

# ESTIMATION OF GENETIC PARAMETERS AND COMPARISON OF RANDOM REGRESSION ANIMAL AND SIRE MODELS OF PRODUCTION TRAITS IN THE FIRST THREE LACTATIONS OF IRANIAN HOLSTEINS

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**Abstract:** This study was conducted to compare of random regression (RR) animal and sire models for estimation of the genetic parameters for production traits of Iranian Holstein dairy cows. For this purpose, the test day records were used belonged to first three lactations of cows and for, milk, fat and protein yields traits where, collected from 2003 to 2010, by the national breeding center of Iran. The genetic parameters were estimated using restricted maximum likelihood algorithm. To compare the model, different criterion  $-2\log L$  value, AIC, BIC and RV were used for considered traits. Residual variances were considered homogeneous over the lactation period. Obtained results showed that 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, fat and protein yields by RR animal and sire models were found to be lowest during early lactation (0.05, 0.04 and 0.07; 0.05, 0.19 and 0.13; 0.14, 0.19 and 0.15, for milk, fat and protein yields and in first, second and third lactation respectively). However, estimated heritabilities during lactation did not vary among different order Legendre polynomials, and also between RR animal and sire models. The variation in genetic correlations estimate in the RR animal and sire models was larger in the first lactation than in the second and third lactations. Thus, based on the results obtained, it can be inferred that the RR animal model is better for modeling yield traits in Iranian Holsteins.

**Keyword:** Dairy cow, random regression model, genetic parameter, test day

## Introduction

The use of appropriate method for the genetic components evaluation of dairy cattle is an important program of dairy animal production. In conventional method, lactation yields are calculated based on the test day (TD) records. TD records are actually repeated observations measured along a trajectory days in milk (DIM) and the mean and covariance between measurements change gradually along the trajectory. Among the models that consider TD production, random regression model (RRM) has been widely observed to increase the accuracy of breeding value predictions (*Strabel et al., 2004*). Several studies have reported that heritability of daily milk yields varied with DIM. In addition, genetic correlations between repeated measurements usually tended to decrease as the time between them increased (*Pander et al., 1992*). The extension of test records to compute 305-day yields is unable to account for these changes in the covariance structure. Secondly, the assumption that 305-day yields across parities measure the same trait suffers from the same limitations. An appropriate model for the analysis of repeated measurements over time or age should account for the mean and covariance structure that changes with time or age and should be feasible in terms of estimating the required genetic parameters.

*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. Although, some investigations have been carried out in Iranian Holstein dairy cows in regard to the estimation of genetic parameters of milk yield traits by RR animal model (*Mohammadi et al., 2012a; Mohammadi et al., 2012b*) and RR sire model (*Bohlouli and Alijani, 2012*), but compare RR animal and sire models in first three lactation has not yet been evaluated. Moreover, in literature several approaches were used lower additive genetic (AG) effect order of fit Legendre polynomial (LP) model than for the permanent environmental (PE) (*Mohammadi et al., 2012c; Takma and Akbas, 2009; Lopez-Romero and Carabano, 2003*). It seems that might be sufficient to capture most of the genetic and permanent environmental variability observed in the shape of daily milk production, producing less oscillatory and less extreme values for both variances and genetic correlations (*Lopez-Romero and Carabano, 2003*). Therefore, the purpose of this study is estimation of genetic parameters and comparison of random regression animal and sire models of production traits, using of LP (lower order LP for the AG effect than for the PE effect) and  $-2\text{LogL}$  value, Akaike's information criterion (AIC), Bayesian information criterion (BIC) and residual variance (RV) of the first three lactations of Iranian Holsteins.

## Materials and Methods

The TD milk yield records obtained from national breeding center of Iran, belonged to the first lactation dairy cow from 2004 to 2010. Age range by parity was 21 to 46 months, 32 to 65 months and 42 to 80 months for first, second and third lactation respectively. Edited data included the following: The TD data were excluded before 5th day and after the 305th day of lactation. In addition, irregular data for milk yield (<1.5 and >70 kg), fat percentage (<1.5 and >9 %), and protein percentage (<1 and >7 %), (then were converted to fat and protein yields) were excluded. Also, only cows with more than 5 TD records, and herds with more than 10 cows per herd in year of calving were kept. The sires having progeny fewer than 10 were eliminated. Four calving seasons (spring, summer, fall and winter) and 6 subclasses for age at calving for the first lactation (<26, 26 to 28, 28 to 30, 30 to 32, 32 to 33 and >33 months), 4 classes for the second lactation (<40, 40 to 43, 43 to 45, and >45), and 3 classes for the third lactation (<54, 54 to 58, and >58) were defined. This resulted to classes of cows calving age-season, which were included in the RRM as fixed regression part. RRM used to fit yield records was:

$$y_{tjklm} = HTD_t + Yc_j + MF_k + \sum_{n=1}^p AS_{mnl} x_n + \sum_{n=0}^r a_{mn} x_n + \sum_{n=0}^r pe_{mn} x_n + e_{tjklm}$$

Where  $y_{tjklm}$  is the  $t^{th}$  record (milk, fat and protein yields) of  $m^{th}$  cow in  $i^{th}$  subclass herd-test-date (HTD),  $j^{th}$  ( $j= 1$  to 7) calving year (YC) and  $k^{th}$  ( $k= 2$  and 3) milking times (MF);  $AS_{mnl}$  is the  $n^{th}$  fixed regression coefficient for  $m^{th}$  cow belong to  $l^{th}$ ,  $a_{mn}$  and  $pe_{mn}$  are in RR animal model, regression coefficients  $n^{th}$  for AG and PE effects on  $m^{th}$  cow and are in RR sire model, random regression coefficients  $n^{th}$  sire for AG and PE effects on  $m^{th}$  cow, respectively;  $p$  is the order fitting of fixed regression coefficients;  $r$  ( $r= 2$  to 6) orders number of LP;  $x_n$  is  $n^{th}$  LP, for  $t^{th}$  day and  $e_{tjklm}$  random residual effect associated with  $y_{tjklm}$ . Estimation of genetic parameters with restricted maximum likelihood (REML) methodology was done by REMLF90 (Misztal et al., 2002) program. For the standardized days in milk, the  $n^{th}$  LP is given as (Krikpatrick et al., 1990);

$$\Phi_{(d_i^*)^t} = \frac{1}{2^t} \sqrt{\frac{2t+1}{2}} \sum_{m=0}^{t/2} (-1)^m \binom{t}{m} \binom{2t-2m}{t} (d_i^*)^{t-2m}, \text{ where } d_i^*, \text{ is the } t^{th}$$

