

Original study

Estimation of genetic parameters and trends for milk fat and protein percentages in Iranian Holsteins using random regression test day model

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Abstract

The aim of the present study was to estimate the genetic parameters and trends for fat and protein percentages of milk in Iranian Holsteins calving between 2001 and 2010 using the random regression test day model. Data set included 505 160 test day records that were collected by the Animal Breeding Centre of Iran. The Legendre polynomial functions of orders (5, 5) and (5, 6) were chosen to fit the additive genetic and permanent environmental effects of fat and protein percentages, respectively. Estimated heritabilities ranged from 0.053 to 0.232 and 0.111 to 0.259 for fat and protein percentages, respectively. The averages of estimated breeding values were -8.61 and -3.15 and annual genetic trends were -0.74 kg and -0.64 kg for fat and protein percentages, respectively. Negative genetic trends for fat and protein percentages are likely the result of major emphasis on milk yield in the breeding plan of Iranian Holsteins.

Keywords: genetic correlation; genetic progress; dairy cow; productive performance

Introduction

The aim of animal breeding is to genetically improve livestock populations for production of more efficient animals to guard against future circumstances. Accurate prediction of breeding values of animals is one of the best tools available for maximising response to selection program (Yousefi-Golverdi *et al.* 2012). To predict the breeding values it is necessary to know the genetic parameters of important traits or to estimate them using a model similar to the

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model of animal evaluation. In the most developed countries, the estimation of variance components from an animal model with restricted maximum likelihood method is spread due to its favourable features and flexibility (Interbull 1992, Kennedy *et al.* 1988).

In dairy farms, milk traits are recorded at various times along with lactation and each cow is expected to have about ten daily records per lactation. In traditional methods of genetic evaluations the daily tests would be transformed to a measure for the whole lactation and there will be one record for each animal per lactation. This will decrease the amount of data and cause computational parsimony. But nowadays, thanks to the progress in computer hardware technology, the analysis of large amounts of data has become feasible (Abdollahpour *et al.* 2010, Szyda & Liu 1999) and then test day models has been developed which can use test day data directly (Abdollahpour *et al.* 2010).

Some advantages of test day models are a greater flexibility about milk recording programs (Schaeffer *et al.* 2000), accounting more accurately for environmental factors that affect cows at different stage of lactation at the time of test (Jamrozik & Schaeffer 1997, Jensen 2001, Schaeffer *et al.* 2000, Swalve 2000), modelling the shape of the lactation curve (Schaeffer *et al.* 2000, Silvestre *et al.* 2005), increasing the accuracy of genetic evaluations, accounting the number of records per cow and the interval between records (Pool & Meuwissen 1999), decreasing the costs of milk recording by making fewer measurements (Pool & Meuwissen 1999), flexibility and the potential to slightly reduce the generation interval by frequent genetic evaluations (Swalve 2000).

The random regression model is presented by Henderson in 1982. Schaeffer & Dekkers (1994) used the random regression model for the analysis of test day milk records. Meyer (2004) showed that increase in the amount of data from each animal and the use of random regression model would increase the accuracy of genetic evaluation. In addition, random regression model describes in a continuous manner the structure of covariances over time and allows the estimation of breeding values for total or partial lactation yield, in contrast to multi-trait models which provide point predictions (Bignardi *et al.* 2009). In general, the Legendre polynomials have largely been used to fit random curves due to their ability of describing the variation along the period. They also avoid overparameterisation of genetic variances and heritability at the beginning and the end of curves (Brotherstone *et al.* 2000, López-Romero & Carabaño 2003, Bignardi *et al.* 2009). The results in the literature have shown that the parameter estimates are highly influenced by the order of the covariance functions used to describe the trends for the additive genetic and permanent environment effects and by the residual variance structure. (Meyer 1998).

The effect of selection on quantitative traits in genetic structure of population always has been considered by animal breeding experts. One of the ways for this purpose is the study of population genetic trends over the past years. Genetic trend evaluates genetic variations over time and also explains the variations of breeding values over consecutive years. A number of methods is available for estimating genetic trends in dairy cattle populations, using either planned selection experiments or data from commercial herds that use control group, regression method and animal model (Nizamani & Berger 1996, Yousefi-Golverdi *et al.* 2012). The precision of genetic trend estimates is enhanced greatly because the number of years, in which it has been studied, increases (Yousefi-Golverdi *et al.* 2012).

