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J Anim Sci Adv 2012, 2(8): 664-667



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Abstract

Several functions were used to model fixed and random part of the lactation curve in Iranian primiparous Holstein cows using random regression analysis. Legendre polynomials of orders three and four as well as parametric lactation curve for the random part of the first lactation milk production were compared to find the best model. The models differed in fixed regression lactation curve part and residual variance assumed heterogeneous during lactation. Based on eigenvalue, associated eigenfunction and residual variance, third order polynomial Quadratic form for random effects and Ali and Schaefer model for fixed part AS33 model is optimal and make parsimonious less parameters for adjustment of test day milk yield records. The maximum residual and permanent environmental variances were obtained at the beginning and at the end of lactation respectively. The greatest additive genetic variance was in the middle of lactation and residual variance decreased during lactation. The highest heritability observed in middle of lactation (170 to 205 d) and ranged from 0.06 to 0.40. The genetic, permanent environmental and phenotypic correlation between extreme parts of lactation was 0.519, 0.317 and 0.240, respectively.

Key words: Eigenvalues, eigenfunction, genetic parameters, model comparison, random regression

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Received on: 07 Aug 2012

Revised on: 15 Aug 2012

Accepted on: 25 Aug 2012

Online Published on: 30 Aug 2012

Introduction

Test day models (TDM) describe longitudinal measurements which change over time. They allow a continuous change of covariance of test day records during lactation (Pool *et al.*, 2000; Melo *et al.*, 2007). These models have several advantages over the traditional 305-d method or lactation model. They allow direct correction for fixed or environmental effects on test day and flexible recording schemes, reduce costs of recording in dairy cattle, decreasing the generation interval, evaluate the genetic potential of the animals more accurately and better accounting of variation in number of test day records in each animal as well as accounting for variation in the shape of lactation curve (Olori *et al.*, 1999; Swalve, 2000; Takman *et al.*, 2007). Different sub-models have been proposed for the adjustment of lactation curve and describing of covariance function in test day models (Jensen, 2001). In random regression model (RRM) proposed by (Jamrozik and Schaeffer, 1997) genetic variance and correlation during lactation among test day records were different. In other words, RRM describe in a continuous manner the structure of covariance over time and allow the estimation of breeding value for lactation in contrast to multiple trait or repeatability models which provide point predictions. Different functions Ali and Schaeffer, Wilmlink, Legendre polynomials in modeling of lactation curve for adjustment of RRM and characterizing of covariance function among test day records proposed by researchers. (Kirkpatrick and Heckman, 1989) introduced Legendre polynomial (LEG) to describe covariance structure of longitudinal traits such as milk yields or body weight, because when both the additive genetic (AD) and permanent environmental (PE) components modeled by Legendre polynomial coefficients during time, the prediction of estimation breeding value and variance components become more accurate (Poll *et al.*, 2000). This structure, which describes the covariance among records of stage of lactation, is a covariance function (CF) which is equivalent to random regression models (Meyer and Hill, 1997). In general, the orthogonal Legendre polynomials have largely been used to fit random curves due to their

ability of describing the variation along lactation or at different stage of lactation, avoiding overestimation of genetic variance and heritability at the beginning and end of curve and achieving a parsimonious model and more accurate results (Bignardi *et al.*, 2008; Meyer, 1998), better convergence and being normalized (Takman *et al.*, 2007), and reduction of estimated correlation among test days and reduction of problems with rounding error because covariables based on LEG are small (Schaeffer, 2004). Accuracy of random regression model for genetic evaluation depends not only on ability of RRM to fit genetic and environmental deviations from the expected curve but also on number of parameters in regression function (Jamrozik and Schaeffer, 1997).

Based on different studies (Bignardi *et al.*, 2008; Kettunen *et al.*, 2000; Olori *et al.*, 1999; Misztal *et al.*, 2000) finding of the best model and order of Legendre are not clearly defined. Moreover, the order of Legendre is important in random regression because of affecting on genetic parameter estimation. It is clear that higher orders of polynomials are more flexible and can model the variance along DIM sufficiently but the lower orders could be also sufficient. (Strabel *et al.*, 2005) used polynomial of order three, (Takman *et al.*, 2007) and (Pool *et al.*, 2000) polynomial of order four, (Costa *et al.*, 2008) polynomial of order five in their studies. For implementation of the random regression model, the minimum order of fit required for modeling observed covariance should be determined in order to obtain reliable estimate of the dispersion parameters. Some studies (Strabel and misztal, 1999; Cobuci *et al.*, 2005) proposed that the residual variance should be homogenous across DIM due to limitation of program, reducing the number of parameters and dimension of the likelihood but it is better to allow residual variance to vary than to fix it in RRM because assumption of constant error variance leads to bias in heritability estimates (Misztal *et al.*, 2000; Jensen, 2001; Bignardi *et al.*, 2008).

The objectives of this study were a) evaluation and comparison of Ali & Schaeffer, Wilmlink and Legendre polynomials with for adjusting lactation curve and different equal power of Legendre polynomials (q=2, 3 and 4) for both additive genetic

and permanent environmental effects and b) selection of the optimum model and estimation of variance components and genetic parameters of milk trait in Iranian primiparous Holstein cows using random regression models.

Materials and Methods

Dataset

Data of 227118 test day milk yield records from 31258 first lactation Iranian Holsteins cows calved between 1999 and 2008 were analyzed which were splitted into 8597 herd-year-season contemporary groups with at least 26.41 records per group and 3.63 animals per group. The number of test day records per cow ranged from 3 to 10, with three milkings per day, both parents known and Age at calving was between 18 and 29 month. The structure of data set and pedigree after editing is summarized in Table 1.

