COMPARISON OF DIFFERENT POLYNOMIAL FUNCTIONS IN RANDOM REGRESSION MODEL FOR MILK PRODUCTION TRAITS OF IRANIAN HOLSTEIN DAIRY CATTLE

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Abstract

The aim of this research was to compare different polynomial functions including Legendre polynomials (LP), Wilmink (WRR) and Ali-Schaeffer (ARR) functions, in random regression model (RRM) for estimation of genetic parameters for milk production traits of Iranian Holstein dairy cattle. For this purpose the performance records obtained from test-day (TD) regarding milk yield. fat and protein contents of the cows calving for the first time were used. The numbers of records for the above mentioned traits were 701212, 657004, and 560775, respectively. These records were collected from the years 2006 to 2010 by the National Breeding Center of Iran. The genetic parameters were estimated using Restricted Maximum Likelihood (REML) method by applying RRM. Residual variances were considered homogeneous over the lactation period. To compare the model, different criteria (-2Logl, AIC, BIC and RV) were used for considered traits. Based on the results obtained, for all traits, RRM with LP function (2,5) were chosen as the best model. Considering residual variance (RV), LP (2,2) was proved to be a model which has the lowest performance, while using -2Logl, AIC, BIC criteria, RRM with ARR function was the worst model. According to the results, it is recommended to use LP with low orders for the additive genetic effects and with more orders for the permanent environment effects in the RRM for Iranian Holstein cattle. Permanent environment variance was higher in early lactation than during lactation and additive genetic variance in the early lactation was lower than at the end of lactation. Heritability range of milk yield, fat and protein contents was estimated to be from 0.08 to 0.23, 0.05 to 0.20 and 0.08 to 0.14, respectively. Phenotypic variance of the considered traits during lactation was not constant and it was higher at the beginning and the end of lactation. The additive genetic correlation between adjacent test days was higher than between distant test days.

Key words: dairy cattle, random regression model, test-day, genetic parameters

Milk production is the most economically important trait in the dairy cattle breeding industry. One of the important breeding programme processes is the estimation of genetic parameters using appropriate models. In the conventional method, lactation

yields are calculated based on the test-day (TD) records. Changes in milk production during the lactation period for any lactating cow follows a shape which is called a lactation curve, and TD measurements are points on the lactation curve (Moradi Shahrbabak, 1990). The TD Model has been described using various models, such as repeatability, fixed regression, multiple-trait and RRM (Swalve, 2000). Among the models that consider TD production, RRM has been widely observed to increase the accuracy of breeding value predictions (Strabel et al., 2004). 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. Genetic parameters of TD milk traits using RRM have been reported for several cow populations from fitting various functions to model additive genetic lactation curves (Jamrozik et al., 1997; Jakobsen et al., 2002; Schaeffer, 2004; Strabel et al., 2005).

Several functions are used to estimate genetic parameters and to model the shape of lactation curves with RRM (Jamrozik et al., 1997; Gengler et al., 1999). Since the choice of appropriate mathematical function to describe the fixed and random effects is the key element in fitting RRM, the correct choice of these functions to estimate genetic parameters leads to more accurate estimates (Misztal et al., 2000). The choice of the polynomial function in RRM influences number of parameters and order of the estimated (co)variance components matrix. Different polynomials such as Legendre polynomial (LP), Wilmink (WRR) and Ali-Schaeffer (ARR) functions have been used in RRM. Takma and Akbas (2009) compared LP, WRR and ARR functions at RRM to TD milk yield in Holstein-Friesian using residual variance (RV), Akaike's information criterion (AIC), -2logL, Bayesian information criterion (BIC) and likelihood ratio test (LRT), and reported that among the acquired functions, LP (6,2), (6,5) and (6,6) were chosen as selected models. Lopez-Romero and Carabano (2003) compared alternative RRM to the analysis of data from the first lactation of daily milk yield in Holstein-Friesian cattle.

