RESEARCH ARTICLE

Comparison of Different Order and Heterogeneous Residual Variances Legendre Polynomials in Random Regression Models

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Abstract

In this study, it was aimed to estimate covariance function, covariance components, permanent environmental effect, additive genetic effect and heritability values, and comparison of models with different order and heterogeneous residual variances Legendre Polynomials in the first lactation Turkish Holstein cows more than 10 test day milk yields. For this aim, 7340 test day records of 386 Holstein Friesian cows in the first lactation raised in private dairy farm calving from 2013 to 2018 in Kırşehir-Turkey were used. The six Legendre polynomial models by random regression described as L(2,2), L(3,3), L(4,4), L(5,5), L(6,6) and L(7,7) were evaluated using first lactation test day records. Heterogeneous residual variances (RV) were modeled by considering five sub-classes. Analyzes were performed using the WOMBAT statistical package. In comparison of the models, -2LogL, Akaike Information Criterion (AIC), Bayes Information Criterion (BIC) and RV were used. Also, the compatibility of random regression models was examined in terms of eigenvalues of covariance matrices. The values of -2LogL (between 28334.16 and 26610.07), AIC (between 28356.16 and 26732.07) and BIC values (between 28432.05 and 27129.21) obtained from the study result decreased as the model order increased. As a result, it was determined that the 3rd degree Legendre polynomial model can provide sufficient compliance. However, when looking at the values for -2LogL, AIC and RV, it was determined that the L(7,7) model fits well according to other models.

Keywords: Heritability, Permanent environmental effect, Additive genetic effect, Holstein Friesian, First lactation

Şansa Bağlı Regresyon Modellerinde Farklı Dereceli ve Heterojen Hata Varyanslı Legendre Polinomlarının Karşılaştırılması

Öz

Bu çalışmada, 10'dan fazla test günü süt verimine sahip birinci laktasyondaki Holstein Friesian ineklerinde farklı dereceli Legendre Polinomları kullanılarak birinci test günü süt verimleri için kovaryans fonksiyonu, kovaryans bileşenleri, kalıcı çevresel etki, eklemeli genetik etki ve kalıtım derecelerinin tahmin edilmesi ve modellerin karşılaştırılması amaçlanmıştır. Bu amaçla Kırşehir-Türkiye'de 2013'ten 2018'e kadar buzağılayan özel süt çiftliğinde yetiştirilen birinci laktasyondaki 386 Holstein Friesian ineklerinin 7340 test günü kaydı kullanılmıştır. L(2,2), L(3,3), L(4,4), L(5,5), L(6,6) ve L(7,7) olarak tanımlanan rastgele regresyon ile altı Legendre polinom modeli birinci laktasyon test günü kayıtları kullanılarak değerlendirilmiştir. Heterojen hata varyansları (RV), beş alt sınıf dikkate alınarak modellenmiştir. Analizler, WOMBAT istatistik paketi kullanılarak yapılmıştır. Modellerin karşılaştırılmasında -2LogL, Akaike Bilgi Ölçütü (AIC), Bayes Bilgi Ölçütü (BIC) ve hata varyansları (RV) kullanılmıştır. Ayrıca, şansa bağlı regresyon modellerinin uyumluluğu kovaryans matrislerinin özdeğerleri açısından incelenmiştir. Çalışma sonucundan elde edilen -2LogL (28334.16 ve 26610.07 arasında), AIC (28356.16 ve 26732.07) ve BIC (28432.05 ile 27129.21 arasında) değerleri model sırası arttıkça azalmıştır. Sonuç olarak, 3. derece Legendre polinom modelinin yeterli uyumu sağlayabileceği belirlenmiştir. Ancak -2LogL, AIC ve RV değerlerine bakıldığında, L(7,7) modelinin diğer modellere göre iyi uyum gösterdiği belirlenmiştir.