Table 1: Description of the database

Animal with record	31258	No. of records	227,118
No. of sire	2064	No. of ¹ CG	8,597
No. of dam	28887	Average No. progeny/sire	15.14
Year of calving	1999- 2008	Average No. progeny/dam	1.08
Age at calving		Milk yield	
Average (day)	742.68	Average (kg)	28.88
² SD (day)	43.52	SD (kg)	7.05
Maximum (day)	931	Maximum (kg)	64.6
Minimum (day)	542	Minimum (kg)	2.10

¹Contemporary group, ² Standard deviation

Models

Several alternative sub-models were defined for modeled days in milk including two parametric functions Ali & Schaeffer, Wilmink in fixed part and different equal orders of Legendre LE3, LE4 and LE5 for additive AD and permanent environmental PE effects.

In this study lactation functions for fitting test days were:

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

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

The Ali-Schaeffer’s regression model has following parameters: **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 the day of lactation.

2- Wilmink exponential function (WL) with three parameters:

$$Y_t = a + b \exp^{-kt} + ct$$

In this model **a** is the level of production, **b** is the initial raise to peak and **c** is the decreasing rate after peak. The factor **k** is equal to 0.05 and is associated to the time of peak yield (Wilmink 1987) and **t** is days in milk.

3- Legendre Polynomial (LE). In calculation of Legendre polynomials it assumed that $p_0(x) = 1$

and $p_1(x) = x$. Then in general, n+1 polynomial is described by the following function:

$$P_{n+1}(x) = \frac{1}{n+1} ((2n+1)xP_n(x) - nP_{n-1}(x))$$

These quantities are normalize using

$$\Phi_n(x) = \left(\frac{2n+1}{2}\right)^{0.5} P_n(x)$$

where n is the order of the polynomials.

Test day records in the interval 5 to 305 t_i days were standardized to the interval -1 to +1 with the following formula:

$$\alpha_i = -1 + 2\left(\frac{t_i - t_{min}}{t_{max} - t_{min}}\right)$$

Where t_{min} and t_{max} are the earliest and latest age represented in data (Schaeffer 2004).

Orders for Legendre polynomials used in this study are 3&3, 4&4 and 5&5 for both AD and PE effects. Similarly, polynomials of equal order were used for Ali & Schaeffer and Wilmink functions for the fixed part of lactation curve, the additive and permanent environmental effects. MME are:

$$Y = Xb + Za + Wp + e$$

where **Y** is the vector of observations measured in animals; **b** is vector of fixed effect; **a** and **p** are vectors of additive genetic and permanent environmental effects; X, Z and W are incidence matrixes of fixed, additive genetic and permanent environmental effects and **e** is the vector of residual. The assumptions of this model are:

$$\text{var} \begin{bmatrix} a \\ p \\ e \end{bmatrix} = \begin{bmatrix} G \otimes A & 0 & 0 \\ 0 & P \otimes I & 0 \\ 0 & 0 & R \end{bmatrix} \quad E \begin{bmatrix} y \\ a \\ p \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

G and P are covariance of additive genetic and permanent environmental effects and \otimes is Kronecker product between matrices. R is diagonal matrix of temporary environmental variance residual with elements that depends on days in milk.

$$R = \text{diag} (\delta_e^2)$$

In this study residual variance assumed to be heterogeneous as function of DIM thorough the lactation to evaluate the parameters and variance

$$Y_{ijlnp} = HYS_i + CS_p + \sum_{k=1}^2 b_j + \sum_m^k \beta_m X_m + \sum_{k=0}^q a_{ln} \Phi_m(t_{ml}) + \sum_{k=0}^q p_{ln} \Phi_m(t_{ml}) + e_{ijlnp}$$

where Y_{ijlnp} = observation of test day record **n** of cow **l** obtained on herd-year-season of production **i** of a cow calved in season **p**, in age of calving **j** as a co-variable with linear and quadratic term, HYS_i = fixed effect of herd-year-season of production $i=1, \dots, 8597$, CS_p = calving season effects, b_j = regression coefficient of age at calving as covariate Linear and Quadratic, β_m is the coefficient of fixed regression for an average population curve, a_{ln} = n^{th} additive genetic random regression coefficient for cow **l**, P_{ln} = n^{th} permanent environmental random regression coefficient for cow **l**, $\Phi_m(t_{ml})$ =the m^{th} standardized lactation age of the l^{th} animal, q is the order of fit for random effects and e_{ijlnp} = residual random effect associated to Y_{ijlnp} . Comparisons of the models were done by eigenvalues associated

components over days in milk more accurately. The following 11 models were evaluated in this study:

LE333, WL33, AS33, LE444, WL44, AS44, LE555, WL55, AS55, WL and AS. For example LE333 shows that the power of Legendre function is two with three coefficients for adjusting lactation curve, additive genetic and permanent environmental effects. Also in AS and WL models, two functions of Ali & Schaeffer and Wilmink were used for fitting fixed regression, additive and permanent environmental effects in each model respectively.

In this study the same power of Legendre polynomial or functions for additive and permanent environment effects were used. This is an important assumption in this study to provide equal opportunity of variation for these effects (Lopez Romero, 2003). Moreover, it is difficult to find a biological reason when using different functions for AD and PE effects (Strabel *et al.*, 2005). The residual variance allowed being heterogeneous, changing with lactation stage. In this study DIM partitioned to 10 monthly classes from 5 to 305 d DIM.

The following equation was used in evaluation of additive genetics and permanent environmental effects on milk production by random regression model:

eigenfunction and residual variance. For both random effects the variation of the first three eigenvalues were considered. Fixed part of the model calculated with SAS package SAS, 2005. The PEST software was used for coding data and estimation of covariance components was based on restricted maximum likelihood REML method using the VCE6 software package (Kovac, Groeneveld and Mielenz, 2008). Using IML procedure in SAS package SAS inst. Inc., 2005 the eigenvalues, corresponding eigenfunction and the other parameters were calculated for covariance matrices of random regression coefficients.