The results of these studies revealed that lactational models (ARR and WRR) showed worse performance than the LP models with the same number of parameters. For LP all criteria (expect the BIC) favoured the most complex model. In many studies in Iran RRM is widely used with LP function, therefore it is necessary to compare different functions of the RRM to determine the best fitting model to TD milk production. The purpose of this study is to compare LP with different orders, WRR and ARR functions using -2logL, AIC, BIC and RV criteria's for the estimation of genetic parameters of TD milk yield, fat and protein contents records of Iranian Holstein dairy cattle.

Material and methods

The TD milk yield records obtained between 2006 and 2010 from the first lactation dairy cows at the National Breeding Center of Iran. The age of cows in the first lactation was from 21 to 46 months. Edited data included the following: rhe TD data were excluded before day 5 and after day 305 of lactation. In addition, irregular data for milk yield (<1.5 and >70 kg), fat content (<1.5% and >9%), and protein content (<1% and >7%) were excluded. Only cows with more than 5 TD records, and herds with more than 4 cows per herd in the year of calving were kept. The sires having progeny fewer than 5 were eliminated. Finally edited data included 701212, 657004 and 560775 TD records for milk yield, fat content and protein content, respectively. Four calving seasons (spring, summer, fall and winter) and 6 subclasses for age at calving (<26, 26 to 28, 28 to 30, 30 to 32, 32 to 33 and >33 months) were defined. This resulted in 24 classes of cows calving age-season, which were included in the RRM as fixed regression part. The RRM used to fit yield records was:

$$y_{iijklm} = HTD_i + Yc_j + MT_k + \sum_{n=1}^{p} AS_{mnl}x_n + \sum_{n=0}^{r} a_{mn}x_n + \sum_{n=0}^{r} pe_{mn}x_n + e_{iijklm}$$

where y_{iijkm} is the *t*th record (milk yield, fat and protein contents) of *m*th cow in *i*th herd-test-date (HTD) effect, *j*th (*j* = 1 to 5) calving year (YC) and *k*th milking frequency (2 or 3 times per day); AS_{mni} is the *n*th fixed regression coefficient of *l*th class of cows calving age-season (*l* = 1 to 24); a_{mn} and pe_{mn} are regression coefficients *n*th for additive genetic and permanent environment effects on *m*th cow respectively; *p* is the number of covariates; *r* (*r* = 2 to 5) orders number of different functions; x_n is *n*th LP, WRR and ARR polynomial for *t*th day; e_{ijklm} random residual effect associated with y_{iiklm} .

Number of records of milk yield, fat and protein contents and other descriptive statistics are summarized in Table 1.

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	Milk (kg)	Fat (%)	Protein (%)
Number of TD records	701212	657004	560775
Means ±SD (kg)	30.56±7.54	3.35±1.83	3.06±1.75
Number of animals with record	83407	79856	67999
Number of total animals	199903	190726	162555
Number of dam with progeny	125651	119661	101818
Number of sire with progeny	3764	3704	3378
Number of HTD	16365	16029	13300
Number of herd-calving year	1519	1463	1207

Table 1. Descriptive statistics of data sets for milk yield, fat and protein contents

To calculate the standard DIM (d*t), the following equation was used:

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

where d_{min} and dmax are minimum and maximum days in milk, and d_i , t^{th} days in milk. For the t^{th} standardized days in milk, the n^{th} polynomial is given as (Kirkpatrick et al., 1990);

$$\Phi(d_t^*, i) = \frac{1}{2^i} \sqrt{\frac{2i+1}{2}} \sum_{m=0}^{i/2} (-1)^m \binom{i}{m} \binom{2i-2m}{i} (d_t^*)^{i-2m}$$

where d_{i}^* is the *i*th days in milk; and *i*, is order LP function. In WRR function, $\phi_{mn} = \phi_{0mn0} + \phi_{1mn1} + \phi_{2mn2}$, where $\phi_0 = 1$, $\phi_1 = \dim_t$ and $\phi_2 = \exp^{(-0.05 \text{dim}t)}$, \dim_t is the considered days in milk, and in ARR function, $\phi_{mn} = (1 \text{ c } c^2 \text{ d } d^2)$, where $c = (t_{mn}/305)$ and $d = \ln(1/c)$, where t_{mn} is the nth days in milk.

