Comparison of Fitting Performance of Random Regression Models to Test Day Milk Yields in Holstein Friesians

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Summary

In this study, random regression models with Ali-Schaeffer functions, Wilmink functions and orthogonal Legendre polynomials were compared for fitting performance to test day milk yields. Legendre polynomials with orders from two to six for additive genetic and permanent environmental effects were fitted under homogeneous error variance assumption throughout lactation. The analyzes were applied to 5918 first lactation test day milk yields of 612 Holstein Friesian cows calving from 1987 to 1993 in Dalaman, Tahirova, Sarımsaklı and Türkgeldi State Farms. To compare the models, residual variances, -2LogL value, Akaike's information criterion, Bayesian information criterion and eigenvalues for additive genetic and permanent environmental random regression (co)variance matrix were used. Among 27 models, the L(6,2), L(6,5) and L(6,6) were chosen as better models.

Keywords: *Random regression model, Holstein Friesian, Test day milk yield*

Siyah Alacalarda Şansa Bağlı Regresyon Modellerinin Denetim Günü Süt Verimlerine Uyum Performanslarının Karşılaştırılması

Özet

Bu çalışmada Ali-Schaeffer fonksiyonu, Wilmink fonksiyonu ve ortagonal Legendre polinomiyal uygulanan şansa bağlı regresyon modellerinin denetim günü süt verimlerine uyum performansları karşılaştırılmıştır. Eklemeli ve kalıcı çevre etkileri için Legendre polinomiyal fonksiyonunun ikinci dereceden altıncı dereceye kadar uyumları yapılmış, hata varyansının ise laktasyon boyunca homojen olduğu kabul edilmiştir. Analizler, 1987 ile 1993 yılları arasında Dalaman, Tahirova, Sarımsaklı ve Türkgeldi çiftliklerinde buzağılayan, 612 adet Siyah Alaca'nın toplam 5918 ilk laktasyon kaydına uygulanmıştır. Modellerin karşılaştırılmasında, modelin hata varyansı, -2LogL değeri, Akaike ve Bayes bilgi kriterleri ile eklemeli genetik ve kalıcı çevre etkisine ait şansa bağlı regresyon (ko)varyans matrisinin özdeğerleri kullanılmıştır. Toplam 27 modelin karşılaştırılması sonucunda, L(6,2), L(6,5) ve L(6,6) modellerinin uyumu daha iyi bulunmuştur.

Anahtar sözcükler: *Şansa bağlı regresyon modeli, Siyah Alaca, Denetim günü süt verimi*

INTRODUCTION

The genetic evaluation of dairy sires and cows for milk traits has been based on the analysis of 305 day lactation yields for many years [1,2]. The genetic and environmental effects are considered as an overall effect for lactation [3]. However, the effects on milk yields change throughout lactation and cause variations.

Recently, test day models have been suggested for genetic evaluation of test day milk yields, instead of using 305 day milk yields [4,5]. Since the correct description of factors for each individual test day milk yield is possible, a higher genetic progress should be expected [6]. Accuracy of genetic evaluations depends on the amounts of information used and methods. For analysis of test day milk yields, several types of models are applied such as

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repeatability model, multivariate model and random regression model [7-11].

A repeatability model assumes genetic correlations between test days records are unity and also assumes constant additive genetic and permanent environmental variances throughout the lactation. In a multivariate model, test day records are considered as separate traits [12]. Random regression models are able to predict covariance structures among the test day points along a continuous scale [13]. Thus, the (co)variances between records for additive genetic and permanent environmental effects can be described by using different covariance functions as Ali-Schaeffer [14], Wilmink [15] or Legendre polynomials. The choice of the function influences number of parameters estimated and level of the estimated (co)variance component [16]. Legendre polynomials were commonly used to estimate (co)variance components due to their easy manipulation and good convergence properties [17].