Anahtar sözcükler: Kalıtım derecesi, Kalıcı çevresel etki, Eklemeli genetik etki, Holstein Friesian, Birinci laktasyon

INTRODUCTION

The main purpose of animal breeding is to increase productivity by choosing the better animals for the next generation. In dairy cattle breeding is usually made over milk yield records. So milk yield records of cows most important for the dairy herds [1]. At the same time sire evaluation is done mainly based on 305-day milk yield in dairy farms. However, in 305-day milk yield models, only average lactation curve of cows is considered [2]. Test day

(TD) yields at monthly intervals are suggested for sire and cow evaluation because the test-day model highly has accuracy due to having a larger number of measurements per daughter. Today, test-day models are much more common than lactation models for genetic evaluations of production traits worldwide [3]. Test-day models provide more accurate genetic evaluations of cows and bulls due to the better definition of contemporary groups and the elimination of environmental effects [4]. Therefore, random regression models (RRM) have been developed to use of test day milk records instead of 305-d lactation milk yield [5]. The RRM is also used to estimate the genetic parameters of TD yields in dairy cows [6]. RRM also allows the evaluation of cows for parameters associated with the shape of the lactation curve simultaneously with the production level [2]. RRM has different approaches to the test day models and attempts to fit the (co)variance structure of repeated measures during the lactation curve [5]. This model assumes standard shapes of the lactation curve for all cows of the same age and season subclass, and the estimated additive genetic effects of the animals reflected the height differences of these curves [7].

Henderson [8] and Laird and Ware [9] developed the RRM. The use of linear RRM as an extension of fixed regression models has been proposed by Schaeffer and Dekkers [10]. Different models can be proposed to estimate the genetic parameters for TD yields of dairy cattle [11]. Thus, the (co)variances between records of additive genetic effects and permanent environmental effects can be described using Legendre polynomials [5]. Legendre polynomials (LP) are orthogonal and normalized and more accurate results than the conventional polynomials [5]. The use of LP has become widespread, as it provides good convergence and is more reliable than other polynomial estimates [12]. LP reduce correlation among estimated regression coefficients in comparison to other functions with the same number of parameters [11]. Olori et al.[13] reported that the critical issues in fitting an RRM include the order of the polynomial used to model the lactation curve at the fixed and random levels. Meyer [14] pointed out that higher-order polynomials are flexible and that changes in means and variances can be modeled along a continuous scale.

In the majority of studies with RRM, the number of test days is usually 10 [1,15-17]. In some studies, the test day is less than 10 [18,19], while in other studies it is more than 20 test days [20,21].

Studies with more test days investigating the use of RRM for estimating genetic parameters for TD yields in dairy cows are scarce. Therefore, the study aimed to estimate covariance function, covariance components, permanent environmental effect, additive genetic effect and heritability values, and comparison of models with different orders and heterogeneous residual variances Legendre Polynomials in the first lactation Turkish Holstein cows more than 10 test day milk yields.

MATERIAL AND METHODS

Data comprised of 7340 TD records of 386 Holstein Friesian cows in first lactation raised in private dairy husbandry calving from 2013 to 2018 in Kırşehir of Turkey. The cows, which produced milk yields on the day of the test, were the daughters of 76 sires and 304 dams. A total test-day milk yields from the morning and evening milking were collected with 15 days intervals from 5 to 305 days of lactation and first record was obtained up to 5 days after calving. There is a minimum of 11 TD records (0.26%) and a maximum of 21 TD (30.83%). The rate of animal records for more than 15 or more TD is 96.63%. The mean and standard deviation of milk yields on the day of the test were 30.03±7.04 kg and a coefficient of variation of 23.46%, respectively. The following RRM was used in the TDMY analysis.

$$y_{ij} = CY + CM + CS + \sum_{m=0}^{k_A-1} \alpha_{im}\phi_m(t_{ij}) + \sum_{m=0}^{k_R-1} \gamma_{im}\phi_m(t_{ij}) + e_{ij}$$

