

Model	K	logL	AIC	BIC
LP (2,2)	7	-2998.460	-3005.460	-3023.724
<b>LP (3,3)</b>	<b>13</b>	<b>-2985.576</b>	<b>-2998.576</b>	<b>-3032.485</b>
LP (4,4)	21	-3068.138	-3089.138	-3143.898
LP (5,5)	31	-3074.508	-3105.508	-3186.321
LP (6,6)	43	-3088.152	-3131.152	-3243.216

The additive genetic (AG), permanent environmental (PE) and phenotypic variances of milk yield and SCS traits as a function of DIM are shown in Fig 2 and 3 respectively. Estimated genetic parameters based on the best model. AG, PE and phenotypic variances of milk yield was higher at the beginning and end of lactation. AG variance of SCS was higher at the beginning of lactation (0.8) and then decreased until about 75 days of lactation also AG highest (0.95) in 160 DIM. AG and phenotypic variances was higher at the beginning of lactation (25.7 and 26.7 respectively) and then decreased until about 95 days of lactation and this trend continued up to 245 DIM and then increased at the end of lactation.

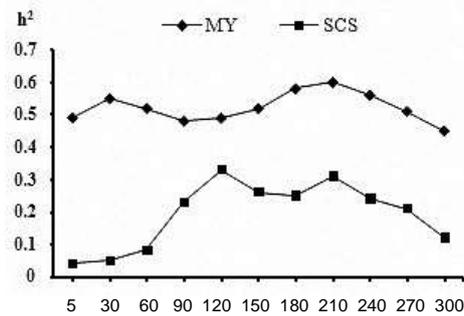


**Fig. 2:** Trajectory of additive genetic (AG), permanent environmental (PE) and phenotypic (P) variances of milk yield as a function of DIM

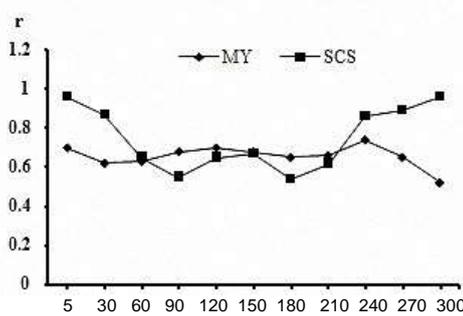


**Fig. 3:** Trajectory of additive genetic (AG), permanent environmental (PE) and phenotypic (P) variances of SCS as a function of DIM

Heritabilities of milk yield and SCS traits as a function of DIM are shown in Fig 4 and 5, respectively. The estimate of heritabilities for different DIM obtained ranged from  $0.45 \pm 0.04$  to  $0.60 \pm 0.05$  and  $0.04 \pm 0.01$  to  $0.31 \pm 0.03$ , for milk yield and SCS traits, respectively. The changes in heritability estimates for TD milk yield was high in the early lactation and then sudden drop in 90th DIM and then trend increased up to 210th DIM and the end of lactation was lower observed. The heritability of SCS in the early lactation was obtained lower than other periods. The estimates of repeatability obtained in the current study were ranged from 0.62 to 0.86 and 0.54 to 0.96 by milk yield and SCS traits, respectively [Fig. 5].



**Fig. 4:** Estimated heritability ( $h^2$ ) of milk yield (MY) and SCS as a function of DIM



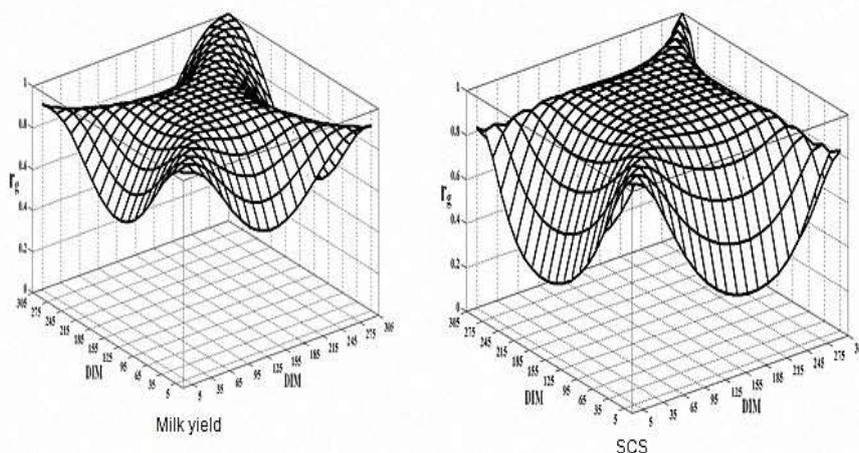
**Fig. 5:** Estimated repeatability ( $r$ ) of milk yield (MY) and SCS as a function of DIM

