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ANIMAL BREEDING AND REPRODUCTION

Appropriate mathematical models to describe the lactation curves of milk production traits of Iranian Holstein dairy cattle

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ABSTRACT. The objective of this study was to compare the goodness of fit of lactation curve models; Wood, Wilmink, Linear Splines (SPL), Cubic Splines (SPC), Quadratic Splines (SPQ), Cobby and Le Du, Ali Schaeffer and Legendre Polynomial (LEG), in random regression model (RRM) for milk production traits of Iranian Holstein dairy cattle. For this purpose the records obtained from Test-day (TD) regarding milk (928513), fat (788577) and protein (653317) yields related to their first parity were used. These data collected from the years of 2003 to 2011 by the Karaj breeding center of Iran. The genetic parameters were estimated using REML method using WOMBAT software. Based on obtained results, RRM with SPL6 (6,6), SPC6 (6,6) and LEG (3,5) for milk yield, SPL6 (6,6), SPQ6 (6,6), LEG (3,5) for fat yield and SPL5 (5,5), SPQ4 (4,4) and LEG (3,4) for protein yield, were selected as better model to describe the lactation curves. The estimated heritabilities by best models were lower in the beginning lactation than other during lactation. The genetic trend of milk yields was showed an increasing during the 10 past years, which indicated Iranian Holstein dairy cattle population genetically was improved for milk yields.

Keywords: dairy cow; model fitting; lactation curves; genetic trend; milk production.

Modelos Matemáticos apropriados para descrever as curvas de lactação dos traços de produção de leite do gado leiteiro Holstein Iraniano

RESUMO. O objetivo deste estudo foi comparar a qualidade de ajustes dos modelos da curva de lactação, Wood Wilmink, Spline Linear (SPL), Spline Cúbico (SPC), Spline Quadrático (SPQ), Cobby e Le Du, Ali Schaeffer e os Polinômios de Legendre (LEG), em um modelo de regressão aleatória (RRM) para as características da produção de leite do gado Holstein iraniano. Para este propósito os registros obtidos no teste, foram referentes ao leite (928513), gordura (788577) e proteína (653317) e os rendimentos relacionados as suas primeiras paridades foram usadas. Estas informações foram coletadas durante 2003 até 2011 por Kraj em um centro de criação no Iran. Os parâmetros genéticos foram estimulados usando o método REML WOMBAT. Baseado nos resultados obtidos, RRM com SPL6 (6.6), SPC6 (6,6) e LEG (3,5) por produção de leite, foram selecionados os melhores modelos para descrever as curvas de lactação. A hereditariedade estimada por esses melhores modelos foi menor no início da lactação do que durante outra lactação. A tendência genética da produção de leite mostrou um aumento ao longo de 10 anos, na qual indicou o melhoramento genético do gado Holstein Iraniano no que diz respeito à produção de leite.

Palavras-chave: gado leiteiro; modelo de regressão aleatório; traços genéticos.