However, there is no more information available for fitting performance of Legendre polynomials with different orders. In literature, several approaches were used for the order of fit in Legendre polynomial model. First one additive genetic effect had generally lower order of fit than that of permanent environmental effect [18-21]. Secondly, same order of fit was considered for additive genetic and permanent environmental effects ensuring flexible modeling for the variances [16,22,23]. Thirdly, in several studies, Legendre polynomials with third order of fit for additive genetic and permanent environmental effects were sufficiently accepted [5,18,19].

Therefore it is needed to compare Legendre polynomial models with all possible orders to determine the best fitting model to test day milk yields. This study was carried out to compare fitting performance of two lactational models (Ali-Schaeffer and Wilmink) and twenty five orthogonal Legendre polynomial random regression models with different order of fit to test day milk yields of Turkish Holstein Friesians.

MATERIAL and METHODS

Data set contained 5918 test day milk yields of 612 Holstein Friesian cows from four state farms (Dalaman, Tahirova, Sarımsaklı and Türkgeldi) in Turkey were analyzed. The cows, produced test day milk yields, were daughters of 92 sires and 130 dams, and calved from 1987 through 1993. Maximum ten test day records (TD1-TD10) were collected at almost successive monthly periods throughout first lactation. Lactation length was restricted to have at least 150 days and maximum 308 days long.

In this study, Ali-Schaeffer (ARR) and Wilmink (WRR) models and twenty five orthogonal Legendre polynomial models (LRR) were fitted for both additive genetic and permanent environmental effects with the DXMRR option of the DFREML statistical package [24]. Residual variance was assumed to be constant throughout lactation for reducing the number of parameters to be estimated and dimension of the likelihood searches. Different orders of fit for additive genetic (α_{jm}, m=2,.,6) and permanent environmental effects (p_{jm}, m=2,.,6) were compared under LRR models. The general random regression model used in this study is as follows:

$$y_{ijl} = HTD_i + \sum_{m=1}^{k_B} \beta_m X_m(t) + \sum_{m=1}^{k_A} \alpha_{jm}\varphi_m(t) + \sum_{m=1}^{k_p} p_{jm}\varphi_m(t) + e_{ijl}$$

where y_{ijk} is the kth test day milk yield of the cow j obtained at i^{th} herd-test day, HTD_i is the ith herd test day (in month), β_m is the mth fixed regression coefficients, $X_m(t)$ is the mth covariate for test day t. In Ali-Schaeffer function, $X_1=1$ $X_2=DIM/c$, $X_3=(X_2)^2$, $X_4=\ln(c/DIM)$, $X_5=(X_4)^2$ where C=305 and in Wilmink function $X_1=1$, $X_2=t$ and $X_3=\exp^{(-0.05t)}$. α_{jm} are the mth additive genetic random regression coefficients for cow j, p_{jm} are the mth permanent environmental random regression coefficients for cow j, φ_m is the mth polynomial evaluated for the age t_{ij}. k_B, k_A and k_p are the order of fit for fixed, random additive and random permanent regression coefficients and e_{ijk} is the random residual effect.

Goodness of fit for the models was examined using likelihood based criteria as -2LogL, Akaike's information criterion-AIC [25], Bayesian information criterion-BIC [26] and also residual variance (RV). AIC and BIC criteria are: AIC = -2 * LogL +2 * p and BIC = -2 * LogL + p * log(N - r(x)) where, p denotes the number of parameters estimated, N is the sample size and r(x) is the rank of the coefficient matrix for fixed effects in the model. The model giving the lower -2LogL, AIC, BIC and RV values is chosen as the better approximating model [20, 27].

Random regression legendre polynomial models are nested models, which allows Chi-square (χ^2) tests over the likelihood ratios to find out the order of polynomial up to where a significant improvement on the model likelihood can be achieved [20]. Therefore, the Legendre polynomial models were compared by Likelihood ratio test (LRT) [28]. Calculation of LRT for model i and j was $LRT_{ij} = 2 * (LogL_i - LogL_j)$. In the LRT, the LogL difference is tested using χ^2 test with the degrees of freedom determined as the number of the parameter differences between the models [29]. Two LRT tests were applied for model comparison. In the first LRT test (called LRT-1), the models with varying order of fit for permanent environmental effects were tested under fixed order of fit for additive genetic effects. In the second LRT test (called LRT-2), likelihood values from models with varying order of fit for additive genetic effects were tested under fixed order of fit for permanent environmental effects. Moreover, eigenvalues of additive genetic, permanent environmental random regression (co)variance matrix were examined to discuss the goodness of fit for the models [18-20].