DIM;  $t$ , is time and  $i$ , is order LP. The matrices notation of the model can be written as,  $y = Xb + Qa + Zpe + e$ ; where  $y$  is the a vector of observations,  $b$  is the a vector of fixed effects,  $a$  and  $pe$  were vectors of AG and PE 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 RR animal model was defined as:

$$\text{var} \begin{bmatrix} a \\ pe \\ e \end{bmatrix} = \begin{bmatrix} G \otimes A & 0 & 0 \\ 0 & I\sigma_P^2 & 0 \\ 0 & 0 & R \end{bmatrix}, \text{ Where } G \text{ is the genetic covariance matrix}$$

among RR 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 PE effects,  $I$  represents an identity matrix, and  $R$  is the diagonal matrices of residual variance. The (co)variance structure for random parts of the RR sire model was defined as:

$$\text{var} \begin{bmatrix} s \\ pe \\ e \end{bmatrix} = \begin{bmatrix} G \otimes A & 0 & 0 \\ 0 & I\sigma_P^2 & 0 \\ 0 & 0 & R \end{bmatrix}, \text{ Where } G \text{ is sire genetic (co)variance matrix}$$

among RR coefficients and  $A$  is additive numerator relationship matrix between sires. For the RR animal model, heritability for  $i^{\text{th}}$  day in the lactation was

$$\text{calculated as: } h_i^2 = \frac{\sigma_{a(t)}^2}{\sigma_{a(t)}^2 + \sigma_{pe(t)}^2 + \sigma_e^2}, \text{ Where } \sigma_{a(t)}^2 = \mathbf{qGq}', \sigma_{pe(t)}^2 = \mathbf{qPq}', \text{ where}$$

$q$  is the vector of the associated LP;  $G$  and  $P$  are the (co)variance matrices for AG and PE, RR coefficients, respectively; and  $\sigma_{a(t)}^2$ ,  $\sigma_{pe(t)}^2$  and  $\sigma_e^2$  are AG, PE and residual variances for  $t^{\text{th}}$  DIM, respectively. For the RR sire model, heritability for

$$i^{\text{th}} \text{ DIM was calculated as: } h_i^2 = \frac{4\sigma_{a(t)}^2}{\sigma_{a(t)}^2 + \sigma_{pe(t)}^2 + \sigma_e^2}$$

Diagonal of above (co)variance matrices were sire AG variances ( $\sigma_{a(t)}^2$ ) and PE ( $\sigma_{pe(t)}^2$ ) for 5<sup>th</sup> day to 305<sup>th</sup> DIM. Number of records of milk, fat and protein yields and other descriptive statistics are summarized in Table 1. AG correlation for 305-days production between LP were calculated as:

$$r_{g(i,j)} = \frac{\text{Cov}_{g(i,j)}}{\sqrt{\text{Var}_{g(i,i)} \text{Var}_{g(j,j)}}}, \text{ Where } \text{Cov}_{g(i,j)}, \text{ is genetic covariance between } i \text{ and}$$

$j$  day,  $\text{Var}_{g(i,i)}$  and  $\text{Var}_{g(j,j)}$  are AG variance  $i$  and  $j$  day, respectively. Goodness of fit for the models (different LP) was examined using likelihood based criteria as -2Logl, AIC, BIC and RV values. AIC and BIC are:  $\text{AIC} = -2\text{Logl} + 2k$  and  $\text{BIC} = -2\text{Logl} + k \cdot \log(N - r(x))$ , where  $k$  is the number of parameters estimated,  $N$  is the sample size and  $r(x)$  is the rank of the coefficient matrix for fixed effects in the model. The model giving the lowest -2Logl, AIC, BIC and RV values is chosen as the better approximating model. Residual variance was 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 (*Costa et al., 2008*). Estimation of genetic parameters with REML methodology was done by REMLF90 program (*Misztal et al., 2002*).

**Table 1. Descriptive statistics of data sets for milk, fat and protein yields**

Parameter	First lactation		Second lactation		Third lactation	
	Model		Model		Model	
	Animal	Sire	Animal	Sire	Animal	Sire
<b>Milk yield</b>						
TD records	928,513		686,871		445,499	
Means $\pm$ SD (kg)	30.14 $\pm$ 7.481		32.74 $\pm$ 10.006		33.26 $\pm$ 10.753	
Number of cows with record	108,873		81,575		53,131	
Number of total animals	225,832	1593	183,407	1410	132,322	1131
Number of HTD	17,820		3,752		3,530	
Number of herd- calving year	1,483		305		289	
<b>Fat yield</b>						
TD records	788,577		586,584		381,896	
Means $\pm$ SD (g)	1 $\pm$ 0.326		1.09 $\pm$ 0.413		1.11 $\pm$ 0.441	
Number of cows with record	96,511		72,518		47,422	
Number of total animals	206,371	1526	162,427	1336	120,414	1063
Number of HTD	16,499		3,465		3,308	
Number of herd- calving year	1400		283		270	
<b>Protein yield</b>						
TD records	653,317		483,048		311,108	
Means $\pm$ SD (g)	0.94 $\pm$ 0.231		1.03 $\pm$ 0.295		1.05 $\pm$ 0.313	
Number of cows with record	79,501		59,147		38,304	
Number of total animals	171,360	142 4	137,950	1247	98,466	982
Number of HTD	14,127		2,938		2,648	
Number of herd- calving year	1,227		254		223	

## Results and Discussion

The values of comparison criteria ( $-2\text{Log}l$ , AIC, BIC, RV) for first three lactations and for the different LP of milk, fat and protein yields traits by RR animal and sire models were given in Tables 2 to 7. The choice for the best RR (animal and sire models) has been commonly taken based on test results of different criteria and genetic parameters. Among the LP models, that a lower order polynomial for the AG component than for the PE effects, the better the results observed by *Mohammadi et al., (2012b,c)*; *Lopez – Romero and Carabano, (2003)*; *Takma and Akbas, (2009)*. Thus, based on the results from most of the comparison criteria, it can be inferred that the models with a better quality fit were those which used lower order polynomial for the AG than for the PE effects.

## a. Model comparison

### a.1. First lactation

Choice of best LP model partly depends on partly the criteria that were used. While RR animal model with LP (2,6) for milk, fat and protein yields, had the lowest -2Logl, AIC and BIC values. Therefore, according to these criteria, the RR animal with LP (2,6) was selected as the best model. Furthermore, LP (2,6) for milk yield and LP (5,6) for fat and protein yields had lowest RV values (Table 2). According to comparison criteria's values, RR sire model with LP (5,6) for milk and protein yields and LP (3,6) for fat yield had the lowest -2Logl, AIC and BIC values. However, LP (2,6) for milk yield and LP (3,6) for fat and protein yield had lowest RV values (Table 3). The values of the criteria's were decreased when the order of fit for the PE effects than AG was increased in the LP models. This results agreeing with the results presented by *Takma and Akbas (2009)*; *Lopez – Romero and Biasus et al. (2011)* for Holstein-Friesian; *Costa et al. (2008)* for Brazilian Holstein and *Carabano et al. (2003)*; *Bignardi et al., (2009)*; *El Faro et al., (2008)*; *Meyer, (2001)*; *Brotherstone et al., (2000)*; *Albuquerque et al., (2005)*. The RV value for the three traits and both models decreased as order PE effect increased.