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 are 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:

$$Var\begin{bmatrix} a\\ pe\\ e \end{bmatrix} = \begin{bmatrix} G \otimes A & 0 & 0\\ 0 & Is_{P}^{2} & 0\\ 0 & 0 & R \end{bmatrix}$$

where *G* is the genetic covariance matrix of the random regression coefficients, o is the kronecker product function, *A* is the additive genetic relationship matrix coefficients among animals σ_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 days in milk was calculated as:

$$h_i^2 = \frac{s_{a(i)}^2}{s_{a(i)}^2 + s_{pe(i)}^2 + s_e^2}$$

where $\sigma_{p(i)}^2 = qGq^1$, $\sigma_{p(i)}^2 = qpq^1$, 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 $\sigma_{p(i)}^2$, $\sigma_{pe(i)}^2$ and σ^2 are additive genetic, permanent environmental and residual variances for *i*th days in milk, respectively.

Heritability for 305-day production was calculated using *G* and *P* matrices and 305-day vector of different functions (q_{305d}). Vector of 305-day polynomials was obtained by summing up the coefficients from day 5 to day 305 (e.g. the additive genetic variance for 305-day production was obtained as: $\sigma_{a(305)}^2 = q_{305g}Gq_{305d}$); therefore, heritability for 305-day production was calculated as:

$$h_{(305)}^2 = \frac{\mathsf{s}_{a(305)}^2}{\mathsf{s}_{a(305)}^2 + \mathsf{s}_{pe(305)}^2 + 301\mathsf{s}_e^2}$$

where $\sigma_{a(305)}^2$ and $\sigma_{pe(305)}^2$ are additive genetic and permanent environmental variances for 305-day production. Additive genetic correlation for 305-day production between LP were calculated as:

$$r_{g(i,j)} = \frac{Cov_{g(i,j)}}{\sqrt{Var_{g(i,i)} \times Var_{g(j,j)}}}$$

were $Cov_{g(i,j)}$, is genetic covariance between *i* and *j* day, $Var_{g(i,j)}$ and $Var_{g(j,j)}$ are additive genetic variance i and j day, respectively.

Goodness of fit for the models was examined using likelihood based criteria as -2Logl, AIC, BIC and RV. AIC and BIC criteria are: AIC = $-2Logl + 2 \times k$ and BIC = $-2Logl + k \times log$ (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 matrices 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 (Misztal et al., 2002) program.

Results

Figure 1 shows changes of the milk yield, fat and protein contents along lactation month and indicates that the amount of fat and protein contents decreased when the milk yield increased.

The values of comparison criteria (-2Logl, AIC, BIC, RV) for the different functions of milk yield, fat and protein contents traits were given in Tables 2, 3 and 4, respectively. Selection of a better function depends partly on the criteria that were used. For milk yield and fat content the RRM with LP (2,5) had the lowest –2Logl, AIC, BIC and RV values (LP (2,5) is 2 and 5 order for additive genetic and permanent environmental effects respectively). Therefore, among 18 models, for milk yield and fat content traits the RRM with LP (2,5) was selected as the best model. For the protein content the LP (2,5) had the lowest –2Logl, AIC, BIC values. Furthermore, for protein content LP (3,5) and (5,5) had the lowest RV value. The ARR model had highest -2Logl, AIC and BIC values in comparison to the other models and for three traits. In milk yield trait, this model had lowest RV compared to WRR and LP (2,2), (2,3), (2,4), (3,2), (3,3), (3,4), (4,2), (4,3), (4,4), (5,2). In milk yield and fat content traits, WRR function compared to LP (2,4), (2,5), (3,5) had the highest values criteria. Moreover, considering milk yield, it has been found that the WRR alone had the lowest RV compared to LP (2,2), (2,3), (3,2) and (3,3), and in fat content had the lowest RV compared to LP (2,2), (2,3), (3,2), (3,3) and (4,2). The results indicated that the performance of WRR was worse than LP (2,4), (2,5). However, this model had the lowest RV value compared to ARR and LP (2,2), (2,3), (3,2), (3,3) and (4,2). For all traits the highest RV value was for LP (2,2) and this model was a worse model.