RESULTS

Level of criteria (-2LogL, LRT, AIC, BIC and RV) for the models were given in Table 1. Values of the AIC, BIC and -2LogL were changed between 16908 and 18484. The values of the criteria were decreased when the order of fit for the effects were increased in the models. The WRR model had the highest values for -2LogL, AIC, BIC and RV (18424, 18456, 18484 and 5.6, respectively). ARR model had generally higher values than that of LRR models except L(2,2), L(2,3), L(3,2) and L(3,3) models. Due to these results, it could be said that the performance of WRR and ARR models was worse than LRR models [Table 1].

Moreover, similar results have been found from the LRT-1 between L(4,3) and L(4,4); L(5,3) and L(5,4); L(5,4) and L(5,5); L(6,4) and L(6,5); and L(6,5) and L(6,6) models with fixed order of fit for additive genetic and varying order of fit for permanent environmental effects. Whereas fitting performance of Legendre polynomials from LRT-2 results were found different (P<0.05) according to varying order of fit for additive genetic effects within fixed order of fit for permanent environmental effect (Table 1).

Table 1. Criteria used for comparison of the models and their levels
Tablo 1. Modellerin karşılaştırılmasında kullanılan kriterler ve düzeyleri

Model	Number of parameters	-2LogL	LRT-1 L (α,...)	LRT-2 L (..., p)	AIC	BIC	RV
ARR	31	17401	-		17473	17536	4.0
WRR	13	18424	-		18456	18484	5.6
L(2.2)	7	18136	-	-	18150	18182	5.5
L(2.3)	10	17602	535*	-	17622	17658	4.2
L(2.4)	14	17340	262*	-	17368	17412	3.4
L(2.5)	19	17219	121*	-	17257	17309	3.6
L(2.6)	24	17060	159*	-	17108	17169	3.1
L(3.2)	10	17571	-	566*	17591	17627	4.2
L(3.3)	13	17562	8*	39*	17588	17630	4.2
L(3.4)	17	17177	386*	163*	17211	17260	3.4
L(3.5)	22	17024	153*	195*	17068	17126	3.0
L(3.6)	27	16989	35*	71*	17043	17109	2.9
L(4.2)	14	17162	-	408*	17190	17233	3.4
L(4.3)	17	17153	9*	409*	17187	17236	3.4
L(4.4)	21	17152	2 N.S.	25*	17194	17250	3.4
L(4.5)	26	17005	146*	19*	17057	17122	3.0
L(4.6)	31	16967	39*	22*	17029	17102	2.8
L(5.2)	19	17006	-	156*	17044	17096	3.0
L(5.3)	22	16995	11*	158*	17039	17097	3.0
L(5.4)	26	16987	8 N.S.	165*	17039	17104	3.0
L(5.5)	31	16978	9 N.S.	28*	17040	17113	3.0
L(5.6)	36	16942	36	25*	17014	17096	2.9
L(6.2)	24	16944	-	62*	16992	17053	2.9
L(6.3)	27	16933	11*	62*	16987	17054	2.9
L(6.4)	31	16922	11*	65*	16984	17058	2.9
L(6.5)	36	16911	10 N.S.	66*	16983	17066	2.8
L(6.6)	41	16908	3 N.S.	34*	16990	17082	2.8

Significant changes (P<0.05) and N.S. is non significant

On the other hand, choice of best model partly depends partly on criteria used. While L(6,2) had lowest BIC value, model L(6,5) had lowest AIC and L(6,6) had lowest value in terms of -2LogL. Furthermore, L(4,6), L(6,5) and L(6,6) models had lowest RV values. Namely, the models with three or greater order of fit for additive genetic effects and sixth order of fit for permanent environmental effects show lower RV values *(Table 1)*.

