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ESTIMATION OF GENETIC PARAMETERS OF FIRST LACTATION TEST-DAY MILK YIELD USING RANDOM REGRESSION MODELS IN IRANIAN HOLSTEIN COWS

M. R. B. Behzadi* and Z. Mehrpoor

Department of Animal Science, Yasouj University, Yasouj, 75918-74831, Iran
*Corresponding author's email: bahreini@yu.ac.ir

ABSTRACT

The objective of the present study was to estimate variance components and genetic parameters for milk yield in Iranian Holstein cows, applying Legendre polynomials functions in random regression models (RRM). A total of 34818 test-day (TD) records from 4033 Holstein cows in their first lactation were analyzed. The genetic parameters were estimated by restricted maximum likelihood method and average information algorithm using the WOMBAT software. Varying order of Legendre polynomials (LP) were used in random regression models. The model considering a 6th-order LP for additive genetic effect, a 5th-order LP for permanent environmental effect and a step function with 10 heterogeneous classes for residual variances (Leg65_10) is more appropriate. Heritability estimates for TD records were highest in the second half part of the lactation, ranging from 0.13 to 0.66. Genetic correlations between TD records were high for consecutive records and decreased as the interval between tests increased, and ranged from -0.41 to 0.99. Genetic correlation estimates of TD records with corresponding lactation yield were highest for mid-lactation. The first eigenfunction suggests that milk yield is mainly controlled by genes with dissimilar effects between early and late stages of lactation. The results suggested that TD yields especially in the second half part of lactation may be used for genetic evaluation.

Key words: Genetic parameters, Holstein cows, Legendre polynomial, Random regression.

INTRODUCTION

Iran has a cattle population of 7.9 million of which 45.9, 43.6 and 10.51 percent are of the indigenous, crossbred and registered (mainly Holstein) cattle, respectively. The contribution of livestock to the national economy is 4 percent of total GDP. FAO (1993) announced that, Iranian dairy production has undergone significant and considerable structural changes during the last two decades due to creating larger herds. According to the FAO (1993), artificial insemination (AI) coverage in several countries including Iran increased remarkably over the 1980s decade (Ebrahimi Hoseinzadeh *et al.*, 2015a). In general, four groups of sires in terms of their origin are available to dairy producers through AI in Iran. These are American, Canadian, European and Iranian sires, which regardless of their origin can be further categorized to two groups: summarized or sampling sires. Summarized sires are those that have been progeny tested; thus, an estimate of their daughter's producing ability is available. Sampling sires are those that have been selected to transmit high production qualities or type-related traits based on their pedigree. However, they also need to be progeny tested to determine more accurately which sires will pass their high production and type-related traits to their daughters. Many Iranian dairy producers are reluctant to use foreign sampling sires because their daughters' performance is considered somewhat unpredictable. However, Iranian sampling sires are very reasonable and hence, some farmers prefer to use them on the repeat breeder cows as well as on the moderate to low foreign cows (Ebrahimi Hoseinzadeh *et al.*, 2015b). On the other hand, according to the latest official statistics of the Iranian Ministry of Agriculture, there are 18830 industrial cattle breeding unit (farm) in Iran that breed 2048563 dairy cattle (Kharrati Koopaei *et al.*, 2011). During 2004 to 2008 years, milk production in Iran has shown a growing trend (Kharrati Koopaei *et al.*, 2011). Despite the increase in milk production in the country, per capita consumption for milk in Iran is lower than the international standard. Per capita consumption of milk for each person is equal to 95 Kg, while in the world it is 169 kg and in the Europe it is 350 Kg. According to available data, it is understandable that the breeding objectives should be to increase milk production in Iran (Kharrati Koopaei *et al.*, 2011).