Introduction

One of the main incomes is milk production for dairy cattle farms and therefore milk yield records are great deal of importance for the dairy herds (Cankaya, Unalan, & Soydan, 2011). Estimation of annual total milk production and operating to breeding plans and management system according with that estimated value in dairy herds depend on both efficiency of milk recording system and accuracy of milk yield calculating methods in the herds (Cankaya et al., 2011). 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. Among the models that consider TD production, RRM has been widely observed to increase the accuracy of breeding value predictions (Strabel, Szyda, Ptak, & Jamrozik, 2005). 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. 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 (Jakobsen et al., 2002; Jamrozik, Schaeffer, & Dekkers, 1997; Schaeffer, 2004; Strabel et al., 2005). Lactation curves in dairy cattle reach to the peak yield after calving and then decrease steadily after peak yield to the drying off (Swalve, 2000). Some characters such as maximum daily milk production, lactating day of maximum milk production and lactation persistency can be obtained directly from the lactation curve models. The shape of the lactation curve provides valuable information which is essential to evaluate the biological and economic efficiency of the animal or herd and is useful for genetic evaluation, health monitoring, feed management decisions and planning purposes (Fadlelmoula, Yousif, & Abu Nikhaila, 2007; Kocak & Ekiz, 2008). Also, knowing when to expect an animal to reach peak yield, would affect the feeding strategy followed, allowing economic management of feed to extent that would satisfy the animal's requirement during various stages of lactation, reduce cost, and possibly maintaining peak yield for as long as possible (Grzesiak, Wojcik, & Binerowska, 2003). A lot of mathematical models as Wood, Wilmink (WIL), Ali and Schaeffer (ASC), Legendre Polynomial (LEG) and Linear Splines (SPL) were used to describe the lactation curve of cows (Bohmanova, Miglior, Jamrozik, Misztal, & Sullivan, 2008; Mohammadi & Alijani, 2014; Soysal, Sirlar, & Gurcan, 2004; Takma & Akbaş, 2007; Val-Arreola, Kebreab, Dijkstra, & France, 2004). 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 estimates genetic parameters leads to more accurate estimates (Misztal, Strabel, Jamrozik, & Mäntysaari, 2000; Mohammadi & Alijani, 2014). The choice of the function influences number of parameters and order of the estimated (co) variance components matrix (Takma & Akbas, 2009).

The objective of the current paper, therefore, was to compare the performance of Wood, WIL, Spline Linear (SPL), Spline Cubic (SPC) and Spline Quadratic (SPQ) fitted by was compared with 4, 5, or 6 knots, ASC, Cobby and Le Du (CLD) and LEG (with orders 3 to 5 for the additive genetic and permanent environment effects) functions at RRM to by fitting these equations to monthly milk production records for an entire lactation from a commercial herd of Iranian Holstein cows using by AIC, -2 logL, BIC and Likelihood ratio test (LRT).

Material and methods

The TD milk yield records obtained from a national breeding center of Iran, belonged to the first lactation dairy cows from 2003 to 2011. The age of cows in the first lactation was from 21 to 46 months. 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 (< 2 and > 75 kg), fat percentage (< 1 and > 9 %), and protein percentage (< 1 and > 8 %) were excluded (Then converted to content). Cows had also, only cows with more than 5 TD records, and herds with more than 5 cows per herd in year of calving were kept. The sires having progeny fewer than 5 were eliminated. Finally, edited data included 928513, 788577 and 653317 TD records for milk yield, fat yields and protein content respectively. Four calving seasons 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 to 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:

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

where y_{tijkm} is the tth record (milk yield, fat and protein contents) of mth cow in ith herd-test-date (HTD) effect, jth calving year (YC) and kth milking frequency (MT) (2 or 3 times per day); AS_{mnl} is the nth fixed regression coefficient of lth class of cows calving age-season; a_{mn} and pe_{mn} are regression coefficients nth for additive genetic and permanent environment effects on mth cow respectively; p is the number of covariates; r is orders number of different functions; x_n is nth lactation curve models (Wood, WIL, SPL, SPC, SPQ, ASC, CLD and LEG) for tth day; e_{tijklm} random residual effect associated with y_{tijklm}. Number of records of milk yield, fat and protein contents and other descriptive statistics are summarized in Table 1.

Table 1. Descriptive statistics of data sets.

	Milk (kg)	Fat (g)	Protein (g)
Number of TD records	928513	788577	653317
Means ±SD (kg)	30.15±7.48	0.999±0.326	0.941±0.231
Number of animals with record	108873	96511	79501
Number of total animals	225832	206371	171360
Number of dam with progeny	127692	128663	111715
Number of sire with progeny	3795	3805	3474
Number of HTD	17820	16499	14127
Number of herd- calving year	1483	1400	1227

Lactation curve models

Mathematical functions were applied to fit the milk production data of individual lactations:

1: The Wood Model: The gamma function described by Wood (1967) is one of the most popular models used to describe the lactation curve:

$$Y_t = at^b e^{-ct}$$

for all models, Y_t is the milk yield in lactation day t. Parameter a is a scaling factor to represent yield at the beginning of lactation, and parameters b and c are factors associated with the inclining and declining slopes of the lactation curve, respectively.