Results and Discussion

Average milk yield, standard deviation and number of records per test day are shown in Table 2. The maximum milk production is in test day 3 and the standard deviations of test days have small variation.

Table 2: Number of test day, means and standard deviation of milk yield in each test day.

Test day	N. of records	Mean	Standard deviation
1	25950	27.28	6.57
2	26657	31.06	6.55
3	26801	31.20	6.69
4	26895	30.59	6.76
5	27203	29.74	6.86
6	27159	28.75	6.94
7	26220	27.78	6.96
8	22223	26.59	6.89
9	14351	25.44	6.77
10	3659	24.42	6.77

In all models, the maximum variation especially phenotypic and permanent environment variance were obtained at the beginning and at the end of lactation. (Van Vleck and Henderson, 1961) found that yield at the start and end of the lactation were subject to more temporary environmental variation than yield in mid-lactation, which is influenced more by genetic and permanent environmental differences between cows. Variance components for test day milk yield by models LE333, WL33, AS33 and WL are presented in Figure 1. Additive genetic variance tend to increase in the WL model along lactation. The only difference of these models related to the sub model which adjusted the lactation curve except for WL model. In these models the maximum range of residual variance related to WL model. Moreover, the Wilmink function has only three parameters and it has reduce flexibility of fitting difference source of variance during lactation so WL model can not produce optimal fit for additive genetic and permanent environmental variance along lactation. Estimation of variance components for test day milk yield by models LE444, WL44 and AS44 were plotted in Figure 2. Increasing permanent environmental variance during lactation suggest that permanent environmental factor had the high

influence on test day milk yield during 305 d milk production especially at the end of lactation. Like the other models, Estimation of variance components for test day milk yield by models LE555, WL55, AS55 and AS are presented in Figure 3. Estimation of the different variance components are related to fixed part of the model except for AS, lactation stage and the order of Legendre polynomial as well as different fixed effects (Olori *et al.*, 1999; Druet *et al.*, 2003).

The residual variance assumed heterogeneous over the lactation and in all models the fluctuation of residual variance was high in early lactation and was gradually constant in mid lactation and the end of lactation. (Olori *et al.*, 1999) reported the similar result using random regression models. From our results it seems that assumption of heterogeneity of variance should be considered in random regression analysis in particular during the first 100 days of lactation. In all models, residual variance slightly decreased as order of Legendre polynomial increased and the highest residual variance associated to LE333, LE444 and LE555 models respectively Figure 1. According to (Olori *et al.*, 1999) decrease of residual variance with increasing order of random regression increase may be due to increased ability of the higher order polynomial to model the lactation stage effect better, especially in the beginning of lactation. Using Ali & Schaeffer function instead of WL as fixed part, resulted to slightly lower residual variance.

The choice of functions for modeling fixed and random parts is an important point in construction of random regression models. In all models additive genetic variance was minimum at the beginning of lactation because of high residual variance in the first of days in milk and increased gradually till the end of lactation. The fluctuation of additive genetic variance in models WL33, WL44 and WL55 was higher than the other models LE333, LE444 and LE555 especially after mid lactation. In models WL33, WL44 and WL55 additive genetic variance overpredict in middle of lactation. Higher estimates of permanent environmental variance at the beginning and especially at the end of lactation were found in models. Lopez Romero *et al.*, (2003) pointed out that difference among models for variance components are more commonly observe

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in lactation. Some problem may produce with the fit of random regressions at the extremes of the trajectory (Meyer, 1999) Because of small number of records, sampling variance and high fluctuation in milk production in the beginning and at the end of DIM. Higher order of Legendre in random parts especially with WL function for fixed regression, follows more oscillatory patterns, which leads to extreme value at the end of lactation (Strabel et. al 2005). In AS model the residual variance was lower than WL model during the lactation and additive genetic variance overestimated at the end of lactation in WL relative to AS model. Comparison of different random regression functions by Melo *et al.*, (2007) showed that Ali & Schaeffer function is

superior to the WL model and the performance of this model was better than Wilmink. It seems that using Wilmink function for random parts is not suitable for random regression analysis in this study. Evaluation of AS and WL showed that When the genetic and permanent environmental components were modeled both by a Legendre polynomial function, predictions became more accurate. The AS33 and AS44 models are similar to LE333 and LE444 but in AS55 additive genetic effect overestimated in the end of lactation. It might be the additive genetic effect is overestimated at the end of the lactation, because of the low number of test day records.