For enhancing the potential of animal improvement programs, knowledge of precise genetic parameters is necessary. Heritability and genetic correlations are fundamental parameters for using in designing animal breeding programs. The use of appropriate method for genetic evaluation of animals is an important aspect of dairy cattle production (Bilal and Khan, 2009). Test-day (TD) milk yield is the quantity of the milk produced by an animal over a period of 24 h (Schaeffer and Jamrozik, 1996). For decades, aggregated TD milk yield records were being applied as a common measure in genetic evaluation of milk yield. Nowadays, using 305-day milk yield had been exchanged by TD milk yield. Test-day milk yield records provide an excellent source of information for managing and breeding programs in dairy cattle. Using TD milk yield data have a number of advantages including removing environmental variation of milk yield data (Visscher and Goddard, 1995); improving the accuracy of genetic evaluation of cows (Rekaya *et al*., 1999); allowing the genetic evaluation of lactation persistency (Jensen, 2001) and increasing the accuracy of parameter estimation that affect milk yield including genetic and permanent environmental effects (Cobuci *et al*., 2005). The use of test-day model in the past decade has made it possible to economize the genetic evaluation with an enhanced accuracy (Bilal and Khan, 2009). Random regression models (RRM) are widely used in many countries to complete genetic evaluations of dairy cows using TD records (Jamrozik and Schaeffer, 1997). In RRM, lactation curve for each individual, stated as deviation from the mean curve of all individuals in the population are fitted. When fitting a RRM, a specific covariance structure between observations is assumed, and this structure is determined by covariances between regression coefficients and can be indicated as a covariance function. This continuous manner of covariance structure allows the estimation of breeding values for total or partial lactation yield (Bignardi *et al*., 2009). Random regression model by using LP functions has been used in modeling the covariance structure of milk yield TD records in dairy cows (Olori *et al*., 1999; Brotherstone *et al*., 2000). These functions have greatly been used to fit random lactation curves due to their ability of explaining the variation along the time period of days in milk (DIM). According to Schaeffer (2004), LP functions of time have much lower correlations between the coefficients and produce estimates of the covariance matrices that tend to be more vigorous over different lactation data sets. The aim of this research was to determine the genetic parameters required for the use of RRM fitting LP functions in order to analyze first lactation milk yield records of Holstein dairy cows, for estimating breeding values for test-day milk yield.

MATERIALS AND METHODS

The originally used data included 51852 test-day milk yield records of Holstein primiparous cows were obtained from the Animal Breeding and Milk Improvement Centre of Iran. After editing, a total of 34818 test-day records from 4033 first lactations primiparous Holstein cows recorded from 1999 to 2015 was analyzed. The cows, progenies of 614 sires, were distributed in 122 herds in Iran, with age at first calving varying from 19 to 36 months. Test-day records after the 301th day of lactation were excluded. In pedigree file, the total number of animals evaluated was 13530 and number of individuals with both known parents was 6806. Test-day milk yield records were taken at monthly intervals starting from day 3th of lactation (TD1) to 301th day (TD11). The lactation records were grouped into 10 month classes of DIM. The number of TD records per cow ranged from 6 to 10, with three milking per day and both parents known. Analyses were carried out using a single trait RRM. The models included direct additive genetic, permanent environmental and residual effects as random effects, contemporary group of herd-year-season as fixed effect and age of cow at calving as covariate. Mean trends of milk production were modeled using second to sixth-order regressions on LP functions of DIM. The random regression model was as follows:

$$y_{\mathrm{ijkl}} = HYS_i + \sum_{k=1}^{2} b_m + \sum_{r=1}^{k} \beta_{jk}\varphi_{jkl} + \sum_{r=1}^{k-1} \alpha_{jk}\varphi_{jkl}(t^*_{jl}) + \sum_{r=1}^{k-1} pe_{jk}\varphi_{jkl}(t^*_{jl}) + \varepsilon_{ijkl} \qquad (1)$$

Where y_{ijkt} = the vector of observations measured in animals; HYS_{i} = fixed effect of i$^{\mathrm{th}}$ herd-year-season; b_{m} = regression coefficient of age at calving as covariate (linear and quadratic form); β_{jkl} = the coefficient of fixed regression for an average population curve; α_{jk} and pe_{jk} = k$^{\mathrm{th}}$ additive genetic and permanent environmental random regression coefficients for the j$^{\mathrm{th}}$ animal, respectively; t^*_{jl} = the l$^{\mathrm{th}}$ standardised lactation age of the j$^{\mathrm{th}}$ animal; φ_{jkl} = the k$^{\mathrm{th}}$ Legendre polynomials for the j$^{\mathrm{th}}$ animal of the l$^{\mathrm{th}}$ standardised lactation age; ε_{ijkl} = residual random effect.

Test-day records in the interval 3 to 301 t_{l} days were standardized to the interval -1 to +1 on the Legendre scale with the following equation:

$$t^* = \frac{2(t_l - t_{\min})}{(t_{\max} - t_{\min})} - 1 \qquad (2)$$

Where t^* = standardised test-day records; $t_{\min}$ and $t_{\max}$ = the earliest and latest age represented in data set, respectively (Schaeffer, 2004).