2: The WIL model is the following:

$$Y_t = a + be^{-kt} + c_t$$

according to Wilmink (1987), the parameter*s a, b, and c are* associated with the level of production, the increase of production before the peak, and with the subsequent decrease, respectively. Parameter k is related to the time of peak lactation and usually assumes a fixed value, derived from a preliminary analysis made on average production.

3: ASC Model can be written as follows:

$$Y_t = a + b_{\gamma t} + c_{\gamma t}^2 + dW_t + eW_t^2$$

where γt = (t_{mn}/305), where t_{mn} is the n^th^ DIM, W_t = ln (305/t), a is a parameter associated with the peak yield, d and e are parameters associated with increasing slope, and b and c are associated with decreasing slope.

4: Splines Model:

$$Y_t = a_i + b_i(t - t_i) + C_i(t - t_i)^2 + d_i(t - t_i)^3,$$
$$\text{for } t_i \leq t \leq t_{i+1}$$

5: CLD Model: The model proposed by Cobby and Le Du (1978) has the particularity that milk yield after peak is modeled as a linear decline function (Val-Arreola et al., 2004). The CLD equation is:

$$Y_t = a - b_t - a\, e^{-ct}$$

6: The LEG model: The Legendre polynomials are polynomial functions of n degree and domain n + 1 and the equation describing a single observation can be written:

$$Yt = \sum_{i=0}^{n} \alpha i\, \Phi i\, (d_t^*)$$

where d_t^* is standardized unit of time ranging from -1 to +1, $d_{t=}^*$ -1 +2 $(\frac{d_t - d_{min}}{d_{max} - d_{min}})$;
where d_{min} and d_{max} are minimum and maximum DIM, and d_t, t^th^ DIM. For the t^th^ standardized DIM, the n^th^ polynomial is given as;

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

where d^*_i, is the i^th^ DIM; and i, is order LEG function; m, index number needed to determine the k^th^ polynomial.

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 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:

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

G is the genetic covariance matrix of the random regression coefficients, ⊗ 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.

Goodness of fit for the models was examined using likelihood based criteria as -2 LogL, AIC, BIC and LRT. AIC and BIC criteria are:

$$AIC = -2\,\mathrm{LogL} + 2 \text{ x } k$$

$$BIC = -2\,\mathrm{LogL} + k \text{ x } \log(N - r(x))$$

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 -2 LogL, AIC, BIC and LRT values is chosen as the better approximating model. For estimated heritability for i^th^ days in milk was calculated as:

$$h_i^2 = \frac{\sigma^2_{a(i)}}{\sigma^2_{a(i)} + \sigma^2_{pe(i)} + \sigma^2_e}$$

where $\sigma^2_{a(i)} = q\,G\,q'$, $\sigma^2_{pe(i)} = q\,P\,q'$, where q is the vector of the associated polynomial functions; G and P are the (co) variance matrices for additive genetic and permanent environmental random regression coefficients, respectively; and $\sigma^2_{a(i)}$, $\sigma^2_{pe(i)}$ and σ^2_e are additive genetic, permanent environmental and residual variances for ith days in milk, respectively. Genetic correlations for 305-days production between functions were calculated as:

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

where $\mathrm{Cov}_{g(i,j)}$, is genetic covariance between i and j day, $\mathrm{Var}_{g(i,i)}$ and $\mathrm{Var}_{g(j,j)}$ are additive genetic variance i and j day, respectively. Estimation of genetic parameters with REML methodology was done using WOMBAT software (Meyer, 2007).

Results

Comparison of the models

For overall lactation numbers, values of comparison criteria (-2 LogL, AIC, BIC, LRT), of the models were given using eight different lactation models of milk, fat and protein yields traits were given in Tables 2, 3 and 4 respectively. Selection of a best function depends partly on the criteria that were used. For milk yield the RRM with SPL6 (6,6), SPQ6 (6,6) and LEG (3,5) had the lowest -2 LogL, AIC, BIC and LRT values.

