Discovery, Vol. 53, No. 255, March 1, 2017

RESEARCH

ISSN
2278–5469
EISSN
2278–5450

Discovery

Use of Test Day Milk Yield by Random Regression Models for Milk Production Traits in Iranian Dairy Cows

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Publication History
Received: 5 January 2017
Accepted: 9 February 2017
Published: 1 March 2017

Citation
Saber Khodaie Ashan. Use of Test Day Milk Yield by Random Regression Models for Milk Production Traits in Iranian Dairy Cows. *Discovery*, 2017, 53(255), 191-204

General Note
Article is recommended to print as color digital version in recycled paper.

ABSTRACT

In this study 203498 test day milk records and 184429 test day fat records of first lactation Holsteins from Iran farms, calving between 2002 and 2009, were analyzed using random regression model. RR/CF models were studied in the respect of different orders of fit for fixed and random regression and also different ways of assuming residual variance in the analysis, including the assumption of constant (homogenous) residual variance and different assumptions about variable (heterogenous) residual variance during lactation. Heterogeneous residual variance considered during days in milk and evaluation of models was based on eigenvalues and associated eigenvectors and residual variance. The heritability estimates obtained by RRM1 (0.34 to 0.56) were higher than those obtained by RRM2 (0.15 to 0.31). Due to the high heritability estimates for milk yield throughout lactation and the negative genetic correlation between test-day yields during different lactation periods, the RRM1 model did not fit the data. Overall, genetic correlations between individual test days tended to decrease at the extremes of the lactation trajectory, showing values close to unity for adjacent test days. The inclusion of random regression coefficients to describe permanent environmental effects led to a more precise estimation of genetic and non-genetic effects that influence milk yield.

Key words: Estimation Breeding Value, Legendre Polynomial, Persistency, Random Regression.

1. INTRODUCTION

Nowadays, genetic evaluation of dairy cows using day milk yield test and random regression method has been officially adopted in several countries (Jensen, 2001). The use of test day records in random regression method has several benefits including flexibility to account for the environmental and genetic components of the shape of lactation curve (Costa *et al.* 2008), reducing generation interval and cost of recording by making fewer measurements, increasing the accuracy of genetic evaluation, direct correction for fixed effects (especially of fixed effects whose impact change along lactation trajectory) (Swalve, 2000) and allowing curve to be estimated for each lactation of every cow. Kirkpatric *et al.* (1994) demonstrated the use of Legendre polynomial (LE) in modeling the covariance structure of test day records for additive genetics and permanent environmental effects. The order of the Legendre polynomial in the random regression model is important in that estimates of genetic parameters can differ. Moreover, the order of Legendre polynomial does not need to be equal for additive genetics and permanent environmental effects (Liu *et al.* 2006). Based on the shape of the lactation curve after peak, it is possible to describe the potential of maintaining the level of milk production or persistency. Nowadays calculation of persistency is based on by-products of random regression test day model. Persistency of lactation is ability of animal to continue producing milk at a high level after the peak of lactation (Jamrozik and Schaeffer, 1997). In other words, high persistency is associated with a slow rate of decline in production and in this situation the lactation curve would be flatter. Cows with higher persistency use better and cheaper roughage around peak yield (Solkner and Fuchs, 1987), improvement of health (less metabolic stress) and fertility (Zimmermann and Sommer, 1973). It's better to calculate persistency in primiparous cows because first parity cows showed an initial and peak milk yield lower than second and third parity cows, however together with greater persistency (Togashi *et al.* 2008). There is no clear consensus on the best way of measuring persistency but generally it refers to the rate of decline in production after peak milk yield (Dzomba*et al.* 2010). Grossman *et al.* (1999) and Gengler (1996) classified persistency measures into three groups: 1) measures based on ratios of yield 2) measures based on variation of test day yields and 3) measures developed by mathematical lactation curve function. According to Jakobsen *et al.* (2002) a good persistence measure should have high heritability and it must be uncorrelated with 305 d yield because there is antagonist relationship between persistency and 305 d yield. Biassus *et al.* (2010) evaluated some measures of persistency using higher order of Legendre polynomials and reported that persistence measurement proposed by Jakobsen*et al.* (2002) it was based on partial estimation breeding value from 106 to 205 d subtracted by partial estimation breeding value from 6 to 105 d] is useful for further genetic evaluation for milk yield persistency. The lower the genetic correlation between persistence measures and EBV_{305} d milk yield, the better the evaluation of persistency. This means that animals with higher estimation breeding value (EBV) for persistency are not necessarily the same as those with larger EBV for this trait (Cobuci*et al.*2007). Togashi and Lin (2006) showed that the first three eigenvector of additive covariance matrix are enough to maximize milk yield and genetic response for persistency together. The object of this study was the evaluation of different unequal order of LE and parametric function of Ali and Schaeffer for fixed and random effects in random regression analysis, finding the optimal model for genetic evaluation and comparison of different measures based on EBV for describing persistency of lactation in Iranian primiparous Holsteins.

2. MATERIALS AND METHODS

The originally used data included 298990 records of test day milk yield of primiparous Holstein in Iran. The number of records per cow was from 3 to 10, three milking per day, both parents were known and age at calving was between 18 and 29 month. The contemporary groups (CG) were defined by grouping the variables herd, year and season of milk production. After editing, data were 227118 test day records for milk yield of 31258 first cows calved from 1999 to 2008. The summary of the data used in this study and the distribution of test days within the classes formed by cow's age and calving season are shown in Tables 1 and 2, respectively.