CY : Fixed effect of calving year

CM : Fixed effect of calving month

CS : Fixed effect of calving season

α_{im} : m^{th} additive genetic random regression coefficients for animal i

γ_{im} : m^{th} permanent environmental random regression coefficients for animal i

k_A : Order of fit for additive genetic random regression coefficients

k_R : Order of fit for permanent environmental random regression coefficients

t_{ij} : j^{th} test day for animal i

$\Phi_m(t_{ij})$: m^{th} Legendre polynomial evaluated for t_{ij}

e_{ij} : Random error $e \sim N(\mu, \sigma_e^2)$

The six Legendre polynomial models by random regression described as L(2,2), L(3,3), L(4,4), L(5,5), L(6,6) and L(7,7) were evaluated using first lactation TD records. In addition, the calving year, calving month and calving season were included in the model as fixed effects. Cows were assigned the six subclasses for calving year (2013-2018), four sub-classes for seasons of calving (summer, winter, spring, autumn) and twelve calving months. Heterogeneous residual variances (RV) were modeled by considering five sub-classes (5-60, 61-120, 121-180, 181-240, 241-305 days). Analyzes were performed using the WOMBAT statistical package.

In comparison of the models, -2LogL, Akaike Information Criterion (AIC) [22], Bayes Information Criterion (BIC) [23] and residual variances (RV) were used. AIC and BIC values were calculated as reported in the Takma and Akbas [24] studies. In comparison, the smallest values of AIC, -2LogL, BIC and RV criteria explain that this model fits well [24,25]. The significance of the change between different order of

Legendre polynomials models was examined by chi-square test (χ^2) [26]. Also, the compatibility of random regression models was also examined in terms of eigenvalues of covariance matrices [1,25,26].

RESULTS

Estimates of the additive genetic effect for TDMY on different test days ranged from 0.09 to 20.10. Especially, the genetic effect in TDMY was generally greater at the beginning of lactation in L(4,4), L(5,5), L(6,6) and L(7,7) models. Genetic effects predicted at the end of lactation were high in all models, but the prediction from the L (7,7) model showed a decreasing trend (Fig. 1).
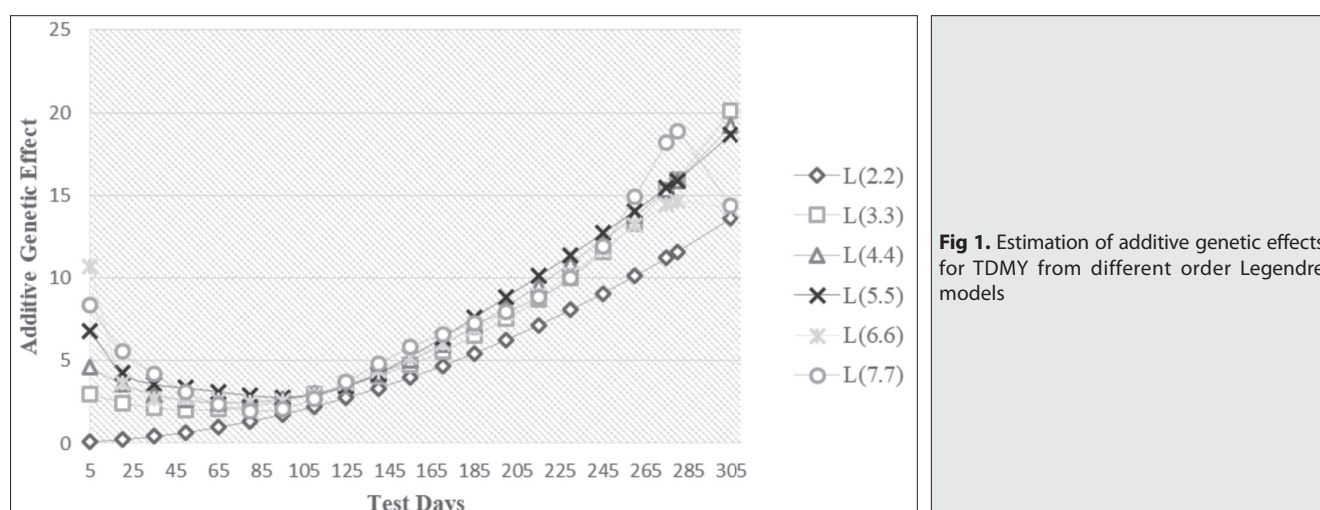
Estimates of the permanent environmental effects of TDMY from the L(2,2), L(3,3), L(4,4), L(5,5), L(6,6), L(7,7) Legendre models have changed between 10.49 and 48.65 and their trends have been illustrated in Fig. 2. This figure shows that the estimates of permanent environmental effects are more stable at the start of lactation and increase during the rest of lactation. Also, there is a very high increase in the L (4,4) model on the last test day.