Heterogeneous residual variances were modelled by a step function with 10 and 4 classes of variance and these two types of residual variance classification were compared. Step functions initially fitted by 10 classes of residual variance. Then, the structure of residual variation had been examined and step function with four residual variances was determined. For the last pattern, because of similarity in residual variances between 61 to 270 days of lactation, the classes were 3-30, 31-60, 61-270 and 271-301 days. There were examined 14 models with orders varying from three to six coefficients for the additive genetic and the permanent environmental effects and heterogeneous residual variances with 10 classes. After finding the best random regression model by fitting 10 heterogeneous residual variances, the model has been fitted with homogenous and four class heterogeneous residual variances and the results of these models were compared. At last, 16 models were investigated and had been reported in this study. The models are showed as LegKaKpe_n, where Ka and Kpe specify the number of regression coefficients fitted for direct genetic and permanent environmental effects and n denotes number of heterogeneous residual variance classes.

The (co)variance components and the genetic parameters were estimated by restricted maximum likelihood method and average information algorithm using the WOMBAT software (Meyer, 2007). For comparing the RRM, the Akaike's (AIC) and Schwarz's Bayesian (BIC) information criteria were used. The information criteria can be described as follow: $AIC=-2logL+2p$; $BIC=-2logL+plog(N-r)$, Where, p is the number of parameters, N is the total number of observations, r is the rank of the incidence matrix of fixed effects, and logL is the logarithm of likelihood function. IML procedure in SAS software (ver. 9.2) was used for calculation of eigenfunctions for covariance matrices of random regression coefficients of the best model.

RESULTS AND DISCUSSION

Mean TD milk yield was 28.63 kg with a standard deviation of 6.26 kg and a coefficient of variation of 21.86 percent. In this study, average milk yield increased until month 3 (31.43 kg), after that there was a slight decline until the end of lactation at month 10 (23.48 kg). The coefficient of variation of milk yield increased as lactation progressed.

Different RRM were fitted and on the basis of the logarithm of the likelihood function (logL), AIC and BIC values best model were recognized (Table 1). Number of parameters ranged from 19 to 52 in the studied models. Comparison of different RRM showed that increasing the order of ka and kpe covariance functions improved logL, AIC and BIC values. The logL functions increased and inversely AIC and BIC decreased when the number of coefficients for additive genetic effect and permanent environmental effects was increased but unequal orders had better fitting. Indeed, improvement of logL, AIC, and BIC values was observed when the order of polynomials for additive genetic effects was fixed, and the order of polynomials for permanent environmental effects was increased. Comparing different models by using second to sixth-order regression for mean trend of lactation indicated that a fourth-order LP of DIM was sufficient for fitting mean trend of milk yield. Therefore, in all random regression models of table 1, the mean trend of milk yield was modeled with a fourth-order LP function. All criteria indicated that the model with ka=6, kpe=5 and 10 classes of residual variances, containing 46 parameters, denoted by LEG65_10, was the most appropriate model for fitting the data of milk yield among the models considering different residual variance classes. Indeed, LEG65_10 model containing fewer parameters being parsimonious form of LEG66_10 model. The result of our study in finding the best model was in agreement with El Faro *et al*. (2008). However, they found that 6th order LP were the best to fit both random effects, according to AIC and BIC criteria. In general, other studies on milk yield records have showed that a lower order of covariance function could be sufficient to fit the data. The results obtained by Strabel *et al*. (2005) and Moghbeli Damane *et al*. (2014) showed that third order Legendre polynomials, for both random effects best described the variation. Singh *et al*. (2016) confirmed that RRM with fourth order LP for additive genetic effect and fifth order LP for permanent environmental effect was the best model.

Analyzing the more suitable model (LEG65_10) by considering four class heterogeneous (LEG65_4) and homogeneous (LEG65_H) residual variances indicated that a 10 class heterogeneous variance structure is better for residual effects since the variances tended to differ across months of lactation period. However, we expected the models with four classes of residual variances (LEG65_4) will have better fitting than the models with ten classes (LEG65_10). Results indicated that finding and using different residual variance classes is often not necessary. Because using new residual variance structures (LEG65_4 and LEG65_H) had worse fitting criteria than the best model (LEG65_10). Olori *et al*. (1999) demonstrated that third-order models for additive genetic and permanent environmental effects resulted in few changes in mean genetic parameter estimates when the residual variance structure was modeled using one, four, 10, and 37 classes. Heterogeneous residual variance has been found in the course of lactation in several studies (Olori *et al*., 1999; Brotherstone *et al*., 2000; Rekaya *et al*., 2000; Moghbeli Damane *et al*., 2014). Rekaya *et al*. (2000) reported that assuming a homogeneous residual variance along the lactation would affect the genetic evaluation. Olori *et al*. (1999) stated that using homogeneous residual variance along the lactation produce bias residual variance estimates in early lactation.