Figure 1. Average of milk yield, fat content (×10) and protein content (×10) along months

Model	Number of Parameters	-2Logl	AIC	BIC	RV
WRR	13	4448693	4448719	4448769	13.97
ARR	31	4667863	4667925	4668043	13.09
LP (2,2)	7	4569470	4569484	4569511	17.03
LP (2,3)	10	4402122	4402142	4402180	14.49
LP (2,4)	14	4380423	4380451	4380505	13.10
LP (2,5)	19	4370066	4370104	4370176	12.29
LP (3,2)	10	4569492	4569512	4569550	14.57
LP (3,3)	13	4559780	4559806	4559856	14.49
LP (3,4)	17	4454900	4454934	4454999	13.22
LP (3,5)	22	4440350	4440394	4440478	12.45
LP (4,2)	14	4571515	4571543	4571596	13.41
LP (4,3)	17	4570368	4570402	4570468	13.33
LP (4,4)	21	4554973	4555015	4555095	13.22
LP (4,5)	26	4483012	4483064	4483164	12.44
LP (5,2)	19	4577063	4577101	4577174	13.24
LP (5,3)	22	4571497	4571541	4571625	12.70
LP (5,4)	26	4564993	4565045	4565144	12.45
LP (5,5)	31	4547413	4547475	4547593	12.44

Table 2. Criteria used for comparison of the models and their levels for the milk yield

WRR (Wilmink), ARR (Ali-Schaeffer), LP (i,j) is i and j order for additive genetic and permanent environmental effects, respectively. For the series of LP models with different orders of fit for additive genetic and permanent environmental effects, the -2Logl of successively nested models were compared using an LRT (P = 0.05). In all cases, the differences observed in the values were large enough to state that a significant improvement was achieved when the order of fit was increased.

Model	Number of parameters	-2Logl	AIC	BIC	RV
WRR	13	1722544	1722570	1722619	0.413
ARR	31	1941215	1941277	1941395	0.407
L (2,2)	7	1793668	1799682	1793708	0.445
L (2,3)	10	1695316	1695336	1695374	0.425
L (2,4)	14	1629550	1629578	1629631	0.409
L (2,5)	19	1626640	1626678	1626750	0.401
L (3,2)	10	1807555	1807597	1807613	0.426
L (3,3)	13	1786486	1786512	1786561	0.425
L (3,4)	17	1728020	1728054	1728118	0.411
L (3,5)	22	1704576	1704532	1704703	0.403
L (4,2)	14	1838209	1838237	1838290	0.415
L (4,3)	17	1828035	1828069	1828133	0.413
L (4,4)	21	1745976	1746018	1746097	0.411
L (4,5)	26	1734037	1734089	1734187	0.403
L (5,2)	19	1846424	1846462	1846534	0.411
L (5,3)	22	1815512	1815556	1815639	0.408
L (5,4)	26	1795545	1795597	1795695	0.408
L (5,5)	31	1723612	1723674	1723792	0.403

Table 3. Criteria used for comparison of the models and their levels for the fat content

Table 4. Criteria used for comparison of the models and their levels for the protein content

Model	Number of parameters	-2Logl	AIC	BIC	RV
WRR	13	459600	459626	459674	0.0611
ARR	31	650230	650292	650407	0.0630
L (2,2)	7	494606	494592	494646	0.0680
L (2,3)	10	394766	394786	394823	0.0640
L (2,4)	14	386092	386120	386172	0.0601
L (2,5)	19	379647	379685	379756	0.0590
L (3,2)	10	495002	495022	495059	0.0650
L (3,3)	13	484158	484184	484232	0.0640
L (3,4)	17	471603	471637	471700	0.0601
L (3,5)	22	471040	471084	471166	0.0580
L (4,2)	14	515531	515503	515611	0.0620
L (4,3)	17	504941	504975	505038	0.0611
L (4,4)	21	482854	482896	482974	0.0611
L (4,5)	26	480841	480893	480990	0.0592
L (5,2)	19	528035	528073	528144	0.0611
L (5,3)	22	526977	526933	527103	0.0591
L (5,4)	26	509920	509972	510069	0.0592
L (5,5)	31	480593	480655	480770	0.0580

The additive genetic variance as a function of DIM for milk yield, fat and protein contents is shown in Figures 2, 3 and 4, respectively. Additive genetic variance was higher at the beginning of lactation and then decreased until about 25 days of lactation. The permanent environment variance as a function of DIM for milk yield, fat and protein contents is shown in Figures 5, 6 and 7, respectively.