2.1. Models

Several different functions have been applied for fixed regression model as well as additive and permanent environmental effects including Ali and Schaeffer (AS) and different unequal orders of Legendre polynomial. Table 2 shows the characteristics of the models used for different random regression analysis.

Ali and Schaeffer (1987), a function with five parameters, which is a regression model of yields on day in lactation (linear and quadratic) and log of 305-day yield divided by day in lactation (linear and quadratic) fitted:

$$Y_t = a + b(t/305) + c(t/305)^2 + d\ln(305/t) + f\ln^2(305/t)$$

1. In this function '*a*'is an intercept, parameters *d* and *f* are connected with the increasing slope, parameters *b* and *c* with the decreasing slope of lactation curve and *t* is time of milking.

2. Legendre Polynomial (LE). In calculation of Legendre polynomials it is assumed that$P_0(\chi) = 1$ *and* $P_1(\chi) = \chi$. Then in general, n+1 polynomial is described by the following function:

$$P_{n+1}(\chi) = (1/n+1)((2n+1)\chi P_n(\chi) - nP_{n+1}(\chi))$$

These quantities are normalized using
$\Phi_n(\chi) = (2n+1/2)^{0.5} P_n(\chi)$

Where:
n: the order of the polynomials.

Test day records in the interval 5 to 305 days were standardized to the interval -1 to +1. In other words, ages or time periods have to be standardized (converted) to the interval between -1 to +1 with the following formula:

$$\alpha_i = -1 + 2\,(t_i - t_{min}/t_{max} - t_{min})$$

Where:
t_{min} and t_{max}: the earliest and latest age represented in data (Schaeffer, 2004). Based on power of Legendre, Random regression analysis provides different coefficients (b) for each animal. For example for animal '*i*' in days in milk '*t*' it can be written as below:
$\lambda = b_{0i} + b_{1i} + b_{2i} + b_{3i} + \ldots$

Models for different power of Legendre (k=2, 3 and 4) with three, four and five coefficients can be written as below:
$\Gamma = (b_0 \times plg_0) + (b_1 \times plg_1) + (b_2 \times plg_2)$
$\Gamma = (b_0 \times plg_0) + (b_1 \times plg_1) + (b_2 \times plg_2) + (b_3 \times plg_3)$
$\Gamma = (b_0 \times plg_0) + (b_1 \times plg_1) + (b_2 \times plg_2) + (b_3 \times plg_3) + (b_4 \times plg_4)$

In these functions Γ is estimation breeding value, plg_0, plg_1… plg_4 are Legendre polynomial coefficients, which standardized based on unite of time and b_0, b_1… b_4 are coefficients of Legendre estimated by VCE6 for each animal in different models.
The model in matrix notation can be represented as:
$Y = Xb + Za + Wp + e$

Where:
Y: the vector of observations measured in animals.
b: vector of fixed effect.
a and ***p***: vectors of additive genetic and permanent environmental effects.
X, Z and W: incidence matrixes of fixed, additive genetics and permanent environmental effects.
e: the vector of residual.

The assumptions of this model are:
G and P are (co)variances of additive genetic and permanent environmental effects, $R= I\ \delta^2_e$is diagonal matrix (residual) with elements related to days in milk and UisKronecker product between matrices. In this study residual variance is assumed to be heterogeneous thorough the lactation (10 residual classes) to evaluate the parameters and variance components over DIM more accurately. The following model shows the parts of the models were used in random regression analysis:

Where:
Y_{ijlnp}: observation of test day n of cow l obtained in herd-year-season ‘i' of a cow calved in season’ p’.
HYS_i: fixed effect of herd-year season of production (i= 1,…., 8597).
CS_p: fixed effect of season of calving (p=1 to 4 for spring, summer, autumn and winter, respectively).
b_j: regression coefficient of age at calving as covariate (Linear and Quadratic form).
$ß_m$: the coefficient of fixed regression for an average population curve (Legendre polynomial or Ali and Schaeffer functions).
$\Phi_m(t_{mL})$: them^{th} standardized lactation age of the l^{th}animalin DIM (t= 5,… , 305).
q: the order of orthogonal Legendre polynomial.
a_{ln}: additive genetic random regression coefficient.
p_{ln}: permanent environmental random regression coefficient.
e_{ijlnp}:random residual effect.

2.2. Persistency

Different measures of persistency based on EBV were used in literature. In this study four different measures of persistency (PSY_1, PSY_2, PSY_3, and PSY_4) were used:

1. The difference between estimation breeding value between day 290 and 90:
$PSY_1= (EBV_{290}-EBV_{90})$ (Cobuci *et al*. 2007)

2. The difference between estimation breeding value between day 280 and 60:
$PSY_2= (EBV_{280}-EBV_{60})$ (Jamrozik and Schaeffer, 1997)

3. Selection based on partial EBV during lactation: (cumulative EBV from DIM 106-205 subtracted from cumulative EBV from DIM 6-105). (Jakobsen*et al*. 2002), (Cobuci*et al*. 2007).