Variances, covariances and correlations between the random regression coefficients and eigenvalues and their proportion for additive genetic and permanent environmental coefficient matrices estimated by model Leg65_10 are presented in Table 3. Eigenvalues illustrate the quantity of variation described by the corresponding eigenfunction (Kirkpatrick *et al*., 1990). Togashi *et al*. (2008) showed that the first three eigenvalues and related eigenfunctions illustrate the highest additive genetic variance. If the amount of first eigenvalue was considerable, selection could generate rapid change in the characteristic that was under selection process (Kirkpatrick *et al*., 1990; Olori *et al*., 1999). In present study, two first eigenvalues of additive genetic effect in Leg65_10 model accounted for about 97.37 percent of genetic variation of milk yield, while other eigenvalues accounted for very small variation about 2.63 percent and could be less important. Elahi Torshizi *et al*. (2013) reported that three eigenvalues for genetic effect in the best model accounted for around 99.9 percent of genetic variation of milk yield in Iranian Holstein dairy cows. Similar results reported by Singh *et al*. (2016) that the first three eigenvalues with 3.26 (86.89%), 0.43 (11.57%) and 0.06 (1.54%) of the additive genetic covariance function accounted for at least 99 percent of all eigenvalues in Karan Fries cattle. For the permanent environmental effect, the first two eigenvalues accounted for 94.62 percent of total variation that was less than 97 percent of genetic variation. Therefore, for the permanent environmental effect, three eigenvalues and corresponding eigenfunctions needed to account for more than 97.37 percent of variation. So, comparing eigenvalues of two random effects in this study confirm that a RRM with unequal order of LP for additive genetic and permanent environmental effects would be an appropriate model. Using equal order of fit for two random effects of additive genetic and permanent environment showed that the results were not suitable. Thus, we can use eigenvalues and their proportion for additive genetic and permanent environmental coefficient matrices for choosing the best RRM. Singh *et al*. (2016) reported that the first four eigenvalues of permanent environmental effect accounted for 99 percent of total variance in Karan Fries cattle. Elahi Torshizi *et al*. (2013) reported that first three eigenvalues for permanent environmental effect accounted for at least 95 percent of total variation.

Figure 1 shows phenotypic (σ_p^2), genetic (σ_a^2), and permanent environmental (σ_{pe}^2) variances estimated with selected RRM (LEG65_10). Phenotypic variance had increasing trend and increased slowly during the lactation trajectory. The phenotypic variance increased until day 65, next decreased until day 215 and then increased until the end of lactation, when the highest value was observed. Similar results have been reported by Bignardi *et al*. (2012), who showed that phenotypic variances were high in the first two weeks of lactation, declined until mid-lactation, and again increased after week 20 until the end of lactation. Additive genetic variance had increasing trend during the lactation trajectory. Genetic variance also increased up to day 65, thereafter a gradual decline was noticed till day 215 and then increased until the end of lactation to obtain the highest value. Figure 1 indicates that additive genetic variances were higher on average in the second half part of the lactation. Additive genetic variances were always lower than phenotypic variances throughout the lactation. A similar finding has been reported by Cobuci *et al*. (2005), Kettunen *et al*. (2000) and Rekaya *et al*. (1999) for Holstein cattle using RR models and different functions. The highest permanent environmental variances estimated with the best RRM were observed at the beginning and at the end of lactation. The same trend has been reported by Bignardi *et al*. (2011), Cobuci *et al*. (2005), Costa *et al*. (2008) and Melo *et al*. (2007) who indicated that environmental factors exerted a marked influence during these periods of time in lactation. The highest permanent environmental variances at the beginning of lactation might be due to this fact that the animals were in an unstable condition due to the effect of parturition. An increase in permanent environmental variance at the end of lactation might be for the reason that the animals were forced to stop milking at this time.