Table 2. Criteria used for comparison of the mathematical models for the milk yield.

Model	Parameters	AIC	BIC	-2 LogL	LRT
Wood	-	4767879	4767783	4767865	-
WIL	13	4878719	4878769	4878693	-
SPL4 (4,4)	27	4439254	4439645	4438824	-
SPL5 (5,5)	37	4438634	4437657	4437835	989*
SPL6 (6,6)	49	4433353	4433575	4437485	350*
SPC4 (4,4)	27	4441678	4442664	4443876	-
SPC5 (5,5)	37	4446356	4446676	4443352	524*
SPC6 (6,6)	49	4434542	4434546	4443253	99*
SPQ4 (4,4)	27	4447845	4447835	4448774	-
SPQ5 (5,5)	37	4447893	4447665	4448438	336*
SPQ6 (6,6)	49	4448783	4445875	4447574	1200*
ASC	31	5667925	5668043	5667863	-
CLD	-	5078564	5077685	5078654	-
LEG (3,3)	13	4459806	4459856	4459780	-
LEG (3,4)	17	4454934	4454999	4458900	880*
LEG (4,4)	21	4455015	4455095	4457973	927*
LEG (3,5)	22	4440394	4440478	4457350	623*

WIL (Wilmink), SPLi (i,j) (Linear Spline knot (order for additive genetic and permanent environmental effects respectively)), SPC(Cubic Spline), SPQ (Quadratic Spline), ASC (Ali-Schaeffer), CLD (Cobby and Le Du) LEG (i,j) is i and j order for additive genetic and permanent environmental effects respectively. Significantly (* $p < 0.05$).

For the fat yield the model SPL6 (6,6), SPC6 (6,6) and LEG (3,5) had the lowest values of comparison criteria. Furthermore, accounted for the protein yield lowest values comparison criteria by the model SPL5 (5,5), SPQ4 (4,4) and LEG (3,4). Moreover, considering it has been found the RRM with ASC, CLD functions have the highest values of comparison criteria than other models by all traits in this study. The results indicated that the performance of ASC, CLD was worse than other functions. For the series of models with different orders of fit for additive genetic and permanent environmental effects, the -2 LogL of successively nested models were compared using a 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.

Table 3. Criteria used for comparison of the mathematical models for the fat yield.

Model	Parameters	AIC	BIC	-2 LogL	LRT
Wood	-	4872623	4873458	4871675	-
WIL	13	4996263	4996745	4996002	-
SPL4 (4,4)	27	4544364	4547645	4545647	-
SPL5 (5,5)	37	4546352	4547842	4545484	163*
SPL6 (6,6)	49	4543718	4543583	4545382	102*
SPC4 (4,4)	27	4566738	4567493	4566747	-
SPC5 (5,5)	37	4565793	4565491	4565785	962*
SPC6 (6,6)	49	4564430	4564842	4565432	353*
SPQ4 (4,4)	27	4575932	4578593	4579493	-
SPQ5 (5,5)	37	4578493	4575279	4579074	419*
SPQ6 (6,6)	49	4563042	4563038	4569029	10045*
ASC	31	6502923	6504076	6502302	-
CLD	-	6276281	6274893	6277363	-
LEG (3,3)	13	4751845	4762325	4751582	-
LEG (3,4)	17	4716374	4717004	4746034	5548*
LEG (4,4)	21	4728962	4729746	4728547	17487*
LEG (3,5)	22	4544043	4544617	4544405	184142*

Table 4. Criteria used for comparison of the mathematical models for the protein yield.