In PSY_1 and PSY_2 measures, persistency was defined as difference in yield between days in milk 280 or 290 and peak DIM. Moreover, Estimation breeding value for a complete 305 DIM for all animals obtained by the sum of EBV of each time of days in milk, and the other criteria (EBV_{5-100}, $EBV_{101-200}$ and $EBV_{201-305}$) are calculated with the following formulas:

According to different measures of persistency, lower values of PSY_1, PSY_2, PSY_3 and PSY_4 indicate higher persistency because it is associated to slow rate of decline in production. Comparisons of the models were done by eigenvalues and associated eigenvectors and residual variance across days in milk. For evaluation of fixed effects and fitting of lactation curve, proc GLM in SAS package (SAS, 2005) was used. The PEST software (Groeneveld *et al*. 2002) was used for coding the original data and then the VCE6 software package (Kovac and Groeneveld, 2008) was applied for estimation of covariance components and obtaining solutions (random regression coefficients of additive genetic and permanent environmental effects of each animal) based on restricted maximum likelihood (REML). Using IML procedure in SAS package (SAS, 2005) the eigenvalues, corresponding eigenfunction and the other parameters were calculated for covariance matrices of random regression coefficients. Finally, calculations of different persistency criteria for each animal using mentioned models were evaluated with SAS programming.

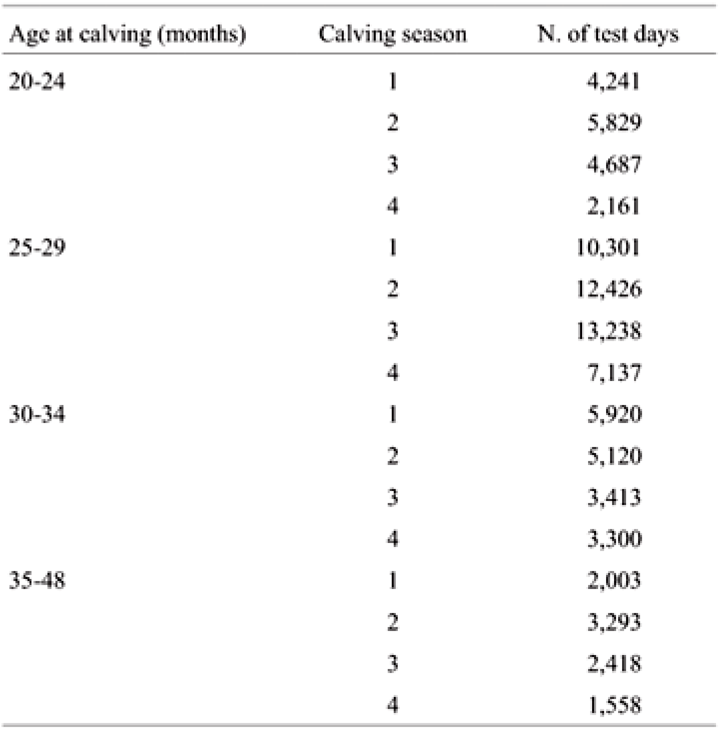
The summary of the data used in this study and the distribution of test days within the classes formed by cow's age and calving season are shown in Tables 1 and 2, respectively.

Table 1

Summary of the infomation used in this study

Animal 1		Animal 2		Animal 3		N. of test days
Age	Wt	Age	Wt	Age	Wt	
28	42	32	30	35	38	5,654
38	53	42	50	45	44	11,543
48	60	52	58	55	51	7,654
58	72	62	68	65	60	12,453
68	83	72	76	75	70	6,721
78	94	82	85	85	77	13,731

Table 2 - Number of test days per class of cow's age and calving season after data edition.



Age at calving (months)	Calving season	N. of test days
20-24	1	4,241
	2	5,829
	3	4,687
	4	2,161
25-29	1	10,301
	2	12,426
	3	13,238
	4	7,137
30-34	1	5,920
	2	5,120
	3	3,413
	4	3,300
35-48	1	2,003
	2	3,293
	3	2,418
	4	1,558

3. RESULTS AND DISCUSSION

Mean milk yield and standard deviation, as well as the number of test-day records and the percentage of cows with the respective number of test-day records per lactation period are shown in Table 3. Small variations were observed in the standard deviation of milk yield of 10 test-day records obtained during the lactation period. In addition, 76.12% of the lactations were incomplete, *i.e.*, there were less than 10 test-day records per lactation.

Table 3

Test day, ages, standardized time values and percentage of cows

Test Day	Age	Mean	Standardized Value	Percentage of Cows
10	31	26.43	-1.000	5.21
20	41	25.65	-0.600	7.12
30	51	25.21	-0.200	7.09
40	61	24.12	0.200	10.23
50	71	23.12	0.600	13.67
60	81	20.12	1.000	15.11