Figure 2. Additive genetic variance (AG) obtained Figure 3. Additive genetic variance (AG) obtained by RRM with LP, WRR and ARR, for milk yield



Figure 4. Additive genetic variance (AG) obtained by RRM with LP, WRR and ARR, for protein content



Figure 6. Permanent environmental variance (PE) obtained by RRM with LP, WRR and ARR, for fat content



by RRM with LP, WRR and ARR for fat content



Figure 5. Permanent environmental variance (PE) obtained by RRM with LP, WRR and ARR for milk vield



Figure 7. Permanent environmental variance (PE) obtained by RRM with LP, WRR and ARR, for protein content

Heritabilities of milk yield, as a function of DIM are shown in Figure 8. The heritability of milk yield by DIM was estimated to be between 0.09 to 0.21, 0.08 to 0.20 and 0.11 to 0.23 by LP, WRR and ARR functions, respectively. The heritability of fat content for different DIM was estimated to be between 0.04 to 0.13, 0.08 to 0.11 and 0.08 to 0.12 by LP, WRR and ARR functions, respectively (Figure 9). The changes in heritability estimates for TD fat content were high in the early lactation, followed by a sudden drop in 40th DIM and the trend increased at the end of lactation. These trends are similar to those observed by El Faro et al. (2009) and Swalve (1995). The heritability of protein content by DIM was estimated to range from 0.07, 0.10 and 0.09 in the early lactation to 0.24, 0.25 and 0.21 in the late lactation by LP, WRR and ARR functions, respectively (Figure 10). Estimates of additive genetic correlation between TD milk yield, TD fat content and TD protein content at different stages of lactation estimated in RRM are shown in Figures 11. As can be seen, 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.



Figure 8. Estimated heritability (h²) as a function of DIM by RRM with LP, WRR and ARR, for milk yield



Figure 9. Estimated heritability (h²) as a function of DIM by RRM with LP, WRR, ARR for fat content



Figure 10. Estimated heritability (h²) as a function of DIM by RRM with LP, WRR and ARR, for protein content







Figure 11. Additive genetic correlation (rg) for milk yield, fat and protein contents as a function of DIM

The additive genetic variance and permanent environmental variance and residual variance for 305-day milk yield, fat and protein contents are shown in Table 5.

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Trait	Model	AG	PE	RV	
	L (2,2)	528203	1232173	5126.03	
	L (3,3)	507504	1274253	4361.49	
Milk yield	L (4,4)	513036	1275342	3979.22	
	L (5,5)	512716	1282048	3744.44	
	ARR	508402	12820916	3940.09	
	WRR	517181	1272244	4204.97	
	L (2,2)	3089	2985	133.51	
	L (3,3)	3063	2997	127.93	
Fat content	L (4,4)	3072	3044	123.71	
	L (5,5)	3059	2988	121.30	
	ARR	3022	2948	122.51	
	WRR	3084	2961	124.31	
	L (2,2)	836	775	20.47	
	L (3,3)	848	748	19.26	
Protein content	L (4,4)	849	757	18.39	
	L (5,5)	858	774	17.46	
	ARR	547	719	18.96	
	WRR	860	792	18.38	

 Table 5. Additive genetic variance (AG), permanent environmental variance (PE) and residual variance (RV) of 305-day milk yield, fat and protein contents

Phenotypic variances of milk yield, fat and protein contents by LP, WRR and ARR are shown in Figure 12, 13, 14, respectively.