Heritability of milk yield during lactation by LEG65_10 model is presented in Figure 2. Heritability had increasing trend and increased during the lactation trajectory but there were a slight decrease at the end of lactation. The range of heritabilities was from 0.13 to 0.66 in this model. The highest heritability was observed in the day 275 of lactation (0.66±0.03) and the lowest was obtained at the beginning of lactation (0.13±0.01). Also, the average heritability was 0.33. This increasing pattern of heritability is in agreement with some reported results (Danell, 1982; Ptak and Schaeffer, 1993; Baffour-Awuah *et al*., 1996; Shadparvar and Yazdanshenas, 2005). Abdullahpour *et al*. (2013) reported the average heritability of 0.22 for daily milk yield. Heritability estimates in different months of lactation were medium to high and indicated that we can have genetic improvement by individual selection for dairy cattle in Iran. Low heritability estimates at the beginning of lactation might have been due to low milk production, stress of cows from calving and insufficiency of energy (Bignardi *et al*., 2009). High permanent environmental variance and decreasing number of records at the end of lactation can generate low heritability. The heritability estimates in our study were higher than those reported by some other scientists on Holstein cattle in Iran. Razmkabir (2011) reported heritability ranges for daily milk yield from 0.11 to 0.25 along the first lactation. Moreover, Abdullahpour *et al*. (2013) estimated range of heritabilities for milk yield from 0.12 to 0.30. Khan *et al*. (2008) studied heritability and breeding values of test-day (TD) and 305-day milk yield of Sahiwal cattle and reported that the heritability estimate of test day milk yield were not very high. These researchers reported that heritability estimates of 0.082 ± 0.0768 and 0.024 ± 0.0464 for 305-day milk yield and test-day (TD). Also, heritability estimates of individual TDs ranged from 0 to 0.274, in another research on Sahiwal cows in Pakistan (Bilal *et al*., 2008). In general, different heritability estimates reported in the literature are due to differences in genetic variances, herd management, statistical models, estimation methods and climatically changes which occur in different area. Our findings confirmed the results of other authors with the highest heritability at the end of lactation (Jakobsen *et al*., 2002; Druet *et al*., 2003).

It is shown in Figure 3 the additive genetic and phenotypic correlations between different DIM. Genetic correlation (ranged from -0.41 to 0.99) between TD were higher (close to unity) in adjacent periods but decreased with increasing period among TD yield. Rekaya *et al*. (1999), Olori *et al*. (1999) and Cobuci *et al*. (2005) also reported high genetic correlation estimates between test-day milk yield records using RRM. The result of Jakobsen *et al*. (2002) showed that the genetic correlation between TD were higher than 0.4. Elahi Torshizi *et al*. (2013) reported that the genetic correlation between TD ranged from 0.47 to 0.98 in primiparous Holstein cows in Iran. Negative genetic correlations were obtained specially between initial and final TD. These negative genetic correlations can be attributed to the difficulty of modeling initial TD milk yields of lactation, a phase during which the cow suffers from post calving stress and also from an energy deficit. Negative genetic correlations estimated by RRM using different functions have also been reported for Holstein cattle by Bignardi *et al*. (2009), Brotherstone *et al*. (2000), Cobuci *et al*. (2005), Costa *et al*. (2008), Jamrozik and Schaeffer (1997), Kettunen *et al*. (2000) and Olori *et al*. (1999). Phenotypic correlations (were ranged from -0.09 to 0.77) between test days and had also higher value in adjacent period but decreased with increasing interval between TD yields. Decrease in additive genetic correlation with increasing interval between TD yields indicated that modeling of additive genetic effect by Random regression coefficients are needed for analysis of genetic data comparing to other methods, e.g. repeatability and fixed regression methods. According to Strabel and Misztal (1999), when the genetic correlation between different test days are close to unity, repeatability model is more suitable than RRM because of less parameters in the model.

Figure 4 shows the two main eigenfunctions obtained with the Leg65_10 random regression model. Two first eigenfunctions accounted for 97.37 percent of total genetic variation. The first eigenfunction explained 82.16 percent of genetic variation and was negative from day 18 to day 196 of lactation period and positive during the other periods. First eigenfunction also illustrate that milk yield is mainly controlled by genes with dissimilar effects between early and late stages of lactation. The change in sign of the first eigenfunction between early and late stages of lactation in our research tends to propose an underlying factor with opposing effects on milk yields in different stages of lactation. However, the change in sign of first eigenfunction values suggests contrasting effects on milk yield between different phases of lactation. The second eigenfunction accounted for 15.21 percent of total genetic variation and had positive and constant behavior during lactation period, suggesting that all of the variation can be explained by genes that operate in similar way during lactation. The participation of the other eigenvalues to the genetic variation was very small. This suggests that the potential of changing in the pattern of milk yield across lactation stage by selection based on factors represented by the third, fourth and fifth eigenfunctions is small.