The estimated heritabilities for AFC, CI and LL were 0.02, 0.04 and 0.10, respectively [Table 5]. The genetic correlation coefficients ranged from -0.31 (the lowest) between AFC and LL to -0.15 (the highest) between AFC and CI. The phenotypic correlations ranged from 0.62 (the lowest) between LL and AFC to 0.93 (the highest) between CI and AFC [Table 4].

**Table 5:** Heritability (diagonal), Genetic (above diagonal) and phenotypic (below diagonal) correlations between age at first calving (AFC), interval between first and second calving (CI) and lactation length (LL) traits

Traits	AFC (day)	CI (day)	LL (day)
AFC (day)	0.02±0.01	-0.15	-0.31
CI (day)	0.93	0.04±0.01	-0.28
LL, (day)	0.62	0.68	0.10±0.01

Estimates of additive genetic correlation between TD milk yield, and TD SCS at different stages of lactation estimated in RRM are shown in Fig. 6. As it is shown, the (co)variance structure of TD data during trajectory was considering RRM, therefore, with this method separate (co)variance components for different days of lactation are estimating that by using them genetic correlation between different days can be calculated. The values of genetic correlations ranged between TD from 0.40 to 0.99 and 0.21 to 0.99 for milk yield and SCS traits respectively.



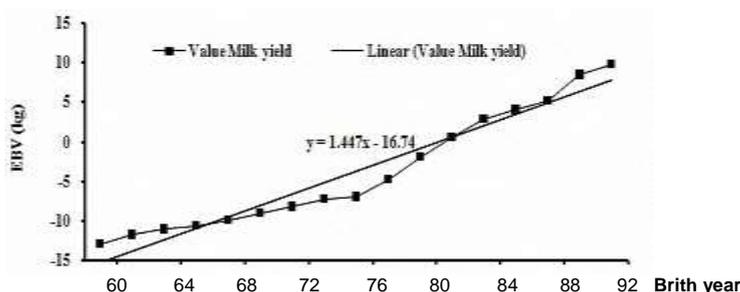
**Fig. 6:** Additive Genetic correlation (rg) milk yield and SCS traits as a function of DIM

The phenotypic correlations of milk yield and SCS traits of between different TD were given in Tables 6. The estimates of phenotypic correlations obtained in this study were ranged from 0.09 to 0.95 and 0.02 to 0.24 by milk yield and SCS traits, respectively.

**Table 6:** Phenotypic correlations of milk yield (diagonal) and SCS (below diagonal)

	305	275	245	215	185	155	125	95	65	35	5	TD
0.45	0.44	0.47	0.51	0.63	0.68	0.71	0.80	0.84	0.87	-	-	5
0.45	0.44	0.47	0.50	0.63	0.69	0.71	0.81	0.84	-	0.24	-	35
0.31	0.28	0.4	0.42	0.60	0.64	0.68	0.91	-	0.20	0.22	-	65
0.09	0.21	0.32	0.51	0.55	0.78	0.84	-	0.21	0.15	0.18	-	95
0.15	0.30	0.64	0.76	0.87	0.92	-	0.10	0.16	0.10	0.12	-	125
0.16	0.20	0.61	0.71	0.88	-	0.11	0.10	0.15	0.11	0.14	-	155
0.22	0.32	0.71	0.77	-	0.14	0.09	0.08	0.11	0.09	0.11	-	185
0.51	0.71	0.95	-	0.15	0.07	0.06	0.07	0.08	0.05	0.08	-	215
0.79	0.90	-	0.18	0.10	0.07	0.03	0.05	0.09	0.04	0.07	-	245
0.93	-	0.14	0.15	0.10	0.04	0.02	0.03	0.04	0.02	0.04	-	275
-	0.12	0.09	0.08	0.06	0.02	0.02	0.04	0.03	0.03	0.05	-	305

Regression coefficients for estimated animal breeding value on animal birth year as the indicator of genetic trend were estimated for milk yield and SCS traits [Fig. 7]. The results showed positive genetic trend for both traits during previous years.