Figure 12. Phenotypic variance of milk yield obtained by LP, WRR and ARR in RRM



Figure 13. Phenotypic variance of protein content obtained by LP, WRR and ARR in RRM



Figure 14. Phenotypic variance of fat content obtained by LP, WRR and ARR in RRM

Discussion

In this study, LP with different orders, WRR and ARR functions were compared for better fitting performance of TD milk productions. The results showed that the criteria of values decreased when the order of fit for the permanent environmental effects increased in the LP models, agreeing with the results presented by Brotherstone et al. (2000), Lopez-Romero and Carabano (2003), Bignardi et al. (2009), El Faro et al. (2008), and Albuquerque and Meyer (2005). Comparison of models based on this criterion showed that a higher order of fit for the permanent environmental effect reduced the RV across DIM. Small differences were observed for estimations of additive genetic variance and permanent environmental variance between different LP of the lactation period. The results demonstrated in this and other studies that use RRM based on parametric functions describing lactation curves (such as WRR and ARR) could result in the overestimation of additive genetic variance. Meanwhile, it was found that when using ARR and WRR in RRM, some part of the permanent environmental variance resulted in the expression of additive genetic variance components. Therefore, the additive genetic variance, especially in early lactation was higher in comparison to the values obtained through LP function. This causes overestimation of heritability, especially in early lactation and low estimation of the genetic correlations of daily production. These results are similar to those estimated in Spanish Holsteins (Lopez-Romero and Carabano, 2003) and Holstein-Friesians (Rekaya et al., 1999).

There was a slight increase following the loss of additive genetic variance in early lactation around 25 days of lactation to later days of lactation and, observed at the end of lactation, maximum additive genetic variance. These results are in agreement with those obtained by El Faro et al. (2008) and Bignardi et al. (2009). On the other hand, the maximum permanent environmental variance was observed at the beginning of lactation. Strabel et al. (2005), Costa et al. (2008) and Biassus et al. (2011) reported similar results for permanent environmental variance. After this period, the permanent environmental variance trend showed a slight decrease followed by a small increase at the end of lactation. These results are consistent with Shadparvar and Yazdanshenas (2005), De Roos et al. (2004), and Biassus et al. (2011). In this study, minimum heritability of milk yield in early lactation by different functions was observed, agreeing with the results presented by Biassus et al. (2011). In general, for all models, a sudden increase in heritability of milk in the early lactation period was observed. This increase in heritability estimation is associated not only with the increases on the values of additive genetic variance components but also with the small reductions in values of permanent environmental components between models. Because heritability is low in early lactation, permanent environmental variance obtained at this stage of lactation is high, given that additive genetic variance was higher in late lactation. These trends are similar to those observed by Jensen (2001), Shadparvar and Yazdanshenas (2005), and Bohlouli and Alijani (2012).

Heritability estimates of fat content were lower compared to milk yield and protein content. Accordingly, phenotypic variance in early lactation was observed to be high, which means that many changes in fat content of animals occur at this stage of lactation and because a proportion of the variance is due to permanent environmental variance, heritability of fat content is lowest in the first months of lactation; this result was observed by Abdullahpour et al. (2010). Heritability of protein content was high in the late stage of lactation. According to the results, the heritabilities of 305day milk yield, fat and protein contents were higher in contrast to their TD heritabilities. This result is in agreement with most studies (Kettunen et al., 1998; Shadparvar and Yazdanshenas, 2005). Using the 305-day model, heritability estimates were 0.28 for milk yield, 0.46 for fat content and 0.48 for protein content (Table 5). Heritability estimates for considered traits during the lactation period were similar between models. The 305-day heritability estimate was higher for fat and protein content than for milk yield. It was very close to most of the estimates reported in other works (Byeong-Woo et al., 2009; Tsvetanova, 2004).

The additive genetic correlation between TD yields was higher when periods were closer to each other. These results agree with results of Biassus et al. (2011), Cobuci et al. (2004), Jakobsen et al. (2002), and Costa et al. (2008). During lactation, the additive genetic correlation of milk yield showed less variation compared to the fat and protein contents. The phenotypic variance of the considered traits during lactation was not constant and it was higher at the beginning and the end of lactation. These trends were similar to results of Costa et al. (2008), Cobuci et al. (2011) and Biassus et al. (2011).

In conclusion, among the different models in this research, it seems that the lowest order LP for the additive genetic component compared to the permanent environmental effect might be sufficient to capture most of the genetic and permanent environmental variability observed in the shape of daily milk production. Thus, according to comparison criterias, among 18 models, the RRM with LP (2,5) were chosen as the better model and can be recommended for estimating genetic parameters of milk production traits of Iranian Holstein dairy cattle.

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