This study discussed the use of RRM by varying order of Legendre polynomials for the estimation of genetic parameters for first lactation milk yield. In general, there is no consensus in the literature about the best model to describe the covariance function for milk yield. Heritability estimates in different stages of lactation were Medium to high and indicated that we can have genetic improvement by using selection. The residual variances have different behavior during the course of lactation and should be modeled through heterogeneous classes. Despite of having technical and computation demands, RRM offers advantage over other methods of genetic prediction and evaluation (as evidenced in the present study and also reported in several previous studies) and may be used for the analysis of TD records of Iranian Holstein dairy cows as well as other dairy breeds under similar circumstances.

Table 1. Models, number of parameters (p), maximum log-likelihood (log L), Akaike's information criterion (AIC) and Schwarz's Bayesian information criterion (BIC) for different analyses.

Model	P	logL	AIC	BIC
Leg32_10	19	-65513.32	131064.64	131225.21
Leg33_10	22	-59228.401	118500.8	118686.72
Leg42_10	23	-65205.610	130457.22	130651.59
Leg43_10	26	-59123.415	118298.83	118518.56
Leg44_10	30	-60491.534	121043.06	121296.6

Leg52_10	28	-648190.08	129694.16	129930.79
Leg53_10	31	-58770.451	117602.9	117864.88
Leg54_10	35	-64786.934	129643.86	129939.65
Leg55_10	40	-58890.765	117861.53	118199.57
Leg62_10	34	-64721.422	129510.84	129798.18
Leg63_10	37	-64717.542	129509.08	129821.77
Leg64_10	41	-59276.562	118635.12	118981.61
Leg65_10	46	**-58187.777**	**116467.55**	**116856.30**
Leg66_10	52	-58288.166	116680.33	117119.78
Leg65_4	40	-58986.421	118052.84	118390.88
Leg65_H	37	-64713.532	129501.06	129813.75

Table 2. Estimates of variances (diagonal), covariances (below the diagonal), and correlations (above the diagonal) between random regression coefficients and eigenvalues (λ) of the coefficient matrix obtained by Leg65-10 model.

0	1	2	3	4	5	λ	λ%
Additive genetic effect							
8.79	0.13	-0.12	0.27	0.11	-0.07	52.09	82.16
2.10	**32.38**	0.94	-0.91	0.79	-0.79	9.64	15.21
-1.58	23.03	**18.73**	-0.98	0.84	-0.77	1.16	1.84
0.67	-4.29	-3.50	**0.69**	-0.79	0.69	0.49	0.77
0.48	6.85	5.49	-0.99	**2.31**	-0.39	0.02	0.03
-0.14	-3.19	-2.38	0.41	-0.42	**0.51**	0.00	0.00
Permanent environmental effect							
23.88	-0.11	-0.38	-0.03	-0.16		24.17	85.45
-0.55	**1.03**	-0.85	-0.08	0.09		2.59	9.17
-2.46	-1.15	**1.77**	0.29	0.03		1.23	4.34
-0.18	-0.09	0.44	**1.28**	0.26		0.29	1.04
-0.46	0.05	0.02	0.17	**0.34**		0.00	0.00