**Table 2. Comparison criteria's used in the first lactation by RR animal model and their levels**

Trait	Model	Number of Parameters	-2Logl	AIC	BIC	RV
Milk	LP(2,4)	14	5,745,809.76	5,745,837.76	5,745,893.19	12.53
	LP(2,5)	19	5,731,287.98	5,731,287.98	5,731,325.98	11.73
	<b>LP(2,6)</b>	<b>25</b>	<b>5,725,100.92</b>	<b>5,725,150.92</b>	<b>5,725,249.90</b>	<b>11.27</b>
	LP(3,4)	17	5,845,163.30	5,845,197.30	5,845,264.61	12.59
	LP(3,5)	22	5,845,163.42	5,831,062.42	5,831,150.53	11.71
	LP(3,6)	28	5,825,896.61	5,825,952.61	5,826,063.47	11.30
	LP(4,5)	26	5,949,498.45	5,949,550.45	5,949,653.39	11.82
	LP(5,6)	37	6,066,980.98	6,067,054.98	6,067,201.48	11.40
Fat	LP(2,4)	14	337,253.53	337,281.53	337,335.96	0.04820
	LP(2,5)	19	336,219.52	336,257.52	336,331.29	0.04729
	<b>LP(2,6)</b>	<b>25</b>	<b>335,652.92</b>	<b>335,602.92</b>	<b>335,800.11</b>	0.04669
	LP(3,4)	17	455,945.73	455,979.73	456,045.82	0.04812
	LP(3,5)	22	454,931.95	454,975.95	455,061.48	0.04724
	LP(3,6)	28	454,265.78	454,321.78	454,430.63	0.04668
	LP(4,5)	26	575,895.08	575,947.08	576,048.16	0.04723
	LP(5,6)	37	696,701.50	696,775.50	696,919.34	<b>0.04656</b>
Protein	LP(2,4)	14	-294,064.67	-294,036.67	-293,983.39	0.01582
	LP(2,5)	19	-296,005.54	-295,967.54	-295,895.23	0.01540
	<b>LP(2,6)</b>	<b>25</b>	<b>-297,002.48</b>	<b>-296,952.48</b>	<b>-296,854.36</b>	0.01508
	LP(3,4)	17	-215,687.16	-215,653.16	-215,588.46	0.01584
	LP(3,5)	22	-217,614.93	-217,570.93	-217,487.21	0.01538
	LP(3,6)	28	-218,500.41	-218,444.41	-218,337.85	0.01508
	LP(4,5)	26	-210,562.43	-210,510.43	-210,411.48	0.01541
	LP(5,6)	37	-21,849.19	-21,775.19	-21,634.38	<b>0.01507</b>

LP (i,j) is i and j order for AG and PE effects respectively

**Table 3. Comparison criteria's used in the first lactation by RR sire model and their levels**

Trait	Model	Number of Parameters	-2Logl	AIC	BIC	RV
Milk	LP(2,4)	14	5484,199.66	5,484,227.66	5,484,283.09	12.53
	LP(2,5)	19	5469,699.11	5,469,737.11	5,469,812.34	11.72
	LP(2,6)	25	5463,526.73	5,463,576.73	5,463,675.71	<b>11.24</b>
	LP(3,4)	17	5451,945.11	5,451,979.11	5,452,046.42	12.57
	LP(3,5)	22	5437,851.36	5,437,895.36	5,437,982.47	11.69
	LP(3,6)	28	5432,759.56	5,432,815.56	5,432,926.42	11.26
	LP(4,5)	26	5424,443.13	5,424,495.13	5,424,598.07	11.81
	<b>LP(5,6)</b>	<b>37</b>	<b>5409,632.05</b>	<b>5,409,852.05</b>	<b>5,409,852.55</b>	11.39
Fat	LP(2,4)	14	97,856.22	97,880.22	97,938.65	0.04813
	LP(2,5)	19	96,475.70	96,513.70	96,587.57	0.04756
	LP(2,6)	25	95,434.10	95,484.10	95,581.29	0.0459
	LP(3,4)	17	97,639.89	97,673.89	97,739.98	0.04784
	LP(3,5)	22	97,469.80	97,513.80	97,599.33	0.04673
	<b>LP(3,6)</b>	<b>28</b>	<b>94,456.61</b>	<b>94,456.61</b>	<b>94,621.01</b>	<b>0.04653</b>
	LP(4,5)	26	95,640.84	95,692.84	95,793.92	0.04718
	LP(5,6)	37	96,184.02	96,258.02	96,401.86	0.04654
Protein	LP(2,4)	14	-491,247.93	-491,219.93	-491,166.65	0.01582
	LP(2,5)	19	-493,173.95	-493,135.95	-493,063.64	0.01540
	LP(2,6)	25	-494,162.09	-494,112.09	-494,016.95	0.01503
	LP(3,4)	17	-512,130.26	-512,096.26	-512,031.56	0.01583
	LP(3,5)	22	-514,043.99	-513,999.99	-513,916.27	0.01536
	LP(3,6)	28	-514,909.18	-514,853.18	-514,746.62	<b>0.01502</b>
	LP(4,5)	26	-516,223.87	-516,171.87	-516,072.92	0.01540
	<b>LP(5,6)</b>	<b>37</b>	<b>-516,885.57</b>	<b>-516,811.57</b>	<b>-516,670.76</b>	0.01505

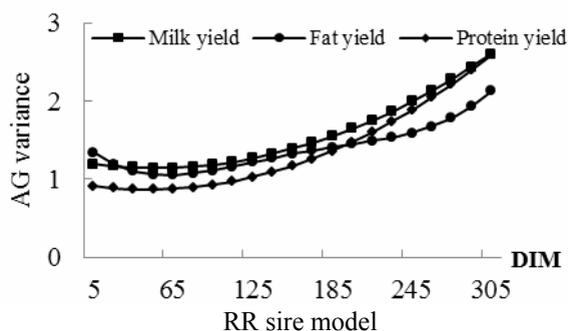
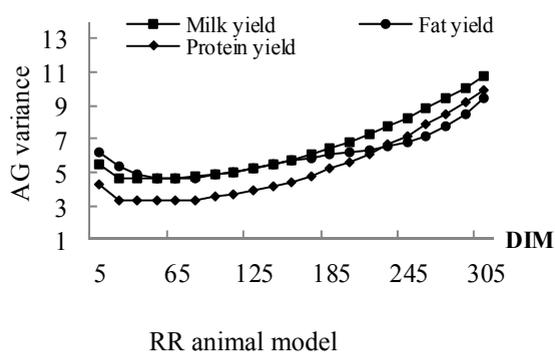
## b. Variances and heritabilities

### b.1. First lactation

The AG and PE variances as a function of DIM for milk, fat and protein yields for RR animal and sire models for first lactation are shown in Figure 1. For all traits studied in each both RR animal and sire models, AG variance was observed higher at the end of lactation. On the other hand, the maximum PE variance was observed at the beginning of lactation, and after this period, PE variance decreased (5-50 DIM) and following by a small increase at the end of lactation. The trends in the AG and PE variances in this study for RR animal model and traits yields in first lactation are consistent with other studies (*Abdollahpour et al., 2010; El Faro et al., 2008; Bignardi et al., 2009; Strabel et al., 2005; Pool et al., 2000; De Melo et al., 2007; De Roos et al., 2004*). On the other hand, inconsistent the results achieved in this study, AG variances was increased as lactation progressed and was highest in middle lactation and subsequently

decreased at the end of lactation for Iranian Holsteins (*Shadparvar and Yazdanshenas, 2005*); and Turkish Holstein-Friesian (*Takma and Akbas, 2007*). Moreover, PE variance was highest in end lactation for Turkish Holstein-Friesian (*Takma and Akbas, 2007*). However, the trend in the AG and PE variances in this study for RR sire model was similar to the results obtained by *Bohlouli and Alijani (2012)*.