Model	Parameters	AIC	BIC	-2 LogL	LRT
Wood	-	5394832	5393922	5394836	-
WIL	13	5139023	5139296	5127492	-
SPL4 (4,4)	27	4638922	4638365	4681723	-
SPL5 (5,5)	37	4636382	4637392	4668523	43200*
SPL6 (6,6)	49	4656352	4625384	4653532	14991*
SPC4 (4,4)	27	4713982	4718283	4728656	-
SPC5 (5,5)	37	4720912	4722942	4727532	1124*
SPC6 (6,6)	49	4665259	4663902	4726372	1160*
SPQ4 (4,4)	27	4658302	4654653	4658364	-
SPQ5 (5,5)	37	4646352	4644994	4655644	2720*
SPQ6 (6,6)	49	4684803	4688476	4654893	751*
ASC	31	6394737	6376362	6394736	-
CLD	-	6123734	6144922	6183726	-
LEG (3,3)	13	4586738	4862832	4761859	-
LEG (3,4)	17	4618393	4613874	4719387	42472*
LEG (4,4)	21	4897213	4893487	4717772	1615*
LEG (3,5)	22	4812165	4812976	4716035	1737*

Estimates of genetic parameters

The additive genetic variance as a function of DIM for milk production traits presented in Figure 1.

The additive genetic variance for milk yield was higher at the beginning of lactation and after this period, the trend showed a slight decrease following by a small increase at the end of lactation. Also, the additive genetic variance of the fat and protein yields during lactation was not constant and it was higher at the beginning and the end of lactation. The permanent environmental variance ranged from 49.57 (beginning lactation) to 23.69 (end lactation), 55.88 to 25.38 and 60.16 to 26.17 for milk yield by best models. Also, for fat and protein yields was higher in beginning lactation (Table 5).

Heritabilities of milk, fat and protein yields as a function of DIM are shown in Figure 1. The heritability of milk yield by DIM was estimated to be between 0.10 to 0.19, 0.11 to 0.22 and 0.08 to 0.21 by SPL6, SPLC6 and LEG (3,5) functions, respectively. Heritability of milk was high in the middle and end lactation by all models. The heritability of fat yield for different DIM was estimated to be between 0.05 to 0.12, 0.07 to 0.20 and 0.08 to 0.121 for SPL6, SPQ6 and LEG (3,5) functions, respectively. The changes in heritability estimates for TD fat yield observed high in the end lactation. The heritability of protein yield by DIM was estimated to be between 0.09, 0.07 and 0.11 in the beginning lactation and 0.23, 0.24 and 0.22 in the end lactation by SPL5, SPQ5 and LEG (3,4) functions, respectively. Estimates of genetic correlation between TD milk, fat and protein yields at different stages of lactation estimated in RRM are shown in Figure 2.

Table 5. Estimated permanent environmental variance obtained as a function of DIM.

	DIM	LEG (3,5)	SPL6	SPC6
Milk yield	5	49.57	55.88	60.16
	65	20.58	18.84	20.68
	125	16.73	17.39	20.51
	185	17.24	17.57	18.57
	245	19.91	19.54	20.78
	305	23.69	25.38	26.17
		LEG (3,5)	SPL6	SPQ6
Fat yield	5	5.56	6.142	6.04
	65	2.01	1.69	2.05
	125	1.57	1.61	1.63
	185	1.59	1.51	1.65
	245	1.76	1.69	1.71
	305	2.32	2.28	2.32
		LEG (3,4)	SPL5	SPQ5
Protein yield	5	3.52	4.43	3.64
	65	1.16	1.27	1.16
	125	1.36	1.44	1.54
	185	1.53	1.56	1.59
	245	1.85	1.76	2.01
	305	2.79	2.63	2.84

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.