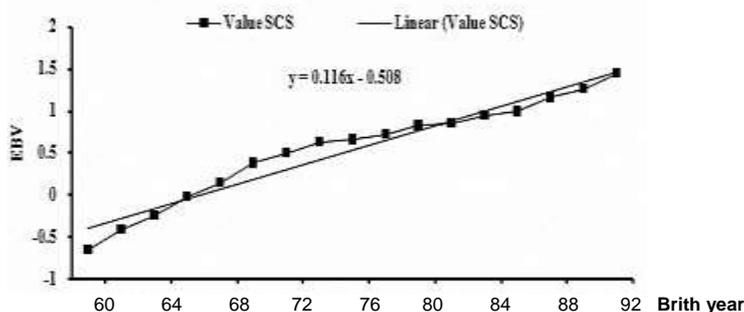


Fig. 7: Genetic trends of milk yield and SCS traits

## DISCUSSION

In this study, LP with different orders was compared for better fitting performance of TD milk yield and SCS. The results showed that the criteria of values changed when the order of fit the effects (AG and PE variances) considered to be various, agreeing with the results presented by Mohammadi et al. (2014a); Bignardi et al. (2009); Albuquerque et al. (2005) [10,18,19].

The trends in the AG and PE variances in this study in the first lactation are consistent with other studies [17,18,20]. On the other hand, inconsistent the results achieved in this study, AG and PE variances of milk yield was increased as lactation progressed and was highest in middle lactation and subsequently decreased at the end of lactation for Iranian Holsteins [21] and Turkish Holstein-Friesian [22]. We speculated that the differences between results may be due to the effects of some parameters such as environmental effects, number of data, software, the method and the breeds. The results of this current study showed that estimates of heritability of SCS were lowest than milk yield. The trend of heritabilities of yield traits in this study, were similar to results obtained in the Iranian Holsteins, by Mohammadi et al. (2014b); Shadparvar and Yazdanshenas (2005) [11,21].

The heritability estimates of first lactation milk yield reported from 0.28 Iranian Holsteins [10] to 0.51 in Holstein-Friesian cows [23]. Some authors reported higher heritabilities at the beginning and at the end of lactation [23]. This increase in heritabilities estimate is associated not only with the increases on the values of AG components but also with the reductions in values of PE components between models. Because heritabilities is low in early lactation for both traits, is obtained PE at this stage of lactation high and given that AG variance was higher in late lactation. The small differences in heritabilities estimate between models do not indicate a preferred order of the LP[10,11]. Estimates for additive genetic variance of fertility traits were less than residual variance; therefore, estimates for heritability for these traits were low. It was very close to most of estimates reported in other studies [8,24,25].

The results indicating that AFC has a relatively low heritability alike other reproductive traits. Thus, under the current conditions, changes in environmental factors would likely have a higher impact than the selection for these traits. The estimate of heritability for AFC in the present study is within the range (0.086 to 0.15) for those estimated for Angus-Blanco Orejinegro Zebu multi-breed cattle population in Colombia [26] and Iranian Holstein [24,27,28]. The estimate of heritability for AFC was lower than Vergara et al. (2009) for Angus Blanco Orejinegro Zebu cattle in Colombia (0.15±0.13); Wasike et al. (2009) for Boran cattle in Kenya (0.04±0.06); Chegini et al. (2015) for Iranian Holstein (0.133) and Suarez et al., 2006 [24,26,29,30] but close to Farhangfar and Naeemipour Younesi (2007), Chookani et al. (2010) for Iranian Holstein (0.014±0.005) [27,31]. Estimates of heritability for CI is similar to that in the reported in the South African cattle by Makgahlela et al. (2008), in the Iranian Holstein Cows by Faraji- Arough et al. (2011); [8,25]. On the other hand, inconsistent the results achieved in this study with results Ghiasi et al. (2011); Vergara et al. (2009); Toghiani Pozveh and Shadparvar (2009) [5,26,32] showed that heritability for CI was between 0.11 and 0.18. The results obtained heritability of LL (0.10±0.01) are supported by previous research, such as Berry and Cromie (2009) in Irish Cattle; Froidmont et al. (2012) [33,34] in Holstein cows but inconsistent with by results Chegini et al. (2015) and Haile-Mariam et al. (2003) [24,35] Different values estimated for heritability of fertility traits in this study could be due to several factors such as: breed of animal, management system, environmental factors, size and structure of data, model of analyses, nutrition or health care and statistical methods employed. The AFC had negative genetic correlations with CI and LL. This suggested that selection for smaller AFC would improve the lactation curve traits and also adversely lengthen CI (Chegini et al. 2015) [24]. The estimated negative genetic correlations of fertility traits Ghiasi et al. (2011) and zero genetic correlations for Iranian Holstein dairy cattle by Farhangfar and Naeemipour (2007); Pozveh and Shadparvar (2009); for Nellore cattle in Brazil by Gressler et al. (2005) [2,27,32,36]. Conversely, Vergara et al. (2009) reported a moderate and positive genetic correlation between AFC and CI (0.33) [26]. Suggested that the differences in sign and value of genetic correlations may be due to differences in breed of animal, environmental conditions, methods of estimation, and accuracies of variance and covariance components [25,26]. The results showed that the