Although the subject of this study has been investigated by other researchers, the novel items in this study included the use of large data set and the interest of including milk constituents in the analyses. On the other hand, comparison of the current estimates of genetic parameters and trends for milk constituents in Iranian dairy herds with other dairy production systems could be interesting in this study. The aim of the present study was to estimate the genetic trend and genetic analyses of test day fat and protein percentages in Iranian Holstein cattle.

Material and methods

Data of 505 160 daily fat and protein percentage records of the first lactation of Holstein cows with calvings between 2001 and 2010 were obtained from the Animal Breeding Centre of Iran. Records were designated using Foxpro 8.0 and ACCESS 2007 software (Microsoft Corporation, Redmond, WA, USA) and the wrong and unusual records were removed from the dataset. Test day observations before day 5 and after day 400 were discarded. The records of cows were deleted if they had fewer than 8 or more than 12 daily fat and protein percentage records or their ages at first calving were below 20 months or above 36 months. All records belonging to the cows, whose sires had less than ten daughters or their herds comprised less than 150 cows, were removed. The pedigree comprised was including seven generations of sire and dam ancestors. Summaries of the pedigree information and the test day data are presented in Tables 1 and 2, respectively.

Table 1
Summary of the pedigree information

Variable	Number
Number of animals	125 115
Number of animals with record	54 960
Number of sires	2 357
Number of dams	79 937
Number of animals with progeny	82 294
Number of animals with progeny and record	12 139
Number of animals without progeny	42 821
Number of inbred animals	236

Table 2
Summary of test day information

Test day	Days in milk	Number of records	Fat		Protein	
			Mean	STD	Mean	STD
1	5-35	46 541	3.47	0.82	3.02	0.41
2	36-65	49 984	3.18	0.75	2.89	0.37
3	66-95	49 362	3.15	0.74	2.93	0.36
4	96-125	50 848	3.16	0.73	2.99	0.36
5	126-155	49 419	3.19	0.73	3.04	0.36
6	156-185	50 816	3.24	0.72	3.07	0.36
7	186-215	49 228	3.29	0.72	3.11	0.36
8	216-245	50 737	3.34	0.72	3.14	0.36
9	246-275	44 801	3.41	0.72	3.18	0.36
10	>275	63 424	3.52	0.74	3.27	0.38
Total	5-305	505 160	3.29	0.75	3.07	0.38

GLM procedure of SAS v9.1 software (SAS Institute Inc., Cary, NC, USA) was used for fitting the fixed effects in the statistical models of analysis. All analyses were performed using the random regression analyses of the WOMBAT v1.0 software package using AIREML algorithm on a Linux operating system (Meyer 2007).

Model

The following random regression model was used in the analysis:

$$Y_{imnptv} = HTD_m + \sum_{f=0}^2 C_f (age_n)^f + \sum_{r=0}^k \beta_r \Phi_r(dim_t) + \sum_{r=0}^{k_a-1} \alpha_{pr} \Phi_r(dim_t) + \sum_{r=0}^{k_p-1} \gamma_{pr} \Phi_r(dim_t) + e_{imnptv} \quad (1)$$

where Y_{imnptv} is the test day record i obtained at dim t of cow p calved at the n -th age in herd-test date m , HTD_m is the fixed effect of m -th herd-test date, C_f is the f -th fixed regression coefficient for calving age, age_n is the n -th calving age, k is the order of fit for fixed regression coefficients ($k=2$), β_r is the r -th fixed regression coefficient, k_a is the order of fit for additive genetic random regression coefficients, k_p is the order of fit for permanent environmental random regression coefficients, α_{pr} is the r -th random regression coefficient of additive genetic value of p -th cow, γ_{pr} is the r -th random regression coefficient of permanent environmental effect of p -th cow, $\Phi_r(dim_t)$ is the r -th coefficient of Legendre polynomials evaluated at days in milk t and e_{imnptv} is the random residual error.