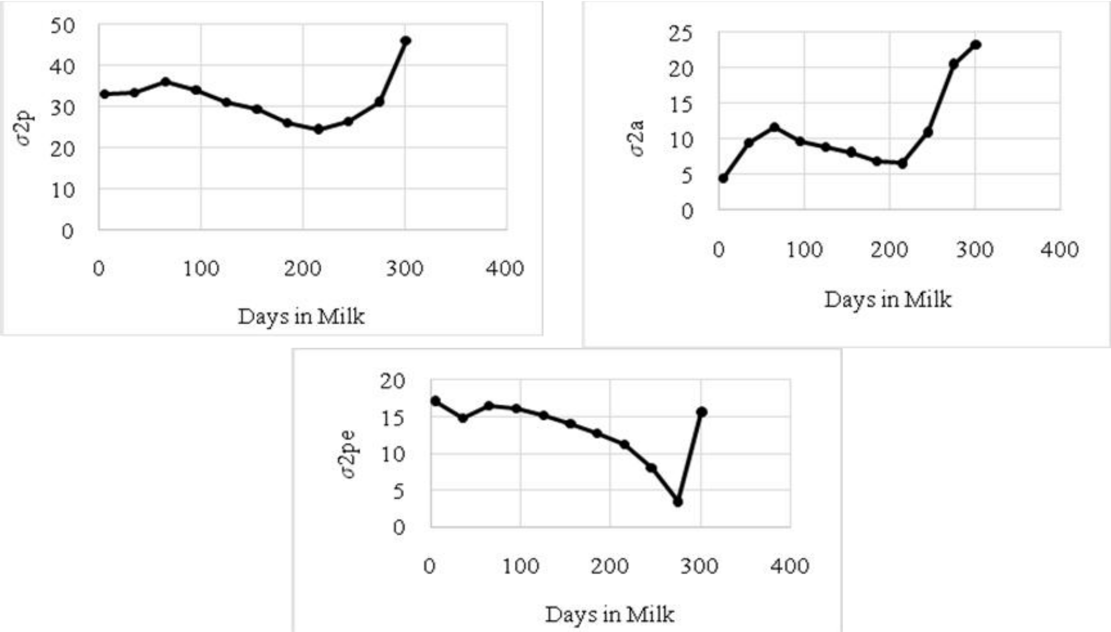

Figure 1. Phenotypic (σ_p^2), additive genetic (σ_a^2) and permanent environmental (σ_{pe}^2) variances estimated by the LEG65_10 random regression model.

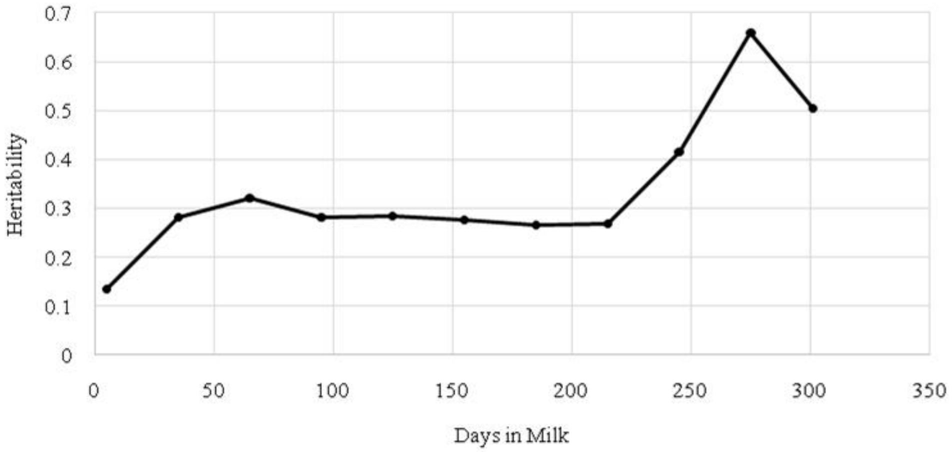

Figure 2. Heritability across days in milk for LEG65_10 model.