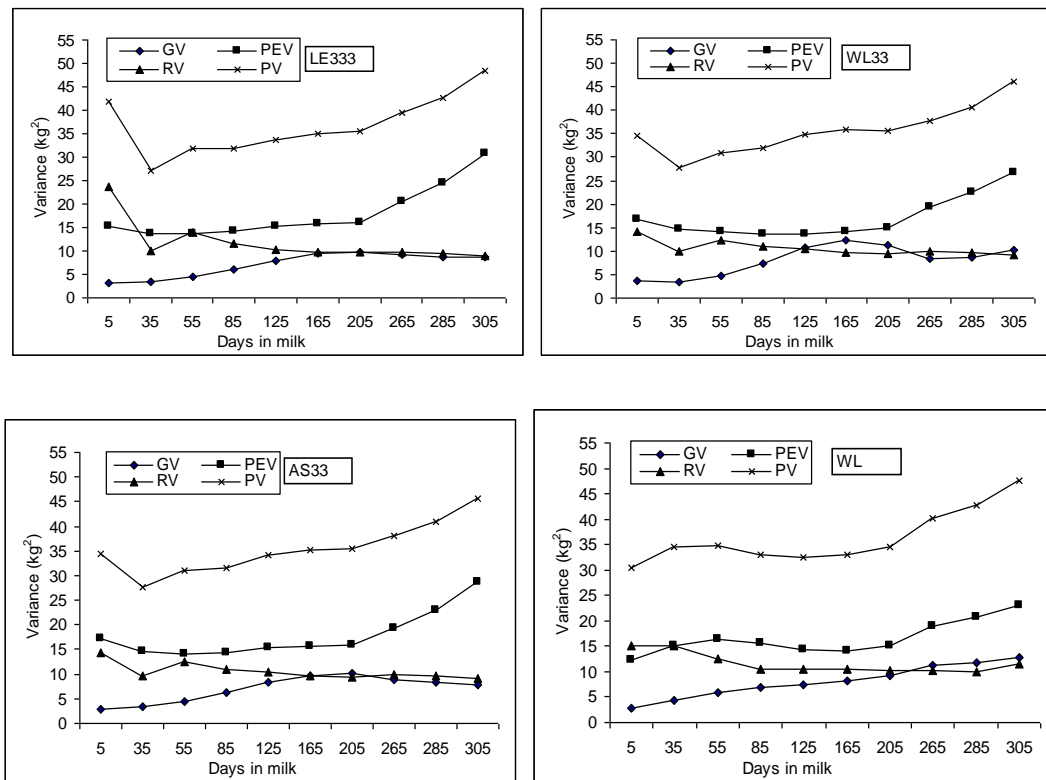


Fig. 1: Estimation of additive genetic (GV), permanent environment (PEV), phenotypic (PV) and residual (RV) variance in the models LE333, WL33, AS33 and WL during lactation period.

Eigenvalues represent the amount of variation explained by the corresponding eigenfunction (Kirkpatrick *et al.*, 1990). For each eigenfunction, a specific eigenvalue is associated. In all models with the same fixed part, with increasing the order of fit for additive and permanent effects, the total amount

of eigenvalues increased and performance of LE333, LE444 and LE555 are similar to AS33, AS44 and AS55. Wilmink model does not fit the lactation curve well compared to Legendre polynomial and Ali and Schaeffer models. Legendre polynomials are flexible enough for the analysis but

higher orders of polynomials require higher computer capacity. The appropriate models were determined by eigenfunction and related eigenvalues and evaluation of residual as well as the number of parameters. The sum of eigenvalues for additive genetic matrices increased with higher orders of polynomials. By using Eigenvalues and eigenvectors it is possible to provide potential for genetic change in average daily milk yield of whole population and also select for persistency (Togashi and Lin, 2008). The first three eigenvalues which are higher in all orders of additive genetic coefficient matrix and the total amount of all eigenvalues is shown in Table 3. In other word, in all models the first three eigenvalues of the additive genetics covariance function accounted for at least 97% of the sum of all eigenvalues but the first three eigenvalues for permanent environment effect accounted at least 95% of total variation data was not shown. It means that little variation was associated to the other eigenvalues especially for additive genetic effects. (Togashi and Lin, 2008) showed that the main three eigenvalue and associated eigenfunction explain the highest additive genetic variance independent of polynomial order should be utilized. In models LE333, LE444 and LE555 the average percent of the first eigenvalue was 93.53%, in models WL33, WL44, WL55 the average was 85.38% and in models AS33, AS44 and AS55 the average first eigenvalues was 91.98%. The size of the first eigenvalue indicated that selection would produce rapid change if this kind of alternation in the mean trajectory was favored (Kirkpatrick *et al.*, 1990). (Druet *et al.*, 2003) reported that the higher first eigenvalue and associated eigenfunction can be used for selection and evaluation of the best model in random regression analysis which resulted quick change on average milk yield and because of biological sense of the first eigenfunctions, it is possible to use it the in selection and evaluation of RRM models. They also pointed out that the first eigenvalue and related eigenfunction might represent the average lactation potential. The use of eigenfunction for selection of the models as proposed by (Van der Werf, 1998) would result in fewer genetic parameters and equation as well as better convergence in mixed model equations. With

respect to this finding, the performance of LE444, LE555 and AS33 models are the optimum but quadratic form Legendre polynomial with three regression coefficients AS33 is more parsimonious and flexible enough with low residual variance during lactation as well as better convergence properties so it can be selected as the best model in this study. This is in agreement with the result of (Lopez Romero *et al.*, 2003) which showed the better performance of Legendre polynomial for random part compare to parametric lactation curve of Wilmink and Ali and Schaeffer. Higher order of polynomials enormously increases computational demands.

The additive genetic eigenfunctions for the AS33 model are shown in Figure 4. The first eigenfunction was positive between 0.3 - 0.83 over lactation. This eigenfunction corresponds to the largest eigenvalue in this model which was positive through lactation and did not show any dramatic change between lactation stages. (Bignardi *et al.*, 2008) observed that the first eigenfunction was always positive and constant throughout lactation. Positive value imply that selection for increased milk yield at any stage of lactation is likely to increase milk yield at all other days in milk. eigenfunction also represent the average lactation potential of the animal (Druet *et al.*, 2003) and also shows the positive genetic correlation between stages of lactation (Olori *et al.*, 1999). The second eigenfunction is associated with the eigenvalue 0.63 and accounted only 4.12% of the total genetic variance. This eigenfunction is negative at the first of lactation up to 175 d and positive during the later days. In this case, a selection before 175 d of days in milk for increasing milk yield, leads to a negative effect on this trait from 175 to 305 d of lactation and selection of cows between 180 and 220 d will improve both milk production and persistency. (Faro *et al.*, 2008) reported the same trend for the second eigenfunction and antagonistic relationship between initial and later milk yield. The third eigenfunction which is less important (Togashi *et al.*, 2008) in milk production, explained 2.26% of the genetic variance. This eigenfunction also shows that there are contrasts between milk yield at the beginning, mid and the end of lactation (Druet *et al.*, 2003).