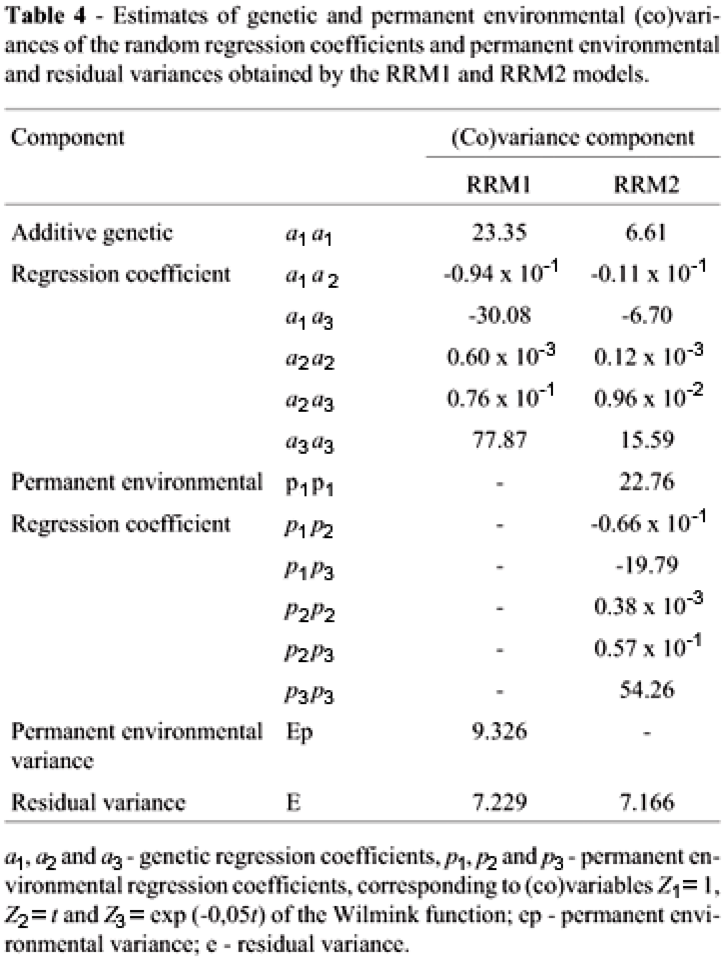


Table 4 - Estimates of genetic and permanent environmental (co)variances of the random regression coefficients and permanent environmental and residual variances obtained by the RRM1 and RRM2 models.

Component		(Co)variance component	
		RRM1	RRM2
Additive genetic	$a_1 a_1$	23.35	6.61
Regression coefficient	$a_1 a_2$	-0.94×10^{-1}	-0.11×10^{-1}
	$a_1 a_3$	-30.08	-6.70
	$a_2 a_2$	0.60×10^{-3}	0.12×10^{-3}
	$a_2 a_3$	0.76×10^{-1}	0.96×10^{-2}
	$a_3 a_3$	77.87	15.59
Permanent environmental	$p_1 p_1$	-	22.76
Regression coefficient	$p_1 p_2$	-	-0.66×10^{-1}
	$p_1 p_3$	-	-19.79
	$p_2 p_2$	-	0.38×10^{-3}
	$p_2 p_3$	-	0.57×10^{-1}
	$p_3 p_3$	-	54.26
Permanent environmental variance	Ep	9.326	-
Residual variance	E	7.229	7.166

a_1, a_2 and a_3 - genetic regression coefficients, p_1, p_2 and p_3 - permanent environmental regression coefficients, corresponding to (co)variables $Z_1 = 1$, $Z_2 = t$ and $Z_3 = \exp(-0{,}05t)$ of the Wilmink function; ep - permanent environmental variance; e - residual variance.

The (-2log$_e$) values of the likelihood function were 301,665.2392 and 301,248.1940 for RRM1 and RRM2, respectively. Application of the likelihood ratio test showed that inclusion of the Wilmink function in the description of the permanent environmental effects significantly increased the fit of the models, considering that the difference between the (-2 $\log_e$) values was greater than the table value. Therefore, based on this test, the RRM2 model would be more adequate for the genetic evaluation of test-day milk yield in Holstein cows from the State of Minas Gerais.

According to Jensen (2001), different models can be proposed to evaluate test-day milk yield traits by random regression models. However, no consensus exists regarding the best model to fit milk yield data. In principle, the model that maximizes the genetic progress of the study population should be selected for the genetic evaluation of animals.

3.1. (Co) variance and correlation between random regression coefficients

In total, 8 and 13 (co)variance components were simultaneously estimated by RRM1 and RRM2, respectively (Table 4).

The inclusion of the random regression coefficients in model RRM2 to describe permanent environmental effects promoted a decrease in the magnitude of the (co)variances and genetic correlations between random regression coefficients (Tables 4 and 5, respectively). However, Rekaya *et al*. (1999) reported that the inclusion of permanent environmental random regression coefficients did not affect in a significant manner the genetic correlation between the coefficients of the model.

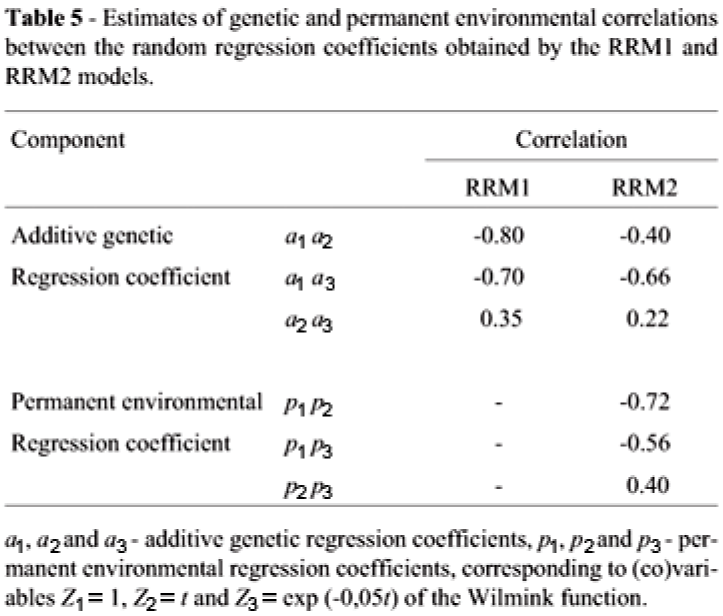


Table 5 - Estimates of genetic and permanent environmental correlations between the random regression coefficients obtained by the RRM1 and RRM2 models.