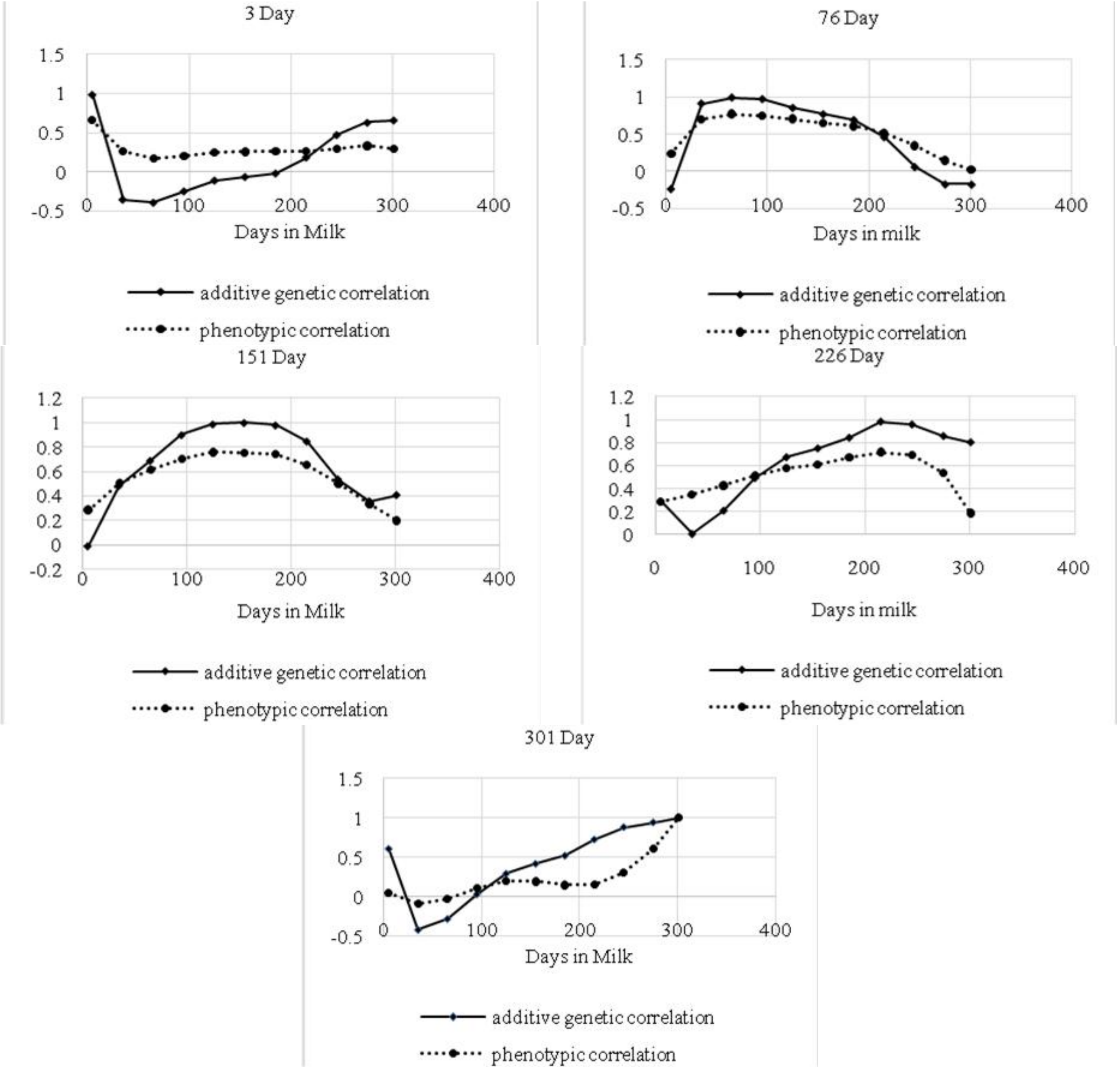

Figure 3. Estimates of additive genetic and phenotypic correlations in LEG65_10 model for milk at 3, 76, 151, 226 and 301 days with milk at all other days.

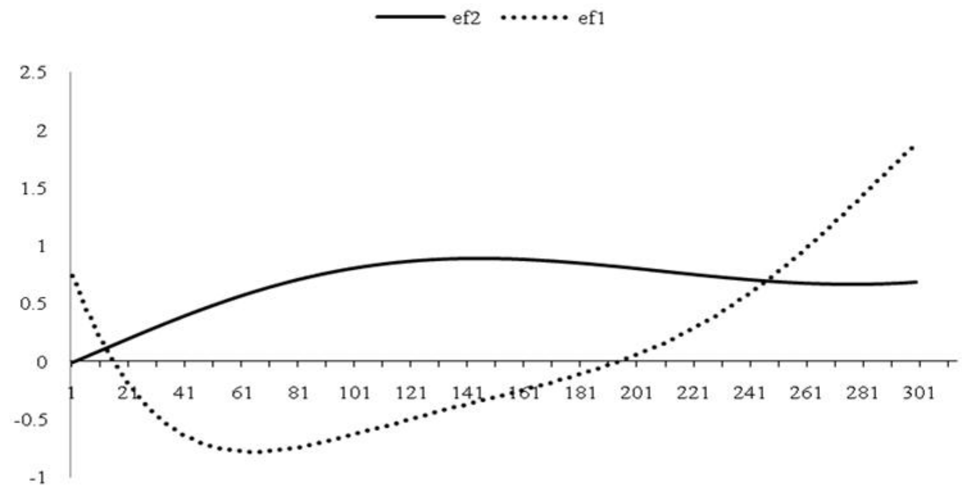

Figure 4. Eigenfunctions related to the first (ef1) and second (ef2) eigenvalues for additive genetic effects obtained with Leg65_10 model.

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