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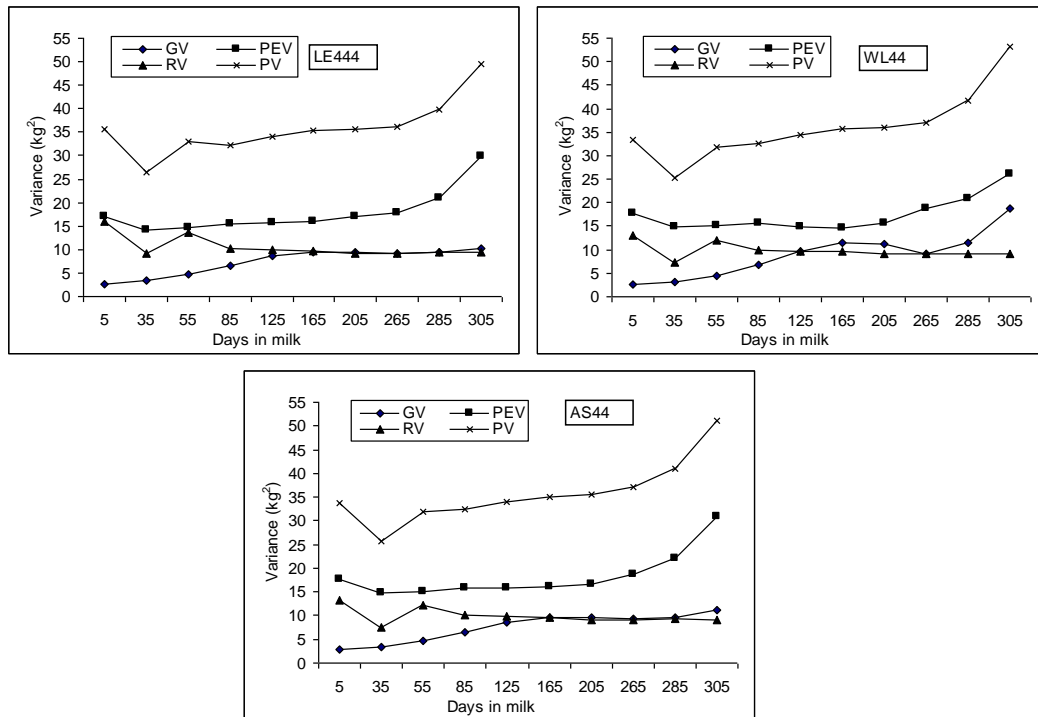


Fig. 2: Estimation of additive genetic (GV), permanent environment (PEV), phenotypic (PV) and residual (RV) variance in the models LE444, WL44 and AS44 during lactation period.

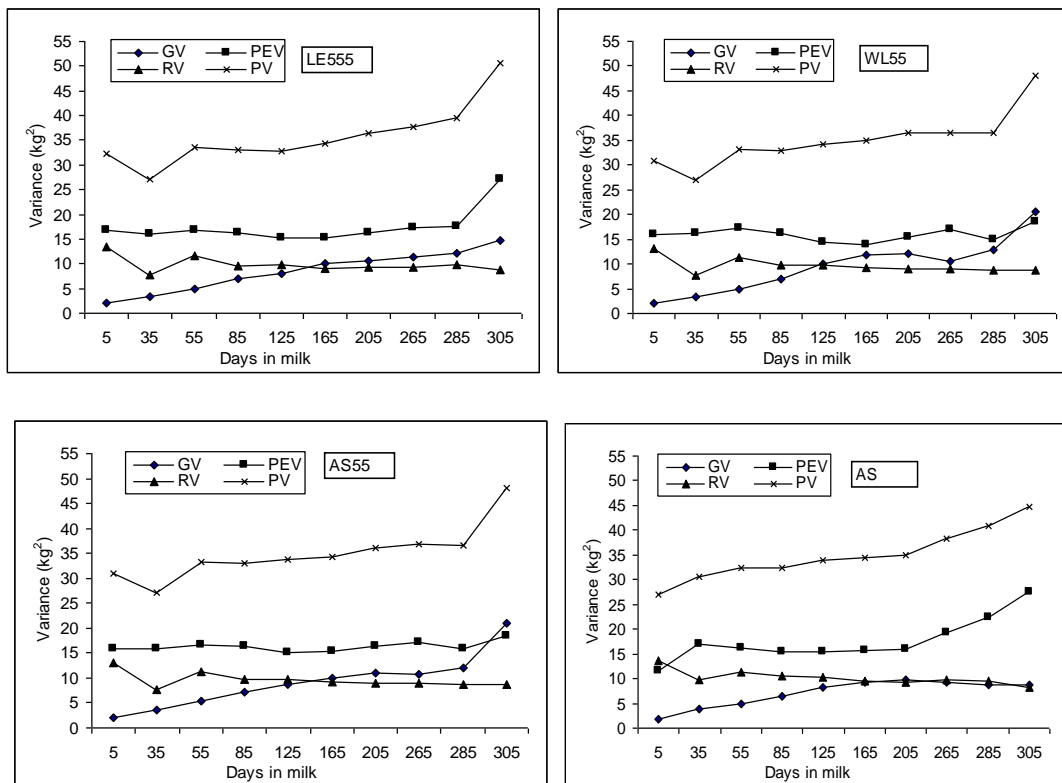


Fig. 3 : Estimation of additive genetic (GV), permanent environment (PEV), phenotypic (PV) and residual (RV) variance in the models LE555, WL55, AS55 and AS during lactation period.

Table 3: The first three eigenvalues, total amount of all eigenvalues and proportions of total variability for additive genetic effect in models with different order of Legendre polynomials.