Measures of 305 d yields

The estimated breeding value (EBV) of animal p for day t was calculated by:

$$EBV_{pt} = \sum_{r=0}^{k_a-1} \alpha_{pv} \Phi_r(dim_t) \quad (2)$$

where EBV_{pt} is the breeding value of cow p at dim t , α_{pv} is the random regression coefficient of additive genetic value of p -th cow, $(dim_t)\Phi$ is the r -th coefficient of Legendre polynomials evaluated at days in milk t .

Therefore, the EBV of animal p for 305 d yields was obtained by summing the EBVs from day 5 to day 305.

$$EBVm = ZC_{305} \alpha_p \quad (3)$$

where α_p is the random regression coefficient of additive genetic value of p -th cow and ZC_{305} is a vector of the summations of Legendre polynomials corresponding to total lactation milk production. ZC_{305} was used for both traits under study as follows: $ZC_{305} = [212.84 \quad -88.66 \quad -58.49 \quad -13.04 \quad 22.25]$

After predicting the breeding values of animals for 305 d yields, the genetic trends of test day fat and protein percentages were calculated using the regression of the means of breeding values on the years. Genetic trend analyses were performed with the regression procedure of the SAS v9.1 software package (SAS Institute Inc., Cary, NC, USA).

Results and discussion

In order to achieve the appropriate random regression model for the analysis of test day fat and protein percentages with the minimum number of parameters to estimate additive genetic and permanent environmental parameters, different orders of fit for random regression coefficients of additive genetic and permanent environmental effects were evaluated. These models are presented in Table 3.

Table 3

Different orders of fit for random regression coefficients in this study

Model	Order of fit		np	logl _{fat}	logl _{protein}
	ka	kpe			
1	3	3	13	–39 354.590	402 203.760
2	3	4	17	–38 283.342	404 519.719
3	3	5	22	–37 428.645	407 466.956
4	3	6	28	–37 015.541	409 554.583
5	4	4	21	–36 534.795	406 060.751
6	4	5	26	–36 021.878	408 193.033
7	4	6	32	–35 659.164	410 164.437
8	5	5	31	–35 293.538	410 601.607
9	5	6	37	–35 057.758	411 791.906

ka, kpe: orders of fit for additive genetic and permanent environmental effects, respectively; np: number of parameter for estimated variance function; logl: maximum log likelihood

In models with different orders of fit for additive genetic and permanent environmental effects, the increase in the maximum log likelihood improved the fit of the model and reduced the residual variances (Liu *et al.* 2006, Meyer 2000, Sesana *et al.* 2010). In the present study, estimates of residual variance decreased as the order of the model increased. Models 8 and 9 were chosen to fit the additive genetic and permanent environmental effects for the analysis of fat and protein percentages, respectively. The maximum log likelihood of model 8 for fat had significant difference with other models, but this model had no significant difference with model 9, considering the higher order of fit for the random effects in model 9. Therefore, the Legendre polynomial functions of orders (5, 5) and (5, 6) were chosen to fit the additive genetic and permanent environmental effects of fat and protein percentages, respectively.

Parameters

Estimates of additive genetic and permanent environmental (co)variances of random regression coefficients for test day fat and protein percentages are presented in Tables 4 and 5, respectively.

As indicated in Figure 1, additive genetic and permanent environmental variances had the highest amounts in the early days of lactation for fat. For protein percentage, additive genetic variances increased in the first and last days of lactation (Figure 2), whereas permanent environmental variances were the highest at the beginning of lactation. Based on the results of Meyer *et al.* (2004) and Zavadilová *et al.* (2005) on Holstein cows, the highest additive genetic and permanent environment variances for dairy traits occurred in the first and last days of lactation (Interbull 1992).