Figure 1 was plotted to clarify the order effect for fitting in LRR models. Since all criteria showed similar pattern for the model, only AIC was given in the *Figure 1*. The figure shows the pattern of AIC for a group of models with a fixed order of fit for permanent environmental effect and varying order of fit for additive genetic *(Figure 1A)* or vice versa *(Figure 1B)*. AIC was decreased with increasing order of fit for additive genetic effect within a series of given permanent environmental effect orders *(Figure 1A)*. Likewise, AIC decreased with increasing order of fit for permanent environmental effects within a series of given additive genetic effect orders *(Figure 1B)*.

In addition, variation of AIC for a group of models with the same order of fit for permanent environmental effect were changed in respect of order of fit for additive genetic effect. For instance,
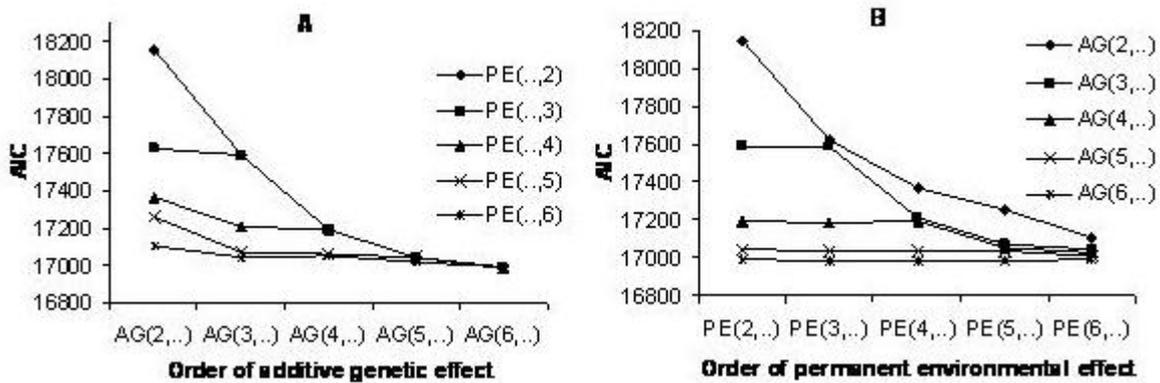
Fig 1. Changes of AIC according to order of fit in LRR models
Şekil 1. LRR modellerinde uyum derecelerine göre AIC değişimi

Table 2. *Eigenvalues of the estimated genetic (co)variance matrix and the proportion of total variance (%) for LRR models*
Tablo 2. *LRR modelleri ile tahminlenen genetik (ko)varyans matrislerinin özdeğerleri ve varyanstaki payı (%)*