phenotypic correlations between fertility traits (AFC, CI and LL) were positive, agreeing with the results presented by Faraji-Arough et al. (2011) [25]. Generally, an genetic correlations between TD yields was highest when periods closer to each other and the lowest was observed between distant TD. These results are in agreement with previous studies which have reported the effect of parity on the estimation of genetic parameters in Holstein-Friesian [11,15,20,37]. According to the results it was observed that phenotypic correlation decreased with increasing distance TD. Phenotypic correlation of SCS was estimated to be lower than of milk yield. These results are in agreement with those obtained by (Shadparvar and Yazdanshenas 2005) [21].

Estimating genetic and environmental trends in a population allows the assessment of the effectiveness of the selection procedure and gives the opportunity for monitoring management conditions. It also supplies the animal breeder with essential information to develop more successful programs in the future [38]. The results obtained of genetic trends, similar trends were reported by Sahebbonar (2010) [39] using the 305 day measures of the traits and Abdollahpour and Moradi Sahrbabak (2010) [17] for milk yield and Cheginiet al. (2015) [24] for SCS. The indicated that Iranian Holstein dairy cattle population genetically improved for milk yield and SCS traits. The interest of farmers to use sperms from genetically superior bulls could be the main factor which caused these changes.

## CONCLUSION

It is assumed that all mates are of similar genetic merit and this can result in bias in the predicted breeding values if there is preferential mating. Among the different models in this research, it seems that the LP (3,3) might be sufficient to capture most of the genetic and permanent environmental variability observed in the shape of daily milk production. The results obtained in this study (Heritabilities, genetic and phenotypic correlation and Etc. parameters of traits) provided population specific parameters with a higher accuracy that could be used in order to develop the national selection index of Holstein dairy cows. Although favourable positive genetic trends obtained for milk yield and SCS traits in Iranian Holstein cows, this could not lead to improvement in the fertility performance. The low heritability for fertility traits suggested that their genetic improvement would be slow. For improving these traits, improvements in nutrition and reproductive management could be useful. The genetic trend was positive for milk yield and SCS traits during previous years.