Component		Correlation	
		RRM1	RRM2
Additive genetic	$a_1\,a_2$	-0.80	-0.40
Regression coefficient	$a_1\,a_3$	-0.70	-0.66
	$a_2\,a_3$	0.35	0.22
Permanent environmental	$p_1\,p_2$	-	-0.72
Regression coefficient	$p_1\,p_3$	-	-0.56
	$p_2\,p_3$	-	0.40

a_1, a_2 and a_3 - additive genetic regression coefficients, p_1, p_2 and p_3 - permanent environmental regression coefficients, corresponding to (co)variables $Z_1 = 1$, $Z_2 = t$ and $Z_3 = \exp(-0{,}05t)$ of the Wilmink function.

The estimates of genetic correlations between random regression coefficients for genetic and permanent environmental effects determined by RRM1 and RRM2 are shown in Table 5. An expressive difference in the genetic correlation estimates was observed between the two models, which might be due to the assumption in RRM1 that the permanent environmental effect was constant throughout the lactation period.

As shown in Table 5, negative associations could be observed between the initial milk yield (a_1), the rate in milk yield decrease after peak lactation (a_2), and the rate in milk yield increase until peak lactation (a_3), whereas positive associations were found between the rate in milk yield decrease after peak lactation and milk yield increase until peak lactation. This indicates that cows with smaller production rates until peak lactation tend to present lactation curves with larger persistency of lactation (a smaller decline rate).

Random regression models also permit inferences regarding the genetic aspects of the lactation curve. However, selection based on components related to different phases of the lactation curve is complex, because the association between these components and the phases of the lactation curve is not well understood (Rekaya *et al*.., 1999). Alternatively, random regression coefficient functions provide the genetic merit of animals during the various lactation periods (Jamrozik *et al*., 1997b).

The estimates of genetic correlations between regression coefficients obtained by the RRM1 model were close to the values (-0.79, -0.65 and 0.43) reported by Jamrozik *et al.* (1997a).

3.2. Variance components for milk yield

The estimates of genetic and environmental variances (sum of the variances of permanent environmental and residual effects), referring to test-day yields obtained during the period from day 6 to day 305 after the beginning of lactation, were calculated from the values shown in Table 6. The genetic variances estimated by the RRM1 model were greater than those estimated by the RRM2 model and were similar to those reported by Rekaya *et al.* (1999).

Table 6 - Estimates of genetic and environmental variances for selected DIM of daily yields obtained by the RRM1 and RRM2 models.

DIM	$Va_{(RRM1)}$	$Va_{(RRM2)}$	$Ve_{(RRM1)}$	$Ve_{(RRM2)}$
6	21.08	5.18	16.555	30.106
30	9.70	3.95	16.555	20.916
60	11.81	5.11	16.555	21.806
90	10.70	5.41	16.555	20.686
120	9.20	5.59	16.555	19.326
150	8.46	5.90	16.555	18.446
180	8.75	6.41	16.555	18.186
210	10.10	7.13	16.555	18.606
240	12.53	8.07	16.555	19.696
270	16.04	9.23	16.555	21.466
305	21.51	10.85	16.555	24.386

$Va_{(RRM1)}$, $Va_{(RRM2)}$, $Ve_{(RRM1)}$ and $Ve_{(RRM2)}$- additive genetic and environmental variances obtained by RRM1 and RRM2, respectively.

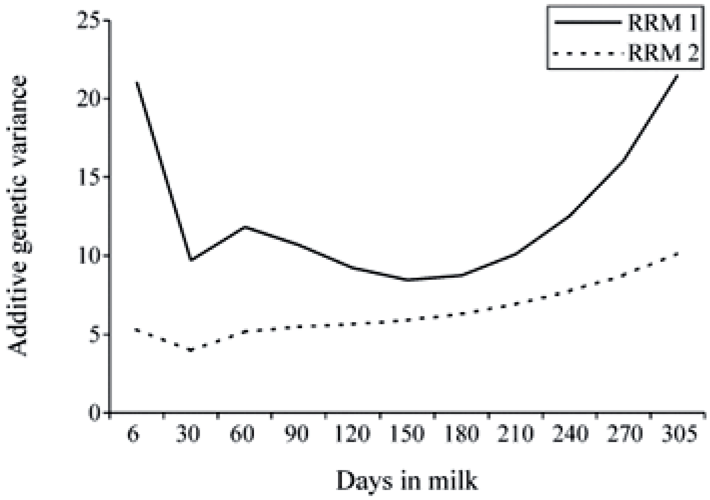


Figure 1 - Additive genetic variances during the different lactation periods estimated by the RRM1 and RRM2 random regression models.