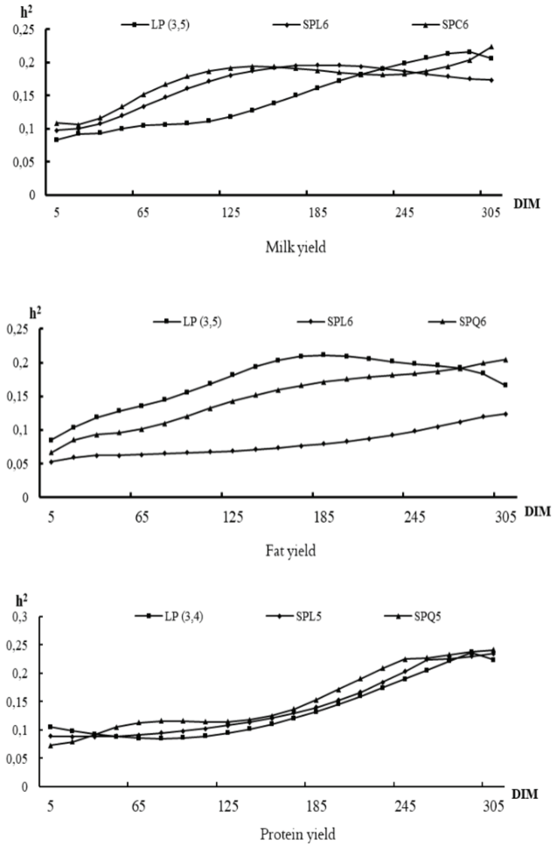


Figure 1. Estimated heritability (h^2) as a function of DIM.

The phenotypic correlation between TD records for milk production traits are shown in Table 6.

The phenotypic correlation coefficients ranged from 0.42 to 0.65 and 0.18 to 0.22 by milk and fat yields, respectively. The phenotypic correlation fat yield was less than milk yield.

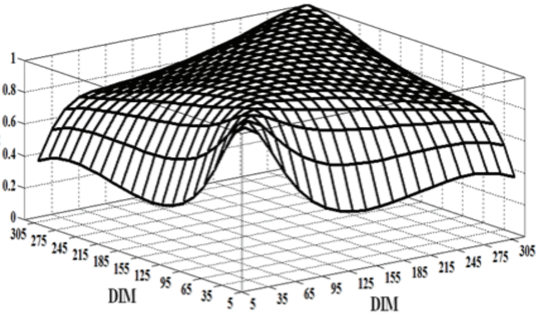
Genetic Trend

Regression coefficients for estimated animal breeding value on animal birth year as the indicator of genetic trend were estimated for milk production traits (Figure 3). The results showed positive genetic trend by milk, fat and protein yields during previous years.

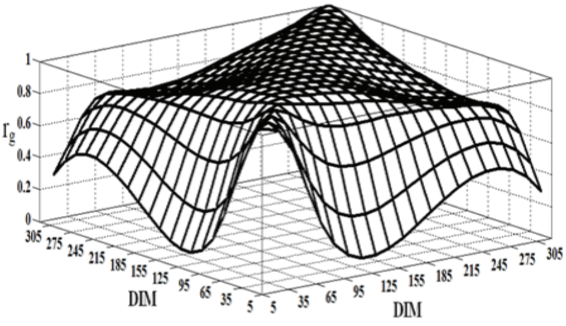
Discussion

In this research, polynomial functions were compared for better fitting performance of TD milk production traits. The comparison results of the models are in agreement with those reported by El

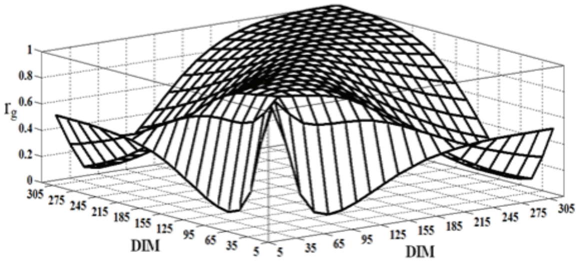
Faro, Cardoso, and Albuquerque (2008), Boujenane (2013) and Mohammadi and Alijani (2014). Small differences were observed for estimations of additive genetic variance and permanent environmental variance between different models of the lactation period. The trends additive genetic and permanent environmental variances are in agreement with those obtained by El Faro et al. (2008), Mohammadi and Alijani (2014) and Laureano et al. (2014).



Milk yield



Fat yield



Protein yield

Figure 2. Genetic correlations milk production traits as a function of DIM.