The minimum heritability for all traits in early lactation was observed (The heritabilities of RR animal model 0.05, 0.04 and 0.07 and heritabilities of RR sire model 0.08, 0.05, 0.05 for milk, fat and protein yields respectively). Generally, heritability for both models and all traits, increased sudden in during the lactation period. The trend of heritabilities of yield traits in this study for first lactation, were similar to results obtained in the Iranian Holsteins, by *Bohlouli and Alijani, (2012)*; *Shadparvar and Yazdanshenas, (2005)*; *Razmkabir. (2008)*. Also, agreeing with the results presented by *Biassus et al., (2011)*; *Gengler et al., (2005)*; *Olori et al., (1999)* and *Gengler et al., (1999)*. 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, 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.



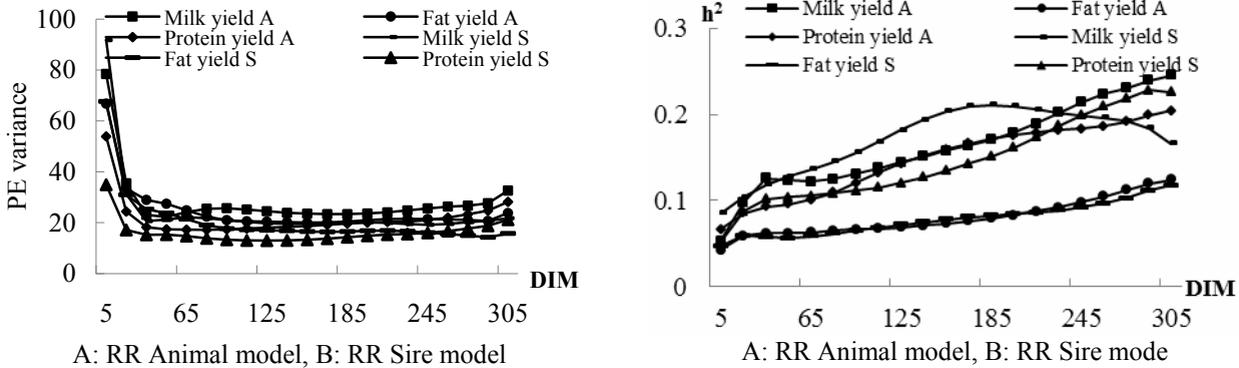


Figure 1. AG and PE variances in first lactation obtained for milk, fat (multiplied by 10<sup>3</sup>) and protein yields (multiplied by 103) and Estimated heritability (h<sup>2</sup>) for traits as a function of DIM

Table 4. Comparison criteria's used in the second lactation by RR animal model and their levels

Trait	Model	Number of Parameters	-2Logl	AIC	BIC	RV
Milk	LP(2,4)	14	4,229,308.22	4,229,336.22	4,229,389.90	19.16
	LP(2,5)	19	4,078,380.18	4,078,418.18	4,078,491.04	19.02
	LP(2,6)	25	3,927,327.79	3,927,377.79	3,927,473.65	18.16
	LP(3,4)	17	3,997,675.53	3,997,709.53	3,997,774.72	19.03
	LP(3,5)	22	3,846,845.05	3,846,889.05	3,846,973.41	18.46
	LP(3,6)	28	3,695,816.86	3,695,872.86	3,695,980.23	<b>17.45</b>
	LP(4,5)	26	3,587,932.73	3,587,984.73	3,588,084.43	18.22
	<b>LP(5,6)</b>	<b>37</b>	<b>3,233,363.09</b>	<b>3,233,437.09</b>	<b>3,233,578.97</b>	17.71
Fat	LP(2,4)	14	511,006.34	511,034.34	511,087.06	0.07081
	LP(2,5)	19	509,667.76	509,705.76	509,777.31	0.06883
	<b>LP(2,6)</b>	<b>25</b>	<b>508,491.09</b>	<b>508,541.09</b>	<b>508,635.23</b>	0.06752
	LP(3,4)	17	606,574.43	606,608.43	606,672.45	0.07067
	LP(3,5)	22	605,039.63	605,083.63	605,166.48	0.06879
	LP(3,6)	28	603,826.87	603,882.87	603,988.31	<b>0.06748</b>
	LP(4,5)	26	645,428.45	645,480.45	645,578.36	0.06763
	LP(5,6)	37	716,087.18	716,161.18	716,300.51	0.06754
Protein	LP(2,4)	14	-6,793.21	-6,765.21	-6,713.67	0.02446
	LP(2,5)	19	-9,019.73	-8,981.73	-8,911.78	0.02354
	<b>LP(2,6)</b>	<b>25</b>	<b>-10,028.62</b>	<b>-9,978.62</b>	<b>-9,886.58</b>	<b>0.02286</b>
	LP(3,4)	17	65,633.83	65,667.83	65,730.41	0.02448
	LP(3,5)	22	63,256.46	63,300.46	63,381.45	0.02352
	LP(3,6)	28	62,196.44	62,252.44	62,355.52	0.02288
	LP(4,5)	26	66,436.65	66,488.65	66,584.36	0.02296
	LP(5,6)	37	67,524.55	67,586.55	67,734.76	0.02291

## a.2. Second lactation

According to comparison criteria's values for second lactation, RR animal model with LP (5,6) for milk yield and LP (2,6) for fat and protein yields had the lowest for -2Logl, AIC and BIC values. However, LP (5,6) for milk yield, LP (3,6) for fat yield and LP (2,6) for protein yield had lowest RV values (Table 4). Furthermore, RR Sire model with LP (5,6) for milk yield and LP (3,6) for fat and protein yields had the lowest -2Logl, AIC and BIC values. Also, LP (2,6) for milk yield and LP (5,6) for fat yield and LP (3,6) protein yield had lowest RV values (Table 5).