Model	Eigenvalues			Total	Proportion %		
	First	Second	Third		First	Second	Third
LE333	14.11	0.62	0.37	15.1	93.44	4.10	2.45
LE444	14.49	0.56	0.32	15.46	93.72	3.63	2.06
LE555	16.17	0.65	0.36	17.31	93.43	3.74	2.05
WL33	15.03	1.66	0.57	17.26	87.07	9.61	3.30
WL44	14.68	2.09	0.55	17.44	84.17	12	3.13
WL55	15.83	2.10	0.55	18.65	84.87	11.22	2.94
AS33	14.24	0.63	0.34	15.21	93.62	4.12	2.26
AS44	14.43	0.59	0.36	15.56	92.76	3.80	2.28
AS55	15.73	1.17	0.41	17.57	89.56	6.66	2.24
AS	68.60	6.47	1.57	76.64	89.50	8.44	2.04
WL	18.98	1.66	0.0	20.64	91.95	8.04	0.00

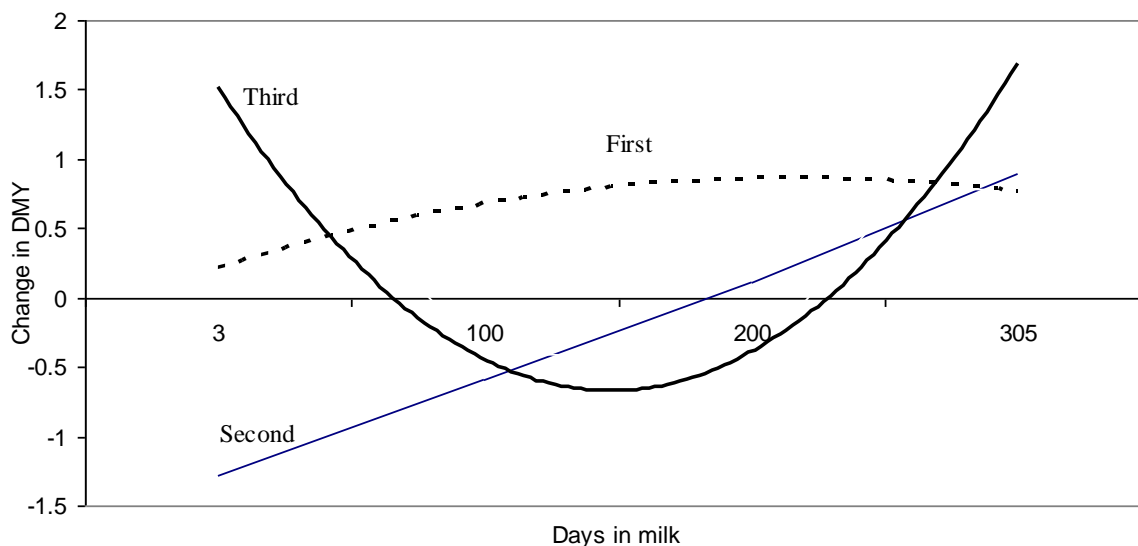


Fig. 4: Additive genetic eigenfunctions estimated by model AS33.

In general, heritability of LE33, AS33, LE444, AS44 and LE555 models were low at the first of lactation, rose toward the middle of lactation and then decreased again at the end of days in milk Figure 5. The rates of decrease in these models are different. In the models WL33, WL44, WL55 and AS55 after day 265 the heritability increased again till the end of days in milk. Low heritability could have been due to low milk production, stress of calving and energy deficit which are important especially at the beginning of lactation (Bignardi *et al.*, 2008). The highest heritability was shown in the middle of lactation between 180 to 205 days.

Several authors also reported the highest heritability in the middle of lactation (Swalve, 1995; Druet *et al.*, 2003; Jakobsen *et al.*, 2002; Szyda, 2001; Misztal *et al.*, 2000). The relatively low heritability at the end of lactation could be the result of small number of records and high permanent environmental variance. The estimation of heritability in all models increase from 0.07 at the beginning of lactation and maximize around 205 d (0.25 to 0.35) and then decrease till the end of lactation. The range of heritability over days in milk in this study was similar to those of (Olori *et al.*, 1999) but lower than (Jakobsen *et al.*, 2002). In the

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latter study residual variance was assumed homogeneous during lactation. Generally, different heritability and genetic parameters among population are related to variation in genetic

potential of milk production, climate changes, herd management, statistical models and estimation methods of co variance.