Table 4
Estimates of genetic and permanent environmental variances (diagonal), covariances (below diagonal) and correlations (above diagonal) for random regression coefficients of test day fat percentage

Additive genetic coefficients						Permanent environmental coefficients					
	a ₀	a ₁	a ₂	a ₃	a ₄		P ₀	P ₁	P ₂	P ₃	P ₄
a ₀	0.0647	0.4200	−0.3918	0.2743	−0.2789	P ₀	0.0595	0.1030	−0.1329	−0.3541	0.0909
a ₁	0.001	0.0087	0.0580	0.2831	−0.2789	P ₁	0.0041	0.0262	0.0201	−0.1616	0.0318
a ₂	−0.0068	0.0004	0.0046	−0.3908	0.3661	P ₂	−0.0045	0.0004	0.019	−0.4044	0.4321
a ₃	0.0062	0.0023	−0.0024	0.0078	−0.9930	P ₃	−0.0055	−0.0016	−0.0035	0.004	0.3864
a ₄	0.0061	−0.0022	0.0022	−0.0076	0.0074	P ₄	0.0021	0.0005	0.0057	0.0023	0.0093

Table 5
Estimates of genetic and permanent environmental variances (diagonal), covariances (below diagonal) and correlations (above diagonal) for random regression coefficients of test day protein percentage

Additive genetic coefficients						Permanent environmental coefficients						
	a ₀	a ₁	a ₂	a ₃	a ₄		P ₀	P ₁	P ₂	P ₃	P ₄	P ₅
a ₀	0.0219	0.5482	−0.3398	−0.2572	−0.0473	P ₀	0.0150	0.2046	0.0653	−0.0608	−0.0880	−0.1156
a ₁	0.0069	0.0072	−0.0821	−0.2630	0.0175	p ₁	0.0021	0.0067	0.2211	0.2298	−0.6627	0.0290
a ₂	−0.0017	−0.0002	0.0011	−0.6723	0.5789	P ₂	0.0006	0.0013	0.0050	0.1995	−0.1039	−0.0748
a ₃	−0.0005	−0.0003	−0.0003	0.0002	−0.4506	P ₃	−0.0006	0.0015	0.0011	0.0065	0.5517	0.6706
a ₄	−0.0004	0.0001	0.0011	−0.0003	0.0032	P ₄	−0.0002	−0.0012	−0.0002	0.0065	0.0005	0.4322
						P ₅	−0.0010	0.0002	−0.0004	0.0038	0.0007	0.0051

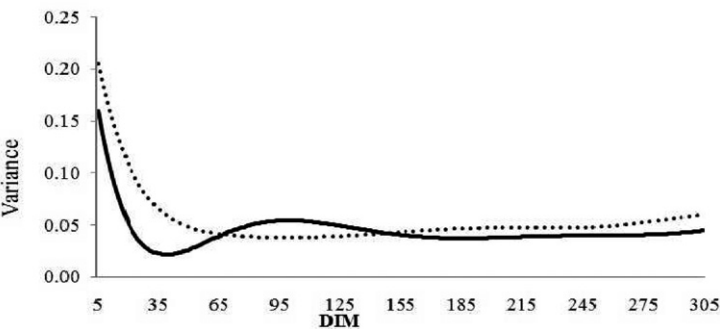


Figure 1
Additive genetic (line) and permanent environmental variances (dash) for test day fat percentage over the lactation

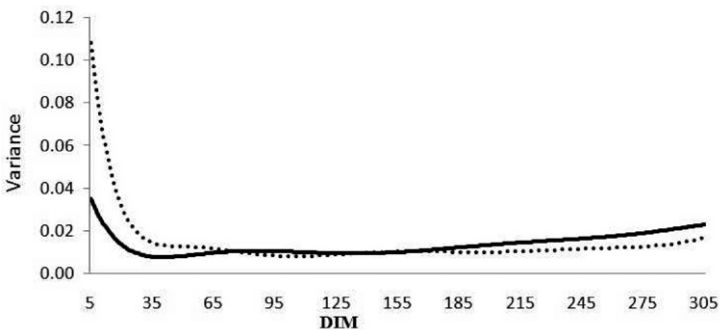


Figure 2
Additive genetic (line) and permanent environmental variances (dash) for test day protein percentage over the lactation