### ACKNOWLEDGMENTS

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### CONFLICT OF INTEREST

There is no conflict of interest

### FINANCIAL DISCLOSURE

None

## REFERENCES

- [1] Pedron O, Tedesco D, Giuliani G, Rizzi R. [1989] Factors affecting calving interval in Italian Holstein-Friesian heifers. *J Dairy Sci*, 72: 1286-1290.
- [2] Schaeffer LR, Dekkers JCM. [1994] Random regression in animal models for test-day production in dairy cattle. In: *Proceedings of the 5th World Congress on Applied Livestock Production*, Guelph, Canada, XVIII, 443-446.
- [3] Bagnato A, Oltenacu PA. [1994] Phenotypic evaluation of fertility traits and their association with milk production of Italian Friesian cattle. *J Dairy Sci*, 77: 874-882.
- [4] Rauw W, Kanis E, Noordhuizen-Stassen E, Grommers F. [1998] Undesirable side effects of selection for high production efficiency in farm animals: A review. *Livest Prod Sci*, 56: 15-33.
- [5] Ghiasi H, Pakdel A, Nejati-Javaremi A, Mehrabani-Yeganeh H, Honarvar M, Gonzalez- Recio O, Jesus Carabano M, Alenda R. [2011] Genetic variance components for female fertility in Iranian Holstein cows. *Livestock Science*, 139(3): 277-280.
- [6] Gonzalez-Recio O, Alenda R. [2005] Genetic parameters for female fertility traits and a fertility index in Spanish dairy cattle. *J Dairy Sci*, 88: 3282-3289.
- [7] Hinojosa A, Franco A, Boliol. [1980] Genetic and environmental factors affecting calving interval in a commercial beef herd in a semi-humid tropical environment. *Trop Anim Prod*, 43: 165-172.
- [8] Makgahlela ML, Banga CB, Norris D, Dzama K, Ngambi JW. [2008] Genetic analysis of age at first calving and calving interval in South African Holstein cattle. *Asia J Anim Vet Adv*, 3(4): 197-205.
- [9] Gonzalez-Recio O, Perez-Cabal MA, Alenda R. [2004] Economic value of female fertility and its relationship with profit in Spanish dairy cattle. *J Dairy Sci*, 87: 3053-3061.
- [10] Mohammadi A, Alijani S, Daghighkia H. [2014a] Comparison of different polynomial functions in Random Regression Model for milk production traits of Iranian Holstein dairy cattle. *Ann Anim Sci*, 14(1): 55-68.
- [11] Mohammadi A, Alijani S. [2014b] Estimation of genetic parameters and comparison of random regression animal and sire models of production traits in the first three lactations Iranian Holsteins. *Biotechnol Anim Husband*, 30(2): 261-279.
- [12] Mohammadi A, Alijani S, Rafat A, Bohlouli M, Latify M. [2012a] Comparison of different polynomial functions in random regression models for estimation of genetic parameters to test day milk yields of Iranian Holstein dairy cattle. *The fifth Iranian Congress on Animal Science*. 29-30 August Isfahan University, Iran [In Persian].
- [13] Mohammadi A, Alijani S, Rafat A, Taghizadeh A, Bohlouli M. [2012b] Comparison of fitting performance of polynomial functions in random regression model for test day milk yield in of Iranian Holstein dairy cattle. *Res Anim Prod*, 6: 46-63 [In Persian].