The behavior of the genetic and environmental variance estimates throughout lactation, obtained by the RRM1 and RRM2 models, is shown in Figures 1 and 2, respectively. In general, the values obtained by the RRM1 model were overestimated. Genetic variance tended to be greater at the beginning and at the end of the lactation period (Figure 1). However, a marked decrease in the course of the genetic variance curve was observed for the first 30 days of lactation, suggesting that the models were less robust to describe the genetic variance in milk yield during this period. A marked decrease in the course of the genetic variance curve during the first days of lactation was also reported by Jamrozik *et al.* (1997b), Rekaya *et al.* (1999) and Kettunen *et al.* (2000). The shape of the genetic variance curve throughout lactation obtained by the RRM1 and RRM2 models was similar to that observed by Jamrozik *et al.* (1997b), Olori *et al.* (1999) and Rekaya *et al.* (1999).

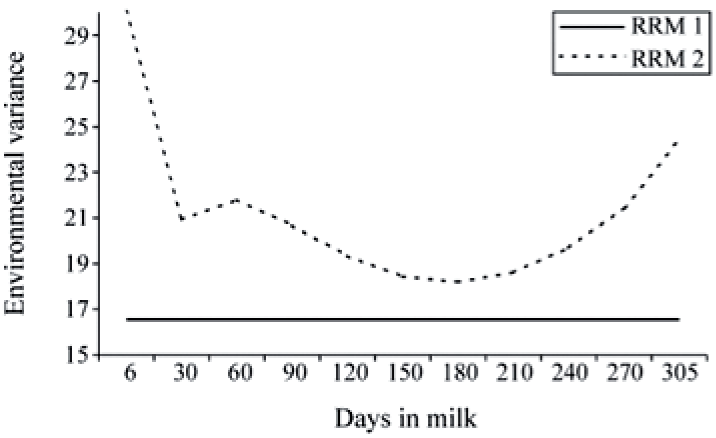


Figure 2 - Environmental variances (sum of permanent environmental and residual variances) during the different lactation periods estimated by the RRM1 and RRM2 random regression models.

The variations in the environmental variance estimates (sum of permanent environmental effects and residual variances) throughout lactation obtained by the RRM2 model (Figure 2) were not observed when the RRM1 model was applied, since in this model the permanent environmental and residual variances were considered to be homogeneous throughout the lactation period.

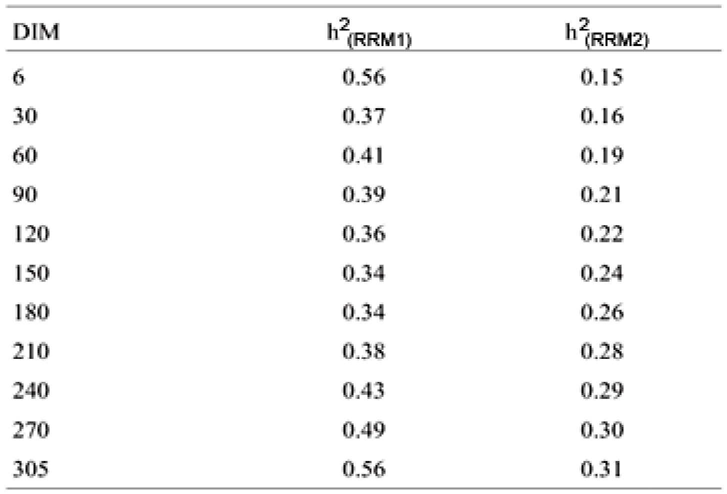
The results obtained with the RRM2 model show that environmental factors were more expressive at the beginning and at the end of lactation (Figure 2), in agreement with the observations of Ludwick and Petersen (1943) that non-genetic factors tend to influence the milk yield in a more expressive manner during the first weeks of lactation.

Comparison of the behavior of genetic and environmental variances estimated by the RRM1 and RRM2 models (Figures 1 and 2, respectively) showed that the absence of permanent environmental random regression coefficients in the RRM1 model did not permit the differentiation between variance estimates for genetic and environmental effects, *i.e.*, part of the genetic variability obtained with the RRM1 model was overestimated due to environmental factors.

3.3. Genetic parameters

The heritability estimates for test-day milk yield obtained for selected periods of lactation by the RRM1 and RRM2 models are shown in Table 7. Graphic representations of these estimates throughout lactation are illustrated in Figure 3.

Table 7 - Estimates of heritability for selected DIM of daily yields obtained by the RRM1 and RRM2 models.



DIM	$h^2_{(RRM1)}$	$h^2_{(RRM2)}$
6	0.56	0.15
30	0.37	0.16
60	0.41	0.19
90	0.39	0.21
120	0.36	0.22
150	0.34	0.24
180	0.34	0.26
210	0.38	0.28
240	0.43	0.29
270	0.49	0.30
305	0.56	0.31

$h^2_{(RRM1)}$ and $h^2_{(RRM2)}$ - heritability estimates obtained by the random regression models RRM1 and RRM2, respectively.