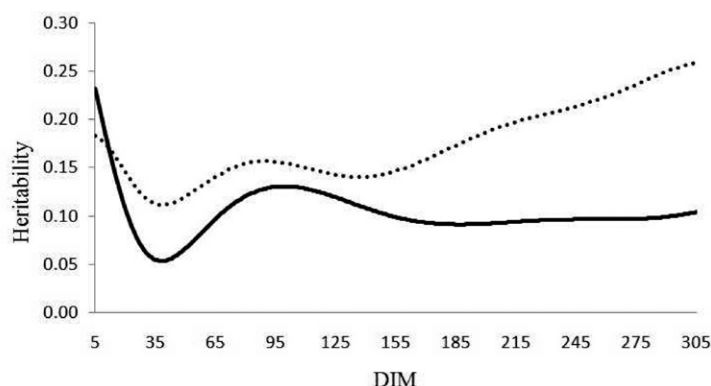


Figure 3
Heritability estimates
for fat (line) and protein
(dash) percentages during lactation

Estimates of heritabilities for fat and protein percentages are presented in Figure 3. Heritability estimates for daily fat and protein percentage records ranged from 0.053 to 0.232 for fat percentage and 0.111 to 0.259 for protein percentage. Repeatability estimates for these traits ranged from 0.187 to 0.529 and 0.272 to 0.745, respectively. Abdullahpour *et al.* (2010) reported on heritabilities of 0.07 to 0.11 and 0.11 to 0.18 and repeatabilities of 0.12 to 0.19 and 0.17 to 0.28 for fat and protein percentages, respectively. Jamrozik & Schaeffer (1997) reported on heritabilities of 0.10 and 0.25 for fat and protein yields, respectively. The heritability estimate for fat percentage was the highest at the beginning of lactation and the heritability estimate for protein percentage was the highest at the end of lactation.

In the present study, the heritability estimates for fat percentage were lower than those for protein percentage over the lactation. Consistent with the current results, Abdullahpour *et al.* (2010), DeGroot *et al.* (2007), Druet *et al.* (2004), Hammami *et al.* (2008) and Silvestre *et al.* (2005) reported lower heritability estimates for milk fat during lactation. The characteristics of fat in the way of being much influenced by temporary environmental effects may be the main reason for its lower heritability (Abdullahpour *et al.* 2010). In addition, since the determination of milk fat and protein percentage requires the application of special laboratory equipment, any measurement error in calculating the percentage of milk fat and protein samples increases the error variance and thus reduces the estimate of heritability for the trait. Estimated parameters for 305 d yields are presented in Table 6.

Table 6
305 d yield parameters for fat and protein percentages in this study

	Additive genetic variance	Permanent environmental variance	Residual variance	Phenotypic variance	Heritability	Repeatability	Mean of EBV
fat	13.23	16.17	97.83	127.24	0.10	0.23	-8.61
protein	4.05	4.26	14.73	23.05	0.18	0.36	-3.15

Genetic trends

The annual genetic trends (standard error) for milk fat and protein percentages in Iranian Holstein cattle were -0.74 kg (0.054) and -0.64 kg (0.033), respectively. Genetic trends were

negative and significant ($P < 0.01$) for both traits. Estimates of genetic trends for both traits are presented in Figure 4. Abdullahpour *et al.* (2010) also reported on negative genetic trends for milk fat and protein percentages in Iranian Holsteins. Negative genetic trends for fat and protein percentages are likely the result of major emphasis on milk yield and neglecting fat and protein percentages in the sire selection at the level of farms during past years. This condition could cause a correlated response for fat and protein percentages as the result of selection for milk because of the probably negative correlation between milk yield and milk fat and protein (Abdullahpour *et al.* 2010). Hashemi & Nayeypoor (2008) reported on negative genetic correlation between milk yield and fat and protein percentages in Iranian Holstein population. Freitas *et al.* (1995) estimated a genetic trend of -0.22 and -0.21 kg for fat and protein yields in the Brazilian dairy cattle. Kunaka & Makuza (2005) reported on genetic trends of 0.127 and 0.39 kg for fat and protein yields. These reports are in contrast with the results of the present study. This discrepancy is probably due to the difference between years of procurement records for these studies. Phenotypic trends (standard error) for fat and protein percentages in this study were -0.007 kg (0.0004) and -0.003 kg (0.0002), respectively. The phenotypic trend (figure 5) for both traits was negative and significant ($P < 0.01$). Considering the negative phenotypic trends for the traits in this study, negative genetic trends did not seem unreasonable.