**Table 5. Comparison criteria's used in the second lactation by RR sire model and their levels**

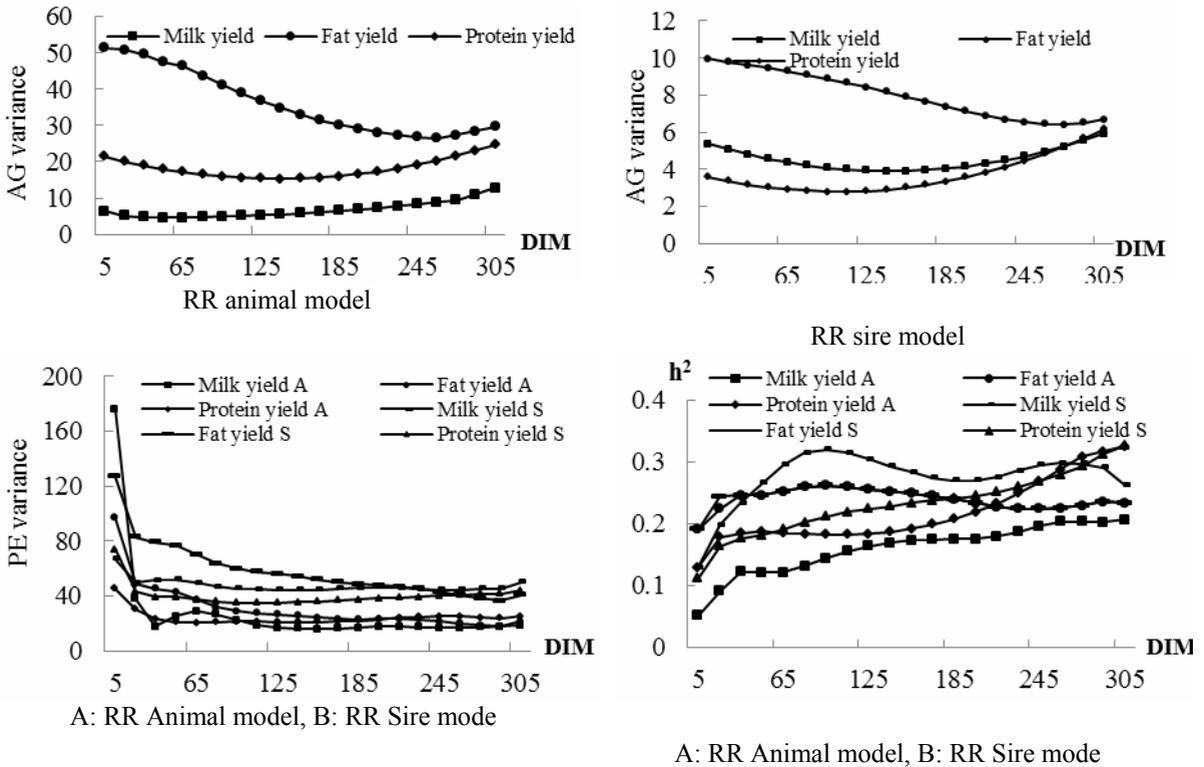
Trait	Model	Number of Parameters	-2Logl	AIC	BIC	RV
Milk	LP(2,4)	14	4,411,819.78	4,411,847.78	4,411,901.46	19.36
	LP(2,5)	19	4,400,704.30	4,400,742.30	4,400,815.16	<b>18.02</b>
	LP(2,6)	25	4,394,670.29	4,394,720.29	4,394,816.15	17.07
	LP(3,4)	17	4,400,252.15	4,400,286.15	4,400,351.34	19.41
	LP(3,5)	22	4,388,902.53	4,388,946.53	4,389,030.89	17.99
	LP(3,6)	28	4,383,316.83	4,383,372.83	4,383,480.19	17.08
	LP(4,5)	26	4,382,730.14	4,382,782.14	4,382,881.84	18.16
	<b>LP(5,6)</b>	<b>37</b>	<b>4,371,164.33</b>	<b>4,371,238.33</b>	<b>4,371,380.21</b>	17.32
Fat	LP(2,4)	14	324,051.78	324,079.78	324,132.50	0.07078
	LP(2,5)	19	322,760.46	322,798.46	322,870.01	0.06878
	LP(2,6)	25	321,536.82	321,386.82	321,680.96	0.06859
	LP(3,4)	17	324,099.90	324,133.90	324,197.92	0.07071
	LP(3,5)	22	322,811.02	322,855.02	322,937.87	0.06872
	<b>LP(3,6)</b>	<b>28</b>	<b>321,228.29</b>	<b>321,284.29</b>	<b>321,389.73</b>	0.06737
	LP(4,5)	26	323,483.46	323,535.46	323,633.37	0.06875
	LP(5,6)	37	323,161.27	323,235.27	323,374.60	<b>0.06734</b>
Protein	LP(2,4)	14	-160,719.99	-160,691.99	-160,640.45	0.02445
	LP(2,5)	19	-162,932.71	-162,894.71	-162,824.77	0.02350
	LP(2,6)	25	-163,948.96	-163,898.96	-163,806.93	0.02287
	LP(3,4)	17	-167,528.72	-167,562.72	-167,432.14	0.02358
	LP(3,5)	22	-168,787.98	-168,743.98	-168,662.99	0.02349
	<b>LP(3,6)</b>	<b>28</b>	<b>-169,779.61</b>	<b>-169,723.61</b>	<b>-169,620.53</b>	<b>0.02282</b>
	LP(4,5)	26	-168,896.18	-168,844.18	-168,748.47	0.02352
	LP(5,6)	37	-169,562.56	-169,488.56	-169,352.35	0.02285

## b.2. Second lactation

The trend of the AG variance estimates during the second lactation for RR animal and sire models and all traits were high at the beginning, then this trend decreased and subsequently increased at the end of lactation. However, the trend of the PE variance estimates during the second lactation was more similar to the first lactation (Figure 2). The AG and PE variances patterns observed in the study were comparable with those obtained by *Cobuci et al. (2011)* on Brazilian Holstein. The

minimum heritabilities for all traits in the second lactation were at the early lactation and trend of heritabilities was also similar to the results obtained of first lactation.

1



**Figure 2. AG and PE variances in second lactation obtained for milk, fat (multiplied by  $10^3$ ) and protein yields (multiplied by  $10^3$ ) and Estimated heritability ( $h^2$ ) for traits as a function of DIMa.3. Third lactation**

According to results obtained of comparison criteria's values for third lactation, RR animal model with LP (2,6) for milk, fat and protein yields had the lowest for -2Logl, AIC and BIC values. However, LP (2,6) for milk yield, LP (3,6) for fat and protein yields had lowest RV values (Table 6). Moreover, RR sire model with LP (5,6) for milk and protein yields and LP (3,6) for fat yield had the lowest for -2Logl, AIC and BIC values. However, LP (2,6) for milk yield and LP (3,6) for fat and protein yields had lowest RV values (Table 7).