In this study, minimum heritability of milk, fat and protein yields in early lactation by different functions was observed, agreeing with the results presented by Biassus et al. (2011), Mohammadi, Alijani, and Daghighkia (2014) and Bohlouli and Alijani (2012). In general, for all models, sudden increase in heritability of milk during the early lactation period was observed. This increase in heritability estimates 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, is obtained permanent environmental variance at this stage of lactation high and given that additive genetic variance was higher in late lactation. The results were in accordance with other reports Biassus et al. (2011), Mohammadi and Alijani (2014) and Laureano et al. (2014).

Table 6. Phenotypic correlation between TD records of milk yield (above diagonal) and fat yield (below diagonal).

TD	1	2	3	4	5	6	7	8	9	10
1	1	0.63	0.63	0.60	0.53	0.52	0.50	0.46	0.47	0.42
2	0.20	1	0.65	0.60	0.54	0.52	0.49	0.48	0.48	0.43
3	0.21	0.22	1	0.61	0.54	0.52	0.49	0.47	0.46	0.45
4	0.20	0.21	0.21	1	0.62	0.51	0.49	0.47	0.47	0.43
5	0.19	0.21	0.21	0.24	1	0.63	0.52	0.50	0.51	0.50
6	0.20	0.20	0.20	0.19	0.25	1	0.63	0.52	0.49	0.47
7	0.19	0.19	0.19	0.19	0.21	0.21	1	0.67	0.55	0.53
8	0.18	0.18	0.18	0.18	0.18	0.19	0.24	1	0.59	0.57
9	0.18	0.19	0.19	0.17	0.19	0.18	0.19	0.25	1	0.60
10	0.17	0.18	0.18	0.18	0.19	0.18	0.20	0.19	0.27	1

The analysis showed less variation in additive genetic correlation of milk yield than fat and protein yields during lactation. For all of the tested models, the highest genetic correlations were observed between adjacent TD, with the magnitude of the correlations decreasing with increasing distance between TD for all traits. These results are in agreement with those reported by Bohlouli and Alijani (2012) and Mohammadi et al. (2014).

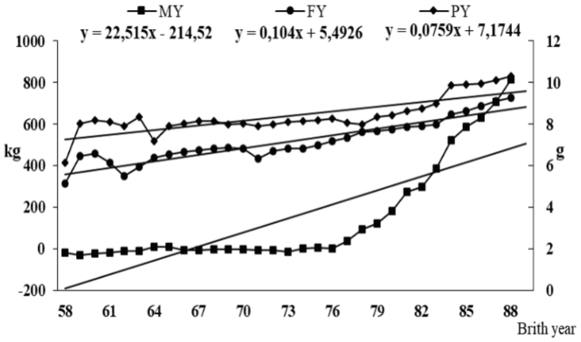


Figure 3. Genetic trend milk (MY), protein (PY) and fat (FY) yields.

Accordance the observed results, phenotypic correlation between TD records milk and fat yields with the increase of distance TD, is decreased. Therefore, it shows that environmental effects involved in production, are difference in herds and cows. The results of this study agree with Naderi (2016), Jensen (2001), Shadparvar and Yazdanshenas (2005) and (Mohammadi and Alijani (2014); Mohammadi et al. (2014)). The results indicated that selection for increase milk production traits at a certain point during lactation has a positive effect on any other point of the curve. These results agree with results of Cobuci, Costa, Braccini Neto, and Freitas (2011) and Laureano et al. (2014). Similar genetic trends were reported by Abdullahpour, Shahrbabak, Nejati-Javaremi, and Torshizi (2010) using the 305 day measures of the traits. They indicated that Iranian Holstein cattle population genetically improved for milk yield. The interest of farmers to use sperms from genetically superior bulls could be the main factor which caused these changes.

Conclusion

The empirical functions have been compared and all of them allowed a suitable description of the shape of the lactation curve of milk production traits of dairy cattle. Thus, the better understanding of the lactation curve of dairy cows will be used as a tool for better management and selection. Although the performance of all models was acceptable, but the RRM with SPL, SPC, SPQ and LEG were chosen as better model and can be recommended for estimate genetic parameters of Iranian Holstein dairy cattle.

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