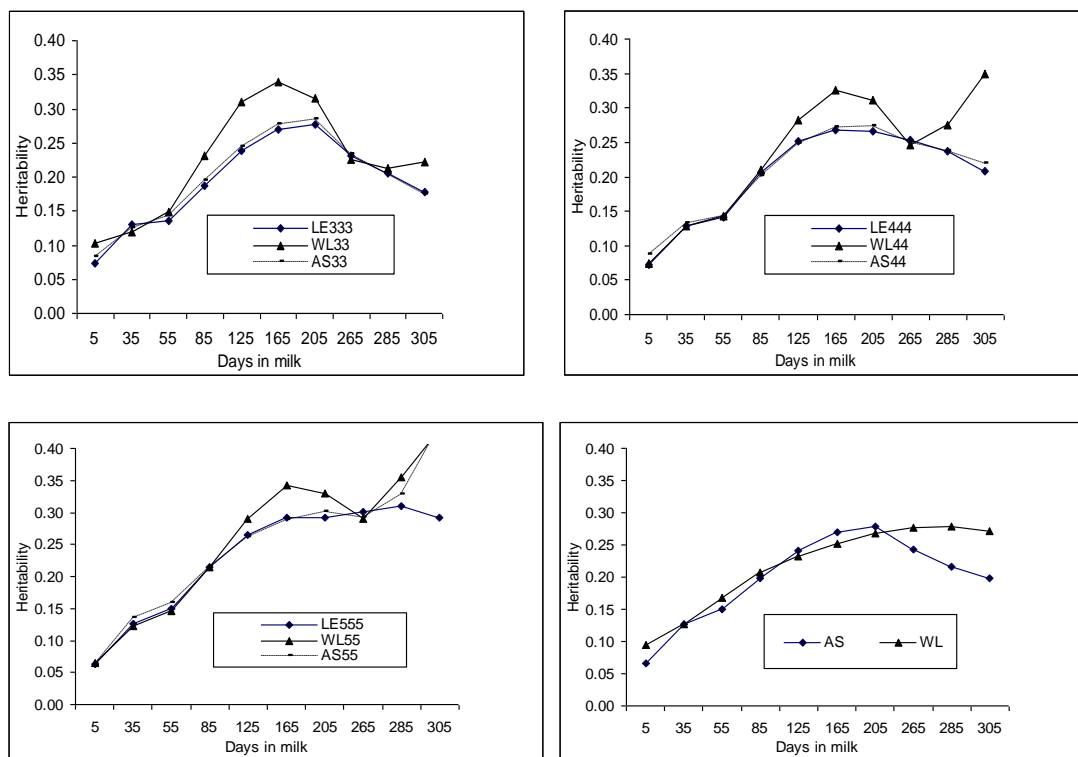


Fig. 5: Estimation of heritability for test day milk yield during lactation in different models.

The heritability in WL33, WL44 and WL55 models was higher compared to other models in the middle and the end of lactation as a result of overestimation of additive genetic variance. (Melo *et al.*, 2007) reported that heritability estimate using Wilmink was higher than those estimated by Ali & Schaeffer and combination of Wilmink and Legendre polynomial especially at the end of lactation. In that study Wilmink model showed convergence problem and Ali and Schaeffer function was superior to other models. Over estimation of heritability is one of the main problems to fit test day milk yield using random regression models (Costa *et al.*, 2008). Heritability estimates were lower in this study in LE333, LE444 and LE555 models than those reported by (Olori *et al.*, 1999) when they assumed the permanent environmental variance was heterogeneous. Medium to high heritability estimates for AS33 model Figure

5 indicate opportunities for genetic gain by selection in this time for primiparous dairy cattle.

Estimates of correlation for additive genetic and permanent environmental effects at different days in milk for AS33 model are presented in Table 4. Permanent environmental correlation between different test days followed a similar pattern as the additive genetic correlations. In general, genetic and permanent environmental correlations between close test days are higher and gradually decline as the distance between test days increase. The correlation between permanent environmental effects decreased much faster than additive genetic effects as test days became more apart (Table 4). The reason is related to high permanent environmental variance during lactation especially at the end of lactation. This means that the effect of environmental variance during DIM is considerable and it should not assume fixed during lactation. (Lopez Romero *et al.*, 2003) reported that higher

order of permanent environment effect produced more improvement than the increasing additive genetic effects. These results agree with those

reported by (Cobuci *et al.*, 2005 and Kettunen *et al.*, 2000).

Table 4: Genetic correlation (above the diagonal) and permanent environment correlation (below the diagonal) between daily milk days at day 5, 35, 55, 85, 125, 165, 205, 265, 285 and 305 in AS33 model.

		DIM								
DIM	5	35	55	85	125	165	205	265	285	305
5		0.901	0.798	0.673	0.527	0.520	0.502	0.511	0.518	0.519
35	0.958		0.980	0.927	0.869	0.833	0.811	0.773	0.745	0.694
55	0.892	0.948		0.984	0.949	0.923	0.902	0.847	0.806	0.741
85	0.775	0.923	0.976		0.991	0.976	0.959	0.894	0.843	0.766
125	0.636	0.826	0.910	0.977		0.996	0.984	0.921	0.868	0.787
165	0.540	0.740	0.837	0.927	0.983		0.995	0.944	0.896	0.819
205	0.575	0.656	0.748	0.842	0.920	0.974		0.970	0.932	0.867
265	0.387	0.471	0.518	0.576	0.657	0.760	0.885		0.992	0.962
285	0.352	0.392	0.416	0.453	0.525	0.639	0.791	0.985		0.988
305	0.317	0.313	0.314	0.329	0.390	0.508	0.681	0.943	0.987	

Additive genetic correlation ranged from 0.502 between first and the last test day and close to unity between adjacent test days but the range of permanent environment correlation is between 0.313 and 0.987. Decreasing of genetic and permanent environmental correlation between beginning and the end of lactation show that modeling of additive and permanent environmental effects by Random regression coefficients are necessary for genetic data analysis compare to repeatability and fixed regression method. When the genetic and permanent environmental correlation between different tests days are close to unity, repeatability model is superior and it has less parameters compare to random regression model (Strabel and Misztal, 1999). The pattern of variation in permanent environment correlation is the same with the other studies (Biassus *et al.*, 2010). Graphic illustrations of phenotypic and genetic correlation between test day milk yields for AS33 are shown in Figure 6. (Danell, 1982) reported that when the genetic correlation between different parts of the lactation curve of cows is less than one, the shape of the lactation curve is not the same for all cows. Moreover, genetic correlations among yields in different stages are positive and higher than 0.5 and suggesting that selection for increased milk yield in each part of lactation have a positive effect on milk yield in the other parts lactation.

(Jakobsen *et al.*, 2002) also reported positive genetic correlation with value above 0.4 for milk trait. Phenotypic correlations estimated between milk yields obtained at consecutive days were positive ranged from 0.240 to 0.771 but they were decreased as the interval between tests days increased. The reason of this diminish could be due to reduction in common environmental effects between two test day measurements and variation of milk production across lactations in each animals.