**Table 6. Comparison criteria's used in the third lactation by RR animal model and their levels**

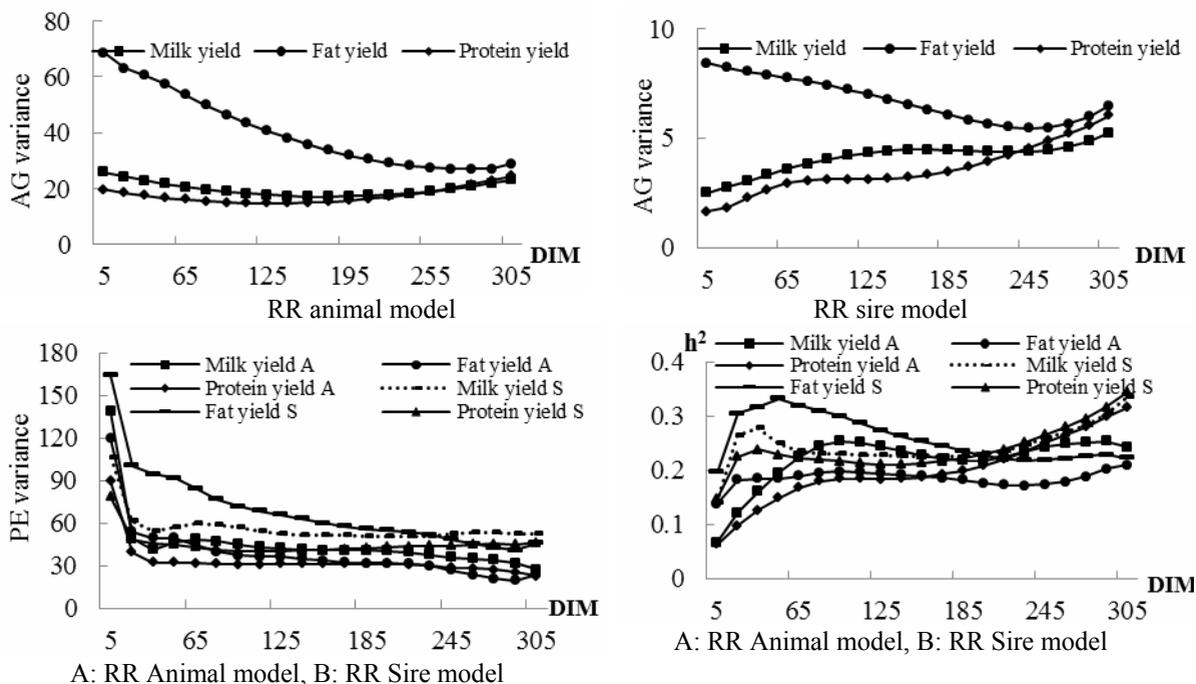
Trait	Model	Number of Parameters	-2Logl	AIC	BIC	RV
Milk	LP(2,4)	14	3,050,656.30	3,050,684.30	3,050,735.34	21.07
	LP(2,5)	19	3,042,083.66	3,042,121.66	3,042,190.92	19.43
	<b>LP(2,6)</b>	<b>25</b>	<b>3,037,826.83</b>	<b>3,037,876.83</b>	<b>3,037,967.96</b>	<b>18.34</b>
	LP(3,4)	17	3,116,815.18	3,116,849.18	3,116,911.15	21.09
	LP(3,5)	22	3,107,908.88	3,107,952.88	3,108,033.08	19.39
	LP(3,6)	28	3,103,942.97	3,103,998.97	3,104,101.04	18.37
	LP(4,5)	26	3,213,432.47	3,213,484.47	3,213,579.25	18.94
	LP(5,6)	37	3,241,645.56	3,241,719.56	3,241,928.44	18.63
Fat	LP(2,4)	14	377,214.95	377,242.95	377,293.04	0.07522
	LP(2,5)	19	376,045.34	376,083.34	376,155.19	0.07280
	<b>LP(2,6)</b>	<b>25</b>	<b>375,140.86</b>	<b>375,190.86</b>	<b>375,285.39</b>	<b>0.07134</b>
	LP(3,4)	17	443,975.77	444,009.77	444,074.05	0.07516
	LP(3,5)	22	442,788.17	442,832.17	442,915.36	0.07274
	LP(3,6)	28	441,831.03	441,887.03	441,992.91	<b>0.07123</b>
	LP(4,5)	26	455,416.16	455,468.16	455,566.48	0.07265
	LP(5,6)	37	576,442.18	576,516.18	576,656.09	0.07128
Protein	LP(2,4)	14	33,618.62	33,646.62	33,695.47	0.02606
	LP(2,5)	19	31,702.01	31,740.01	31,806.30	0.02488
	<b>LP(2,6)</b>	<b>25</b>	<b>30,889.61</b>	<b>30,939.61</b>	<b>31,026.84</b>	<b>0.02406</b>
	LP(3,4)	17	83,516.39	83,550.39	83,609.93	0.02605
	LP(3,5)	22	81,469.32	81,513.32	81,590.08	0.02483
	LP(3,6)	28	80,616.94	80,672.94	80,770.64	<b>0.02404</b>
	LP(4,5)	26	81,034.64	81,086.64	81,177.36	0.02495
	LP(5,6)	37	82,751.44	82,825.44	82,954.54	0.02407

Table 7. Comparison criteria's used in the third lactation by RR sire model and their levels

Trait	Model	Number of Parameters	-2Logl	AIC	BIC	RV
Milk	LP(2,4)	14	2,889,766.33	2,889,794.33	2,889,845.37	19.64
	LP(2,5)	19	2,896,038.46	2,896,080.46	2,896,145.72	19.38
	LP(2,6)	25	2,891,858.66	2,891,908.66	2,891,999.79	<b>18.28</b>
	LP(3,4)	17	2,897,117.58	2,897,151.58	2,897,213.55	21.09
	LP(3,5)	22	2,888,251.98	2,888,295.98	2,888,376.18	19.33
	LP(3,6)	28	2,887,742.47	2,887,798.47	2,887,900.54	18.37
	LP(4,5)	26	2,882,782.41	2,882,834.41	2,882,929.19	19.57
	<b>LP(5,6)</b>	<b>37</b>	<b>2,874,637.55</b>	<b>2,874,711.55</b>	<b>2,874,846.43</b>	18.58
Fat	LP(2,4)	14	245,627.43	245,655.43	245,705.52	0.07515
	LP(2,5)	19	244,507.21	244,545.21	244,613.19	0.07270
	LP(2,6)	25	243,622.79	243,672.79	243,762.24	0.07110
	LP(3,4)	17	245,594.39	245,628.39	245,689.22	0.07510
	LP(3,5)	22	244,444.14	244,488.14	244,566.86	0.07267
	<b>LP(3,6)</b>	<b>28</b>	<b>243,506.91</b>	<b>243,562.91</b>	<b>243,663.09</b>	<b>0.07103</b>
	LP(4,5)	26	244,861.89	244,913.89	245,006.92	0.07271
	LP(5,6)	37	244,584.23	244,658.23	244,790.62	0.07105
Protein	LP(2,4)	14	-73,910.45	-73,882.45	-73,833.60	0.02605
	LP(2,5)	19	-75,821.63	-75,783.63	-75,717.11	0.02482
	LP(2,6)	25	-76,592.40	-76,542.40	-76,455.17	0.02399
	LP(3,4)	17	-78,291.81	-78,257.81	-78,198.49	0.02604
	LP(3,5)	22	-80,310.36	-80,266.36	-80,189.60	0.02475
	LP(3,6)	28	-81,120.91	-81,064.91	-80,967.21	<b>0.02397</b>
	LP(4,5)	26	-80,921.91	-80,869.91	-80,779.19	0.02483
	<b>LP(5,6)</b>	<b>37</b>	<b>-81,559.19</b>	<b>-81,485.19</b>	<b>-81,559.19</b>	0.02402