Models	1	2	3	4	5	6	Number of substantial eigenvalues
L(2.2)	5.18 (71.0)	2.12 (29.0)					2
L(2.3)	5.88 (70.8)	2.42 (29.2)					2
L(2.4)	16.63 (82.0)	3.64 (18.0)					2
L(2.5)	14.17 (87.3)	2.06 (12.7)					2
L(2.6)	13.91 (78.8)	3.74 (21.2)					2
L(3.2)	8.34 (69.5)	2.37 (19.8)	1.29 (10.8)				3
L(3.3)	15.01 (88.8)	0.00 (0.0)	1.89 (11.2)				2
L(3.4)	7.05 (72.9)	2.14 (22.1)	0.48 (5.0)				2
L(3.5)	12.31 (82.7)	2.15 (14.4)	0.43 (2.9)				2
L(3.6)	13.29 (83.5)	2.34 (14.7)	0.28 (1.8)				2
L(4.2)	8.02 (62.5)	3.08 (24.0)	1.37 (10.7)	0.36 (2.8)			3
L(4.3)	8.00 (66.4)	2.84 (23.6)	0.94 (7.8)	0.27 (2.2)			2
L(4.4)	7.39 (64.3)	2.93 (25.5)	0.96 (8.3)	0.22 (1.9)			3
L(4.5)	7.31 (65.9)	2.86 (25.8)	0.86 (7.8)	0.06 (0.5)			2
L(4.6)	7.69 (69.6)	2.75 (24.7)	0.68 (6.1)	0.00 (0.0)			2
L(5.2)	8.90 (62.1)	3.42 (23.8)	1.25 (8.7)	0.69 (4.8)	0.08 (0.6)		3
L(5.3)	8.34 (65.8)	2.94 (23.2)	0.49 (3.9)	0.84 (6.6)	0.07 (0.6)		3
L(5.4)	7.36 (65.0)	2.70 (23.8)	0.78 (6.9)	0.49 (4.3)	0.00 (0.0)		3
L(5.5)	7.84 (66.6)	2.69 (22.9)	0.77 (6.5)	0.47 (4.0)	0.00 (0.0)		3
L(5.6)	7.67 (67.7)	2.58 (22.8)	0.41 (3.6)	0.67 (5.9)	0.00 (0.0)		2
L(6.2)	8.17 (59.9)	3.32 (24.3)	1.23 (9.0)	0.70 (5.1)	0.20 (1.5)	0.03 (0.2)	3
L(6.3)	8.01 (63.1)	3.13 (24.7)	0.56 (4.4)	0.77 (6.1)	0.20 (1.6)	0.02 (0.2)	3
L(6.4)	6.92 (63.5)	2.76 (25.3)	0.56 (5.1)	0.00 (0.0)	0.60 (5.5)	0.05 (0.5)	3
L(6.5)	7.52 (65.5)	2.73 (23.8)	0.64 (5.6)	0.55 (4.8)	0.00 (0.0)	0.04 (0.3)	3
L(6.6)	7.65 (65.4)	2.78 (23.8)	0.66 (5.6)	0.58 (5.0)	0.00 (0.0)	0.02 (0.2)	3

Table 3. *Eigenvalues of the estimated permanent environmental (co)variance matrix and the proportion of total variance (%) for LRR models*
Tablo 3. *LRR modelleri ile tahminlenen kalıcı çevre (ko)varyans matrislerinin özdeğerleri ve varyanstaki payı (%)*

Models	1	2	3	4	5	6	Number of substantial eigenvalues
L(2.2)	7.30 (84.8)	1.31 (15.2)					2
L(2.3)	8.25 (79.7)	0.44 (4.3)	1.66 (16.0)				3
L(2.4)	3.16 (60.1)	0	2.10 (39.9)	0			2
L(2.5)	0	1.67 (37.4)	2.80 (62.6)	0	0		2
L(2.6)	3.43 (80.7)	0	0	0.82 (19.3)	0	0	2
L(3.2)	6.56 (93.3)	0.47 (6.68)					2
L(3.3)	0	3.38 (100.0)	0				1
L(3.4)	7.07 (70.6)	1.57 (15.7)	0	1.38 (13.8)			3
L(3.5)	4.62 (73.1)	0	1.25 (19.8)	0	0.45 (7.1)		2
L(3.6)	3.75 (68.8)	0	1.24 (22.8)	0	0.46 (8.4)	0	2
L(4.2)	6.81 (93.3)	0.49 (6.7)					1
L(4.3)	6.33 (80.2)	1.56 (19.8)	0				2
L(4.4)	6.72 (80.8)	1.53 (18.4)	0	0.07 (0.8)			2
L(4.5)	6.89 (81.2)	1.51 (17.8)	0.09 (1.1)	0	0.57 (6.3)		2
L(4.6)	6.96 (75.3)	1.46 (15.8)	0.52 (5.6)	0	0.30 (3.2)	0.00	2
L(5.2)	6.43 (100.0)	0					1
L(5.3)	6.11 (79.1)	1.61 (20.9)	0				2
L(5.4)	6.84 (77.6)	1.62 (18.4)	0	0.35 (4.0)			2
L(5.5)	6.32 (75.1)	1.55 (18.4)	0.46 (5.5)	0.09 (1.1)	0		2
L(5.6)	6.48 (73.8)	1.52 (17.3)	0.71 (8.1)	0	0.07 (0.8)	0.17 (6.9)	2
L(6.2)	6.64 (93.7)	0.45 (6.3)					1
L(6.3)	6.30 (80.2)	1.56 (19.8)	0				2
L(6.4)	7.25 (77.6)	1.57 (16.8)	0.52 (5.6)	0			2
L(6.5)	6.61 (74.7)	1.49 (16.8)	0.64 (7.2)	0.11 (1.2)	0		2
L(6.6)	6.49 (75.0)	1.46 (16.9)	0.59 (6.8)	0.11 (1.3)	0	0	2