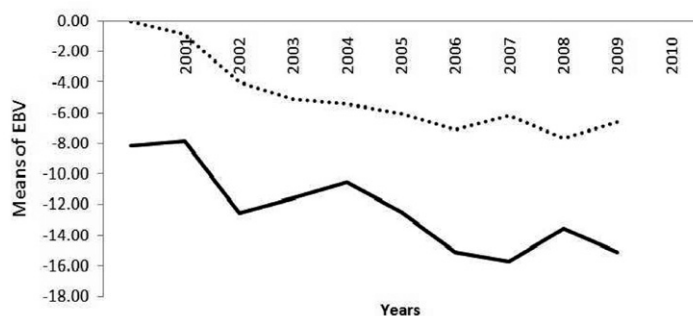


Figure 4
Genetic trend for fat (line) and protein (dash) percentages

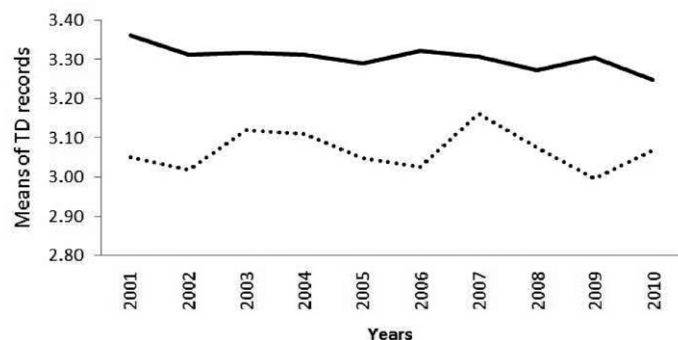


Figure 5
Phenotypic trend for fat (line) and protein (dash) percentages

In conclusion, the results of the present study indicate that heritability of fat percentage was the highest in the beginning days, third and fourth months of lactation and heritability of protein was the highest in the last months of lactation. Therefore, it was suggested to select for these traits in these periods of lactation. The relatively low heritability estimates obtained in this study indicate that studied traits are more influenced by environmental factors than by genetic effects. Negative genetic trends for fat and protein percentages are likely the result of major emphasis on milk yield and neglecting fat and protein percentages in the sire selection at the level of farms during past years. Therefore, studied traits have not been considered to be improved in the breeding program.

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References

- Abdollahpour R, Moradi Shahrbabak M, Nejati-Javaremi A, Vaez Torshizi R (2010) Genetic Analysis of Daily Milk, Fat Percentage and Protein Percentage of Iranian First Lactation Holstein Cattle. *World Appl Sci J* 10, 1042-1046
- Bignardi AB, El Faro L, Cardoso VL, Machado PF, de Albuquerque LG (2009) Random regression models to estimate test-day milk yield genetic parameters Holstein cows in Southeastern Brazil. *Livest Sci* 123, 1-7
- Brotherstone S, White IMS, Meyer K (2000) Genetic modelling of daily yield using orthogonal polynomials and parametric curves. *Anim Sci* 70, 407-415
- DeGroot BJ, Keown JF, Van Vleck LD, Kachmen SD (2007) Estimation of genetic parameters for Holstein cows for test-day yield traits with a random regression cubic spline model. *Genet Mol Res* 6, 434-444
- Druet T, Jaffrézic F, Ducrocq V (2004) Estimation of genetic parameters for test day records of dairy traits in the first three lactations. *Genet Sel Evol* 37, 257-271
- Freitas JA, Silva RAG, Nascimento JAC (1995) [Características do leite fluido consumido em Belém, Pará]. *Arq Bras Med Vet Zootec* 47, 435-445 [in Portuguese]
- Hashemi A, Nayeypoor M (2008) Estimation of Genetic and Phenotype Parameters for Milk Production in Iran Holstein-Friesian Cows. *Res J Biol Sci* 3, 678-682
- Henderson CR Jr. (1982) Analysis of Covariance in the Mixed Model: Higher-Level, Nonhomogeneous, and Random Regressions. *Biometrics* 38, 623-640
- Hammami H, Rekik B, Soyeurt H, Ben Gara A, Gengler N (2008) Genetic Parameters for Tunisian Holsteins Using a Test-Day Random Regression Model. *J Dairy Sci* 91, 2118-2126
- Interbull (1992) Sire evaluation procedures for dairy production traits practiced in various countries. Bulletin No. 5. Department of animal breeding and genetics, SLU, Uppsala, Sweden
- Jamrozik J, Schaeffer LR (1997) Estimation of Genetic Parameters for a Test Day Model with Random Regressions for Yield Traits of First Lactation Holsteins. *J Dairy Sci* 80, 762-770
- Jensen J (2001) Genetic Evaluation of Dairy Cattle Using Test-Day Models. *J Dairy Sci* 84, 2803-2812
- Kennedy BW, Schaeffer LR, Sorensen DA (1988) Genetic Properties of Animal Models. *J Dairy Sci* 71, 17-26
- Kunaka K, Makuza SM (2005) Genetic and Environmental Trends for Milk Traits in the Zimbabwean Holstein-Friesian Population. *PJBS* 8, 1011-1015
- Liu YX, Zhang J, Schaeffer LR, Yang RQ, Zhang WL (2006) Optimal Random Regression Models for Milk Production in Dairy Cattle. *J Dairy Sci* 89, 2233-2235