### b.3. Third lactation

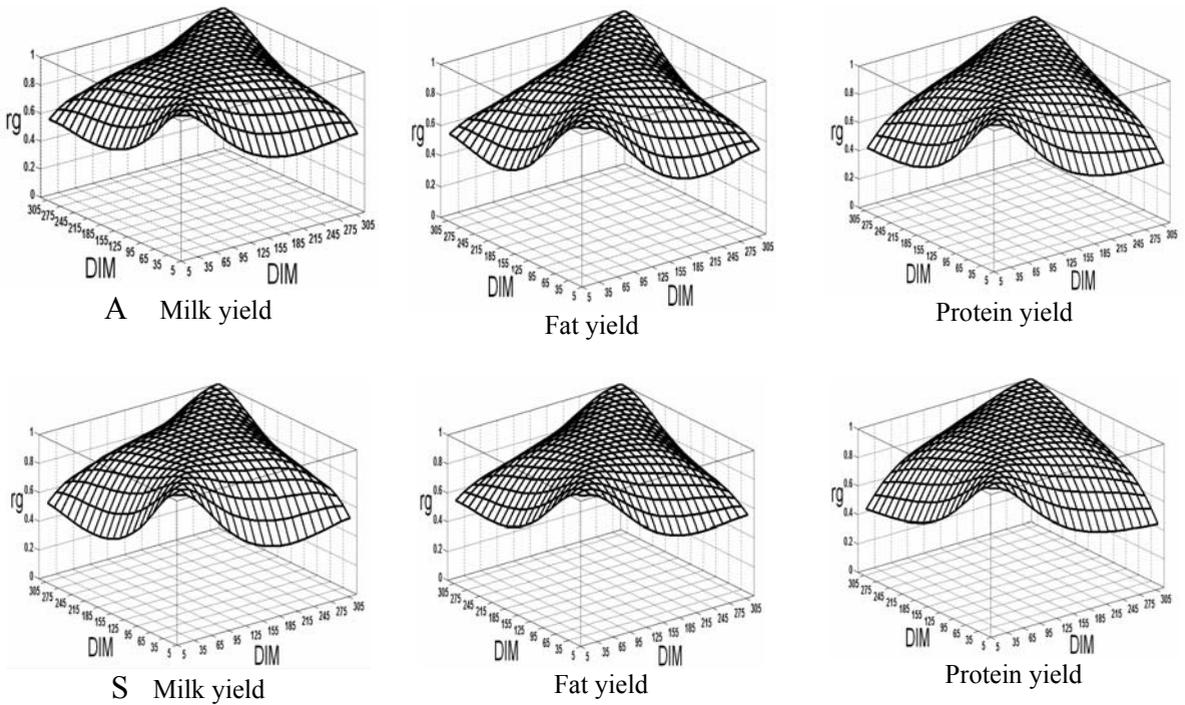
The AG variances pattern of RR animal model in the third lactation was similar to those obtained in the second lactation. However, AG variances for milk and protein yields by RR sire model lowest was at beginning of lactation. Shape of heritability for all traits in third lactation and by RR animal model was similar to the obtained in the first and second lactations. Moreover, the patterns of heritability by RR sire model were the minimum at around 210 DIM.



**Figure 3.** AG and PE variances in third lactation obtained for milk, fat (multiplied by  $10^3$ ) and protein yields (multiplied by  $10^3$ ) and Estimated heritability ( $h^2$ ) for traits as a function of DIM

### Genetic correlations

Generally, genetic correlations between TD yields for both RR animal and sire models was highest when periods closer to each other and the lowest was observed between distant TD. These results agree with results of *Biassus et al. (2011)*; *Cobuci et al. (2011)*; *Jakobsen et al. (2002)* and *Costa et al. (2008)*. The variation in genetic correlation estimates was larger in the first lactation than in the second and third lactations, although the trends within lactation were similar for both RR animal and sire models. These results are in agreement with previous studies which have reported the effect of parity on the estimation of genetic parameters in Holstein-Friesian (*Liu et al., 2000*; *Guo et al., 2002*; *Cobuci et al., 2011*).



**Figure 4. Genetic correlations in the first lactation obtained by RR animal model (A) and RR sire model (S) as a function of DIM. (Genetic correlations are presented only first lactation)**

## 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. According to in the RR animal model using of all animal records, therefore is for estimation of genetic parameters high accuracy. Thus, based on the results from the comparison of RR animal and sire models and comparison criteria, it can be inferred that the RR animal model which used lower order polynomial for the AG component than for the PE effects is better for modeling yield traits in Iranian Holsteins. Variations in heritability estimates across lactation were associated to different trends in genetic and PE variances. Trends of the heritability estimates during the second and the third lactation were more similar than those between the first and the second or the third lactation. Genetic correlations between individual TD records within traits and both RR animal and sire models and for different lactations were high for adjacent tests and decreased as the interval between tests increased.

## Acknowledgment

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## Procena genetskih parametara i poređenje modela slučajne regresija grla i oca (random regression animal and sire models) za proizvodne osobine u prve tri laktacije goveda rase iranski holštajn

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## Rezime

Cilj ovog istraživanja je bio da se uporede modeli slučajne regresije (RR) životinje i oca u proceni genetskih parametara za proizvodne osobine muznih krava rase iranski holštajn. U tu svrhu, dan testiranja korišćeni su podaci dnevnog testiranja u prve tri laktacije krava za osobine prinosa mleka, masti i proteina, koji su prikupljeni od 2003 do 2010 godine, od strane nacionalnog oplemenjivačkog centra Irana. Genetski parametri su ocenjivani koristeći algoritam ograničene maksimalne verodostojnosti. Da bi se uporedili modeli, korišćeni su različiti kriterijumi -  $2\log L$  vrednost, AIC, BIC i RV u razmatranju osobina. Rezidualne varijanse su smatrane homogenim tokom perioda laktacije. Dobijeni rezultati su pokazali da je aditivna genetska varijansa bila je najveća u početku i na kraju laktacije i stalna varijansa životne sredine bila je veća u početku laktacije nego u drugim periodima laktacije. Procene heritabiliteta za prinosa mleka, masti i proteina, utvrđeni prema modelima slučajne regresije (RR) životinje i oca, utvrđeno je da su najniže tokom rane laktacije (0.05, 0.04 i 0.07, 0.05, 0.19 i 0.13, 0.14, 0.19 i 0.15, za prinose mleka, masti i proteina u prvoj, drugoj i trećoj laktaciji, respektivno). Međutim, procenjeni heritabiliteti tokom laktacije nisu varirali između Ležandra polinoma različitog redosleda a takođe između modelaslučajne regresije (RR) životinje i oca. Varijacija procenjenih genetskih korelacija u modelima slučajne regresije (RR) životinje i oca bila je veća u prvoj laktaciji nego u drugoj i trećoj laktaciji. Stoga, na osnovu dobijenih rezultata, može se zaključiti da je model slučajne regresije (RR Animal model) životinje bolji za modelovanje osobina prinosa goveda rase iranski holštajn.