when the order of fit for permanent environmental effect was two, range of AIC was 1158 (18150-16992). When the orders of fits were four and six, the range values were 384 (17368-16984) and 118 (17108-16990), respectively.

As compare to these results, ranges of AIC were less for the models with the same order of fit for additive genetic effect. For instance, when the order of fit for additive genetic effect was two, AIC range of the models was 1042 (18150-17108) while it was 161 (17190-17029) and 2 (16992-16990) for four and six orders of fit for additive genetic effect, respectively. In this study, changes in order of fit for additive genetic effect are more effective on performance of models as compared to changes in order for permanent environmental effect.

For Legendre models, eigenvalues and their relative proportions (in parenthesis) were given in *Table 2* and *Table 3* for the additive genetic and permanent environmental random regression (co)variance matrix, respectively. First two or three eigenvalues for additive genetic effect and first two for permanent environmental effect account for over 90% of total variation. Number of substantial eigenvalues was also listed in *Table 2* and *Table 3*.

DISCUSSION

In this study, several random regression models have been compared for better fitting performance of test day milk yields. The results showed that the WRR model had the worst performance among models in terms of all criteria used. The decreasing of AIC for series LRR models with increasing order of fit for additive genetic and permanent environmental effects was similar with the pattern reported previously [20].

While some eigenvalues were close to zero or small compared to the others two eigenvalues for additive genetic effect and three eigenvalues for permanent environmental effects were accounted for over 90% of total variation. This implies that we might obtain a more parsimonious fit of the CF by using a reduced rank [30]. Therefore, according to eigenvalues L(2,2) and L(3,2) models were sufficient and one can generally say that third order of fit for both effects was enough for fitting performance of LRR models. This result mainly agreed with preliminary studies [5,18,19] which stated that third order of fit was sufficient. However, considering other criteria used in this study, the best fit was found in the sixth order of fit for additive

genetic and fourth or more order of fit for permanent environmental effects. These results are not consistent with previous results [18-21]. Some studies [18-21] obtained good fit by using L(3,4), L(2,3), L(2,5), L(3,6), L(2,7), L(4,7) and L(5,7) models. The outcomes in literature reveal that the best fit model has generally lower order of fit for additive genetic effect than order of fit for permanent environmental effect.

In conclusion, overall evaluation of the RV, -2LogL, AIC, BIC, LRT and eigenvalues for the models indicate that the L(6,2), L(6,5) and L(6,6) models provided better performance among 27 different models in this study. This result was consistent with the findings of the study [20] which indicate that L(6,6) model had lowest -2LogL and AIC values. The mentioned three models have also higher order of additive genetic effect than that of permanent environmental effect. This may be explained by higher additive genetic variance than the permanent environmental variance due to comparatively small data set with high number of sires and less number of daughters per sire.

Alternatively, the model L(3,3) with small order of fit and less number of parameters, which was found according to the model eigenvalues of models, can be recommended for computational simplicity, since in several studies L(3,3) was accepted sufficient in several studies [5,18,19]. Besides, same order of fit for both genetic and permanent environmental effects may allow an equal chance for genetic evaluation of the variances. Although same order of fit actually doubles number of parameters to be estimated per animal, equal flexibility for modeling of the genetic and permanent environmental (co)variances is achieved with this same function [22,23].

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