Genetic correlation between 30, 150 and 250 days and the other days in milk was shown in Figure 7. Low genetic correlation at the beginning and the end of trajectory was shown in this graphs which similar to heritability. The Closer test days to 30, 150 and 250 d, the higher genetic correlation were shown in this Figure. This figure also shows that genetic Correlations were greater during mid lactation than during early or late lactation.

Various results of genetic correlations in different studies probably related to the fixed part of lactation curve including different environmental factors and lactation curve functions in random regression analysis (Druet *et al.*, 2003). Moreover, high genetic correlations between adjacent test days imply that both traits are influenced by similar genes (Ilatsia *et al.*, 2007). Phenotypic correlations between test day milk yields were lower than additive genetic correlations. (Kominakis *et al.*, 2001; Kettunen *et al.*, 2000) reported the same trend

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for phenotypic correlation of milk trait in dairy sheep and Ayreshire cows respectively. They

mentioned that this decline is more evident in the first lactation.

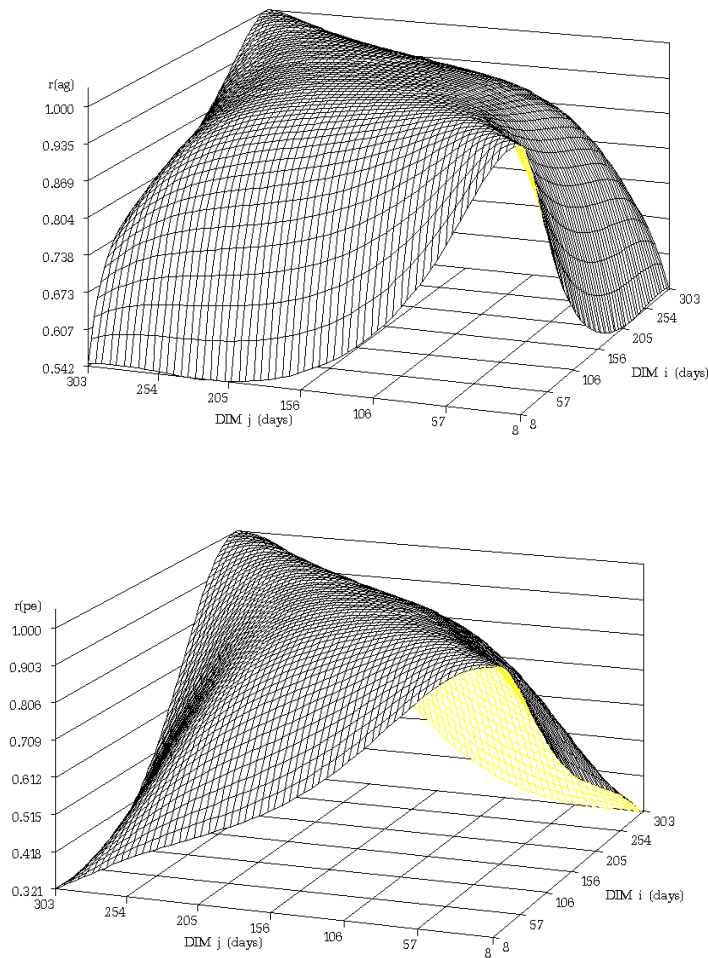


Fig. 6: Genetic correlation (r_g) above and phenotypic correlation (r_p) below between different test day milk yields using Quadratic order of Legendre polynomial AS33.

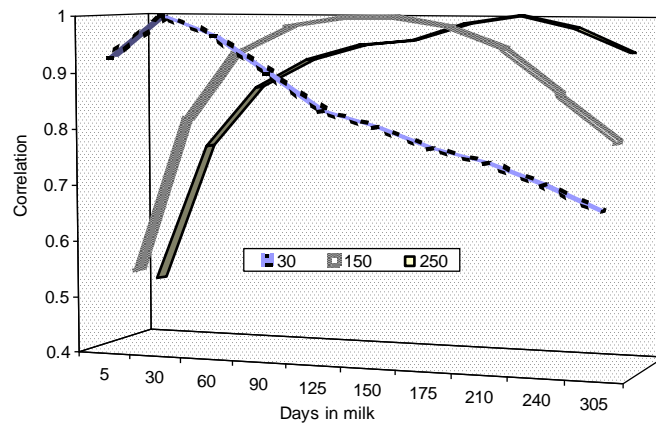


Fig. 7 : Genetic correlation between day milk yields at 30, 150 and 250 days in milk and the remaining part of lactation in model AS33.

Conclusion

Genetic parameters for random regression test day models with different fixed and random parts functions including parametric function and Legendre polynomials in Iranian Holstein were estimated in this study. The Residual variance, Eigenfunctions and corresponding eigenvalues were calculated for covariance matrices of random regression coefficients to evaluate the models. It is necessary to consider heterogeneity of residual variance to model the change in variance during lactation especially at the beginning of lactation in Iranian Holstein. Increasing the order of Legendre polynomial provided better fit of the data. Because of computational limitation in random regression model, using lower order has preference. Different among the optimal models LE333, LE444 and AS33 models are negligible but according to criteria utilized a lower order for both additive genetic and permanent environmental effects are enough. Model AS33 is suitable and selected as the best for genetic parameter estimation in Iranian primiparous Holstein. The main three eigenvalues for additive genetic effects were responsible for 99.9% of total variation. Using Legendre polynomial, the highest heritability estimation 0.28 was observed at the middle of lactation between 180 and 205 d. in model AS33, higher values of additive genetic variance obtained in the middle of lactation and lower values at the extremes but for permanent environmental variance in this model the higher and lower values observed in the extremes and the middle of lactation respectively. Genetic correlation estimates ranged between 0.51 to 0.99. the higher and lower genetic correlation observed between adjacent test days in middle of lactation and at the beginning and at the end of lactation respectively.

Acknowledgement

The Centre of Animal Breeding of Iran is greatly acknowledged for providing the data used in this study.

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