- López-Romero P, Carabaño MJ (2003) Comparing alternative random regression models to analyse first lactation daily milk yield data in Holstein–Friesian cattle. *Livest Prod Sci* 82, 81-96
- Mayeres P, Stool J, Boormann J, Reents R, Gengler N (2004) Prediction of daily milk, fat, and protein production by a random regression test-day model. *J Dairy Sci* 87, 1925-1933
- Meyer K (2007) WOMBAT – A tool for mixed model analyses in quantitative genetics by restricted maximum likelihood (REML). *J Zhejiang Univ Sci B*. 2007 November; 8 (11), 815-821
- Meyer K (1998) Estimating covariance functions for longitudinal data using a random regression model. *Genet Sel Evol* 30, 221-240
- Meyer K (2004) Scope for a random regression model in genetic evaluation of beef cattle for growth. *Livest Prod Sci* 86, 68-83
- Meyer K (2000) Random regressions to model phenotypic variation in monthly weights of Australian beef cows. *Livest Prod Sci* 65, 19-38
- Nizamani AH, Berger PJ (1996) Estimates of Genetic Trend for Yield Traits of the Registered Jersey Population. *J Dairy Sci* 79, 487-494
- Pool MH, Meuwissen THE (1999) Prediction of Daily Milk Yields from a Limited Number of Test Days Using Test Day Models. *J Dairy Sci* 82, 1555-1564
- Schaeffer LR, Jamrozik J, Kistemaker GJ, Van Doormaal J (2000) Experience with a Test-Day Model. *J Dairy Sci* 83, 1135-1144
- Schaeffer LR, Dekkers JCM (1994) Random regressions in animal models for test-day production in dairy cattle. In: *Proc 5th World Congr Genet Appl Livest Prod* 18, Guelph, Ontario, Canada, 182-186
- Sesana RC, Bignardi AB, Borquis RRA, El Faro L, Baldi F, Albuquerque LG, Tonhati H (2010) Random regression models to estimate genetic parameters for test-day milk yield in Brazilian Murrah buffaloes. *J Anim Breed Genet* 127, 369-376
- Silvestre AM, Petim-Batista F, Colaço J (2005) Genetic Parameter Estimates of Portuguese Dairy Cows for Milk, Fat and Protein Using a Spline Test-Day Model. *J Dairy Sci* 88, 1225-1230
- Swalve HH (2000) Theoretical Basis and Computational Methods for Different Test-Day Genetic Evaluation Methods. *J Dairy Sci* 83, 1115-1124
- Szyda J, Liu Z (1999) Modelling test day data from dairy cattle. *J Appl Genet* 40, 103-116
- Yousefi-Golverdi A, Hafezian H, Chashnidel Y, Farhadi A (2012) Genetic parameters and trends of production traits in Iranian Holstein population. *Afr J Biotechnol* 11, 2429-2435
- Zavadilová L, Jamrozik J, Schaeffer LR (2005) Genetic parameters for test-day model with random regressions for production traits of Czech Holstein cattle. *Czech J Anim Sci* 50, 142-154