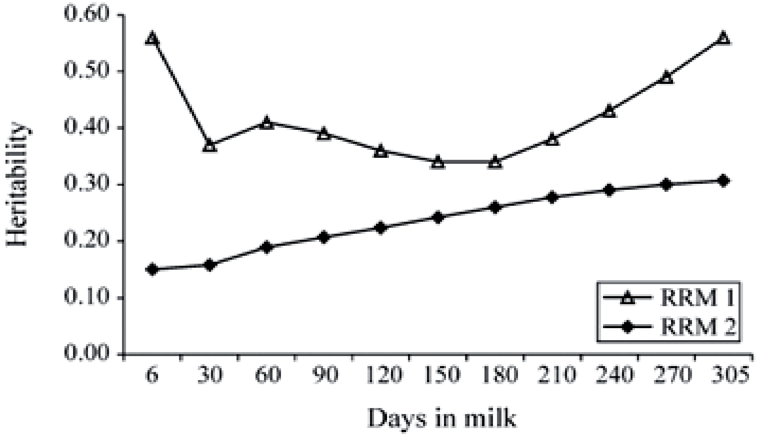


Figure 3 - Heritability estimates for milk yield during the different lactation periods estimated by the RRM1 and RRM2 random regression models.

The heritability estimates obtained with the RRM1 model ranged from 0.56 (first and last test day) to 0.34 (sixth and seventh test day), corresponding to 150 and 180 days of lactation (Table 7). A marked decrease in the heritability estimates was observed between day 6 and day 30 after the beginning of lactation, followed by an increase up to day 60, and remaining unchanged up to day 240, when an increase was again observed. Variations in heritability estimates throughout lactation have also been reported by Jamrozik and Schaeffer (1997) and Rekaya *et al*. (1999) for Holstein breeds and by Kettunen *et al*. (2000) for the Ayrshire breed, with the authors considering permanent environmental variances to be constant during lactation.

High heritability estimates for milk yield during different lactation periods were also observed by Jamrozik and Schaeffer (1997), Kettunen *et al*. (1997, 1998, 2000) and Costa *et al*. (2002). According to Costa *et al*. (2002), the overestimation of heritability has been one of the main problems to fit test-day milk yields by random regression models.

Heritabilities were always higher when estimated by the RRM1 model (Table 7), probably due to incorrect partition of the genetic and environmental components, based on the assumption of variance homogeneity for the permanent environmental effect. Similar results were obtained by Rekaya *et al.* (1999) in Holstein herds.

The heritability estimates obtained with the RRM2 model ranged from 0.15 to 0.31 (Table 7), with a gradual increase throughout lactation (Figure 3). This finding is in contrast to those of Rekaya *et al.* (1999) for Holstein cattle, and of Costa *et al.* (2002) for the Gir breed, considering residual variance heterogeneity between milk yield records throughout lactation. On the other hand, the present findings are similar to those reported by Olori*et al.* (1999) for Holstein cows, using Legendre polynomials to model permanent environmental effects.

Ferreira (1999), using data from the Milk Recording Organization of the Minas Gerais Association of Breeders of Holstein Cattle collected between 1989 and 1998 in a multiple-trait analysis, obtained heritability estimates for monthly test-day milk yields ranging from 0.11 to 0.21. A gradual increase in heritability estimates was observed up to the eighth test day (240 days of lactation), followed by a decrease on the two subsequent test days.

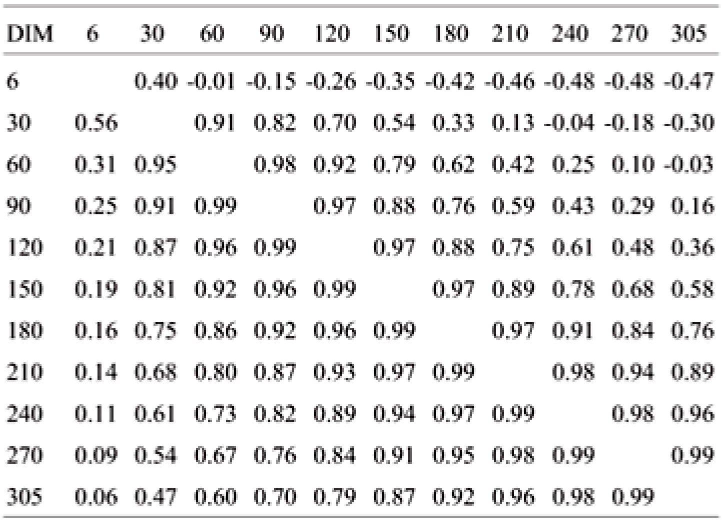
Genetic correlation estimates between test-day milk yields during the selected lactation periods obtained by the RRM1 and RRM2 models are shown in Table 8. In general, genetic correlations between individual test days tended to decrease at the extremes of the lactation trajectory, showing values close to unity for adjacent test days. These results agree with those reported by Rekaya*et al.* (1999) and Olori *et al.* (1999) for Holstein cows, and by Kettunen *et al.* (2000) and Costa *et al.* (2002) for Ayrshire and Gir breeds, respectively.

Negative genetic correlation estimates between test-day milk yields measured during the selected lactation periods were obtained by the RRM1 model (Table 8), a fact also observed by Rekaya *et al.* (1999), Liu *et al.* (2000), Kettunen *et al.* (2000) and Costa *et al.* (2002).

Permanent environmental correlation estimates between milk yields during selected lactation periods obtained by the RRM2 model are shown in Table 9. For example, permanent environmental correlations were greater between adjacent test days and tended to decrease between test-day pairs at the extremes of the lactation trajectory.

Milk yields at the beginning (DIM30) and at the end of lactation (DIM270) and midlactation yields (DIM150) were chosen to represent the character of the genetic correlations for milk yield between different lactation periods, estimated by the RRM1 and RRM2 models (Figures 4 and 5). The lowest genetic correlation estimates were obtained at the beginning and at the end of lactation.