- [14] Kirkpatrick M, Lofsvold D, Bulmer M. [1990] Analysis of the inheritance, selection and evolution of growth trajectories. *Genetics*, 124: 979-993.
- [15] Costa NC, Melo CMRD, Pakcer LUFAD, Teixeira NM, Cobuci JA. [2008] Genetic parameters for test day milk yield of first lactation Holstein cows estimated by random regression using Legendre polynomials. *Revista Brasileira de Zootecnia*, 37: 602-608.
- [16] Meyer K. [2007] WOMBAT - a tool for mixed model analysis in quantitative genetics by REML *J Zhejiang Univ Sci*, 8: 815-821.
- [17] Abdollahpour R, Moradi Sahrbabak M. [2010] Genetic analysis of daily milk, fat percentage and protein percentage of Iranian first lactation Holstein cattle. *World Appl Sci J*, 10: 1040-1046.
- [18] Bignardi AB, El Faro L, Cardoso VL, Machado PF, Albuquerque LGD. [2009] Random regression models to estimate test-day milk yield genetic parameters Holstein cows in Southeastern Brazil. *Livest Sci*, 123: 1-7.
- [19] Albuquerque LG, Meyer K. [2005] Estimates of covariance functions for growth of Nelore cattle applying a parametric correlation structure to model within-animal correlations. *Livest Prod Sci*, 93: 213-222.
- [20] Naderi Y, Emam Jome Kashan N, Vaez Torshizi R, Amin Afshar M. [2015] Genetic analysis of milk yield in Iranian Holstein cattle by the test day model. *Iran J Appl Anim Sci*. 5: 839-844.
- [21] Shadparvar AA, Yazdanshenas MS. [2005] Genetic parameters of milk yield and fat percentage test day records of Iranian Holstein cows. *J Anim Sci*, 9: 1231-1236.
- [22] Takma C, Akbas Y. [2009] Comparison of fitting performance of random regression model to test day milk yields in Holstein Friesians. *Kafkas Univ Vet Fak Derg*, 15: 261-266.
- [23] Olori VE, Brotherstone S, Hill WG, Mc Guirk BJ. [1999] Fit of standard models of the lactation curve to weekly records of milk production of cows in a single herd. *Livest Prod Sci*, 58: 55-63.
- [24] Chegini A, Shadparvar AA, Ghavi Hosseini-Zadeh N. [2015] Genetic parameter estimates for lactation curve parameters, milk yield, age at first calving, calving interval and somatic cell count in Holstein cows. *Iran J Appl Anim Sci*, 5: 61-67.
- [25] Faraji-Arough H, Aslaminejad A, Farhangfar H. [2011] Estimation of genetic parameters and trends for age at first calving and calving interval in Iranian Holstein COWS. *J Res Agr Sci*, 7: 79-87.
- [26] Vergara O.D, Elzo MA, Ceron-Muno MF. [2009] Genetic parameters and genetic trends for age at first calving and calving interval in an Angus-Blanco Orejinegro Zebu multibreed cattle population in Colombia. *Livest Sci*, 126: 318-322.
- [27] Farhangfar H, Naeemipour Younesi H. [2007] Estimation of genetic and phenotypic parameters for production and reproduction traits in Iranian Holsteins. *J Sci Technol Agr Nat Res Water Soil Sci*, 11: 431-441.
- [28] Nilforooshan MA, Edriss MA. [2004] Effect of age at first calving on some productive and longevity traits in Iranian Holsteins of the Isfahan province. *J Dairy Sci*, 87: 2130-2135.
- [29] Suarez M, Ossa G, Perez J. [2006] Environmental and genetic aspects that influence on age at first calving in a native cattle of Colombia (Romosinuano). *Rev MVZ Cordoba*, 11: 738-743.
- [30] Wasike CB, Indetie D, Ojango JMK, Kahi AK. [2009] Direct and maternal (co)variance components and genetic parameters for growth and reproductive traits in the Boran cattle in Kenya. *Trop Anim Health Prod*, 41: 741-748.
- [31] Chookani A, Dadpasand M, Mirzaei HR, Rokouii M, Sayad Nezhad MB. [2010] An estimation of genetic parameters for some reproductive traits and their relationships to milk yield in Iranian Holstein cattle. *Iran J Anim Sci*, 40(4): 53-61.
- [32] Toghiani Pozveh S, Shadparvar AA, Moradi Shahrababak M, Dadpasand Taromsari M. [2009] Genetic analysis of reproduction traits and their relationship with conformation traits in Holstein cows. *J Livest Sci*, 125: 84-87.
- [33] Berry DP, Cromie AR. [2009] Associations between age at first calving and subsequent performance in Irish spring calving Holstein-Friesian dairy cows. *Livest Sci*, 123: 44-54.
- [34] Froidmont E, Mayeres P, Picron P, Turlot A, Planchon V, Stilmant D. [2013] Association between age at first calving, year and season of first calving and milk production in Holstein cows. *Anim*, 7: 665-672.
- [35] Haile-Mariam M, Bowman PJ, Goddard ME. [2003] Genetic and environmental relationship among calving interval, survival, persistency of milk yield and somatic cell count in dairy cattle. *Livest Prod Sci*, 80: 189-200.
- [36] Gressler MGM, Pereira JCC, Bergmann JAG, Andrade VJ, Paulino MF, Gressler SL. [2005] Genetic aspects of weaning weight and some reproductive traits in Nelore cattle. *Arquivo Brasileiro Med Vet Zootec*, 57: 533-538.
- [37] Cobuci JA, Costa CN, Neto JB, Freitas AF. [2011] Genetic parameters for milk production by using random regression models with different alternatives of fixed regression modeling. *R Bras Zootec*, 40: 557-567.
- [38] Hollowell G, Van Der Westhuizen J, Van Wyk J. [1998] Genetic and environmental trends for first lactation milk traits in the south African Ayrshire breed. *South Afr J Anim Sci*, 28: 38-45.
- [39] Sahebbonar M, Moradi Shahr Babak M, Miraei Ashtiani SR, Sayaadnejad MB. [2010] Estimation of genetic trends and factors affecting production traits in Iranian Holstein Cattle. *J Anim Sci Iran Period* 41: 173-184 (In Persian).