## References

- ABDULLAHPOUR R., MORADI SHAHRBABAK M., NEJATI JAVAREMI A., VAEZ TORSHIZI R. (2010): Genetic analysis of daily milk, fat percentage and protein percentage of Iranian first lactation Holstein cattle. *World Applied Science*, 10, 1042-1046.
- ALBUQUERQUE L.G., MEYER K. (2005): Estimates of covariance functions for growth of Nelore cattle applying a parametric correlation structure to model within-animal correlations. *Livestock Production Science*, 93, 213-222.
- BIASSUS L.D.O., COBUCI J.A., COSTA C.N., RORATO P.R.N., NETO J.B., CARDOSO L.L. (2011): Genetic parameters for production traits in primiparous Holstein cows estimated by random regression models. *Revista Brasileira de Zootecnia*, 40, 85-94.
- BIGNARDI A.B., EL FARO L., CARDOSO V.L., MACHADO P.F., ALBUQUERQUE L.G.D. (2009): Random regression models to estimate test-day milk yield genetic parameters Holstein cows in Southeastern Brazil. *Livestock Science*, 123, 1-7.
- BOHLOULI M., ALIJANI S. (2012): Genotype by environment interaction for milk production traits in Iranian Holstein dairy cattle using random regression model. *Livestock Research for Rural Develment*, 24,7.
- BROTHERSTONE S., WHITE I.M.S., MEYER K. (2000): Genetic modeling of daily milk yield using orthogonal polynomials and parametric curves. *Journal of Animal Science*, 70, 407-415.
- COBUCI J.A., COSTA C.N., NETO J.B., FREITAS A.F. (2011): Genetic parameters for milk production by using random regression models with different alternatives of fixed regression modeling. *Rev. Bras. Zootec.* 40, 557-567.
- COSTA N.C., MELO C.M.R.D., PAKCER L.U.A.F.D., TEIXEIRA N.M., COBUCI J.A. (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.
- DE MELO C.M.R., PACKER I.U., COSTAAND C.N., MACHADO P.F. (2007): Genetic parameters for test day milk yields of first lactation Holstein cows by random regression models. *Journal of Animal Consortium*, 1, 325-334.
- DE ROOS A.P.W., HARBERS A.G.F., DE JONG G. (2004): Random herd curves in a test-day model for milk, fat, and protein production of dairy cattle in the Netherlands. *Journal of Dairy Science*, 87, 2693-2701.
- EL FARO L., CARDOSO V.L., ALBUQUERQUE L.G.D. (2008): Variance component estimates applying RRM for test-day milk yield in Caracu heifers (*Bos taurus Artiodactyla*, *Bovidae*). *Genetics and Molecular Biology*, 31, 665-673.

- GENGLER N., WIGGANS G.R., GILLON A. (2005): Adjustment for Heterogeneous Covariance due to Herd Milk Yield by Transformation of Test-Day Random Regressions. *Journal of Dairy Science*, 88, 2981-2990.
- JAKOBSEN J.H., MADSEN P., JENSEN J., PEDERSEN J., CHRISTENSEN L.G., SORENSEN D.A. (2002): Genetic parameters for milk production and persistency for Danish Holsteins estimated in random regression models using REML. *Journal of Dairy Science*, 85, 1607-1616.
- KIRKPATRICK M., LOFSVOLD D., BULMER M. (1990): Analysis of the inheritance, selection and evolution of growth trajectories. *Genetics*, 124, 979-993.
- LIU Z., REINHARDT F., REENTS R. (2000): Estimating parameters of a random regression test day model for first three lactation milk production traits using the covariance function approach. *Interbull Bulletin*, 25, 74-80.
- LOPEZ-ROMERO P., CARABANO M.J. (2003): Comparing alternative random regression models to analyse first lactation daily milk yield data in Holstein-Friesian cattle. *Livestock Production Science*, 82, 81-96.
- MEYER K. (2001): Estimating genetic covariance functions assuming a parametric correlation structure for environmental effects. *Genetics Selection Evaluation*, 33, 557-585.
- MISZTAL I., TSURUTA S., STRABEL T., AUVRAY B., DRUET T., LEE D.H. (2002): BLUPF90 and related programs (BGF90). In: Proc 7th World Congress Genetics Applied Livestock Production, Montpellier, France CD-ROM communication. 28, 07
- MOHAMMADI A., ALIJANI S., RAFAT A., BUHLOLI M., LATIFY M. (2012a): Estimation of genetic parameters for milk yield test day records by random regression model of Iranian Holstein dairy cattle. The fifth Iranian Congress on Animal Science, 29-30 August Isfahan University, Iran [In Persian].
- MOHAMMADI A., ALIJANI S., RAFAT A., BUHLOLI M., LATIFY M. (2012b): 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].
- MOHAMMADI A., ALIJANI S., RAFAT S.A., TAGHIZADEH A., BUHLOLI M. (2012c): Comparison of Fitting Performance of Polynomial Functions in Random Regression Model for Test Day Milk Yield in of Iranian Holstein Dairy Cattle. *Research on Animal Productions*. 6: 46-63 [In Persian].
- OLORI V.E., HILL W.G., MC GUIRK B.J., BROTHERSTONE S. (1999): Estimating variance components for test day milk records by restricted maximum likelihood with a random regression animal model. *Livestock Production Science*, 61, 55-63.
- PANDER B.L., HILL W.G., THOMPSON R. (1992): Genetic parameters of test day records of British Holstein heifers. *Journal of Animal Production*, 55, 11-21.

- 
- POOL M.H., JANSS L.L.G., MEUWISSEN T.H.E. (2000): Genetic parameters of Legendre polynomials for first parity lactation curves. *Journal of Dairy Science*, 83, 2640-2649.
- SCHAEFFER L.R., DEKKERS J.C.M. (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, pp, 443-446.
- SHADPARVAR A.A., YAZDANSHENAS M.S. (2005): Genetic parameters of milk yield and milk fat percentage test day records of Iranian Holstein cows. *Asian-Australian Journal of Animal Science*, 9, 1231-1236.
- STRABEL T., PTAK E., SZYDA J., JAMROZIK J. (2004): Multiple-lactation random regression test-day model for Polish Black and White cattle. *Interbull Bulletin*, 32, 133-136.
- STRABEL T., SZYDA J., PTAK E., JAMROZIK J. (2005): Comparison of Random Regression Test-Day Models for Polish Black and White Cattle. *Journal of Dairy Science*, 88, 3688-3699.
- TAKMA C., AKBAS Y. (2009): Comparison of Fitting Performance of random regression model to Test Day Milk Yields in Holstein Friesians. *Kafkas Universitesi Veteriner Fakultesi Dergisi*, 15: 261-266.
- TAKMA C., AKBAS Y. (2007): Estimates of genetic parameters for test day milk yields of a Holstein Friesian herd in Turkey with random regression models. *Journal Archiv Tierzucht Dummerstorf*, 50, 327-336.