Table 8 - Genetic correlation estimates between selected DIM of daily yields obtained by the RRM1 (above the diagonal) and RRM2 (below the diagonal) models.



DIM	6	30	60	90	120	150	180	210	240	270	305
6		0.40	-0.01	-0.15	-0.26	-0.35	-0.42	-0.46	-0.48	-0.48	-0.47
30	0.56		0.91	0.82	0.70	0.54	0.33	0.13	-0.04	-0.18	-0.30
60	0.31	0.95		0.98	0.92	0.79	0.62	0.42	0.25	0.10	-0.03
90	0.25	0.91	0.99		0.97	0.88	0.76	0.59	0.43	0.29	0.16
120	0.21	0.87	0.96	0.99		0.97	0.88	0.75	0.61	0.48	0.36
150	0.19	0.81	0.92	0.96	0.99		0.97	0.89	0.78	0.68	0.58
180	0.16	0.75	0.86	0.92	0.96	0.99		0.97	0.91	0.84	0.76
210	0.14	0.68	0.80	0.87	0.93	0.97	0.99		0.98	0.94	0.89
240	0.11	0.61	0.73	0.82	0.89	0.94	0.97	0.99		0.98	0.96
270	0.09	0.54	0.67	0.76	0.84	0.91	0.95	0.98	0.99		0.99
305	0.06	0.47	0.60	0.70	0.79	0.87	0.92	0.96	0.98	0.99	

Table 9 - Permanent environmental correlation estimates between selected DIM of daily yields obtained by the RRM2 model.

DIM	30	60	90	120	150	180	210	240	270	305
6	0.65	0.40	0.34	0.31	0.28	0.24	0.19	0.14	0.10	0.05
30		0.95	0.91	0.87	0.80	0.71	0.60	0.47	0.35	0.22
60			0.99	0.96	0.90	0.82	0.71	0.58	0.46	0.33
90				0.99	0.95	0.88	0.79	0.68	0.57	0.44
120					0.98	0.94	0.87	0.78	0.68	0.57
150						0.98	0.94	0.87	0.79	0.69
180							0.98	0.94	0.89	0.81
210								0.98	0.95	0.90
240									0.99	0.96
270										0.99
305										-

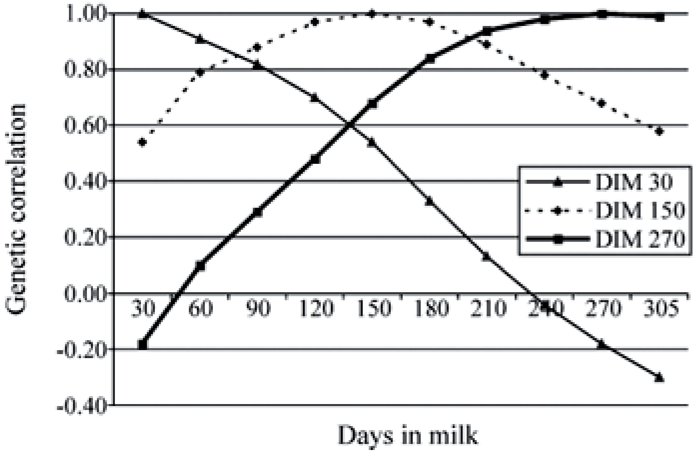


Figure 4 - Genetic correlations between daily milk yield at 30, 150 and 270 days and the other lactation periods obtained by the RRM1 model.

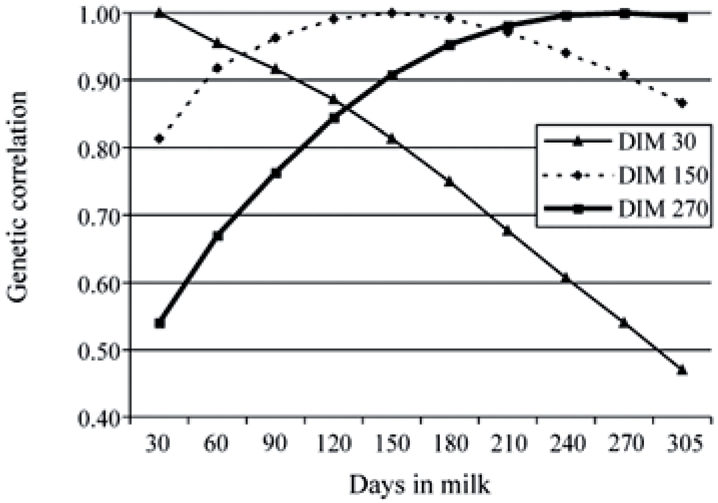


Figure 5 - Genetic correlations between daily milk yield at 30, 150 and 270 days and the other lactation periods obtained by the RRM2 model.

4. CONCLUSION

In this study, modeling of test day records using different random regression models was conducted for evaluation of milk yield in Iranian first parity cows. In view of the capacity of random regression models to provide mechanisms for the estimation of individual lactation curves, it seems feasible to predict the genetic merit of animals, using random regression coefficients. We therefore recommend the inclusion of random regression coefficients in random regression models to describe permanent environmental effects, in order to define more precisely the genetic and non-genetic effects that influence milk yield.

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