Heritability values estimates of TDMY ranged from 0.002 to 0.389. This change resembled the results obtained from the estimates of genetic effects. Heritability values estimates were lowest with the L (2,2) model at the beginning of lactation, while the highest with the L (7,7) model. On the 8th and 9th test days (110 - 125th days), while all models formed close estimates, the highest heritability value estimation at the end of lactation was found with the L (3,3) model (Fig. 3).
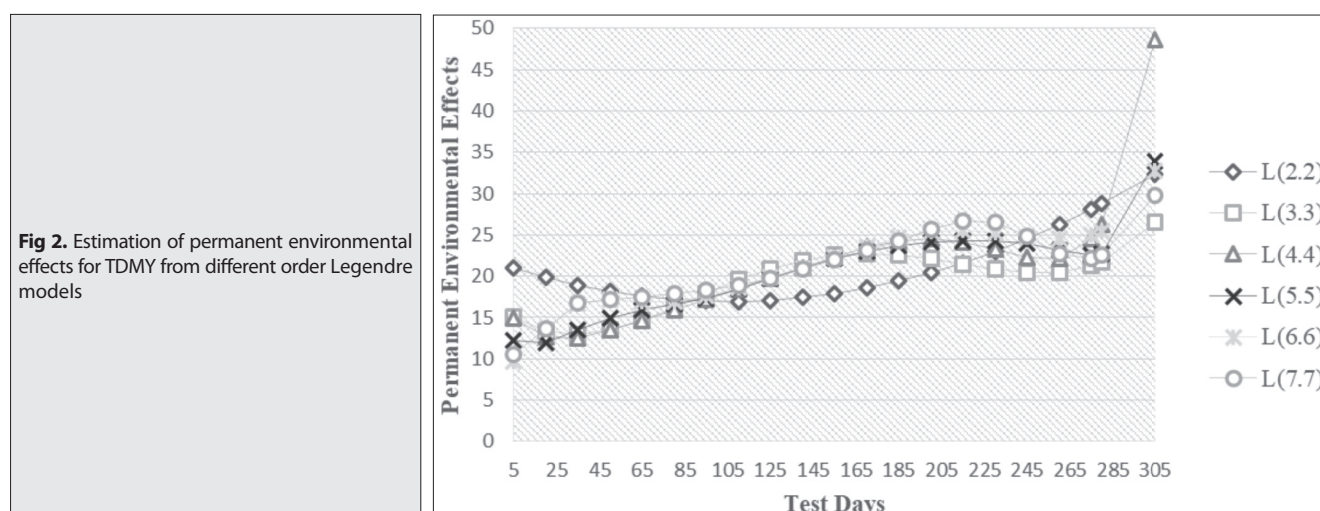
The findings of the criteria used for comparing different orders Legendre models are given in Table 1. In the table seen that -2LogL, AIC and BIC values vary between 26610.07 and 28432.05, while RV value varies between 5.09 and 30.32.

The maximum log-likelihood (LogL) values and the LogL changes of models with different orders are shown in Table 2. As seen in the table, LogL values varied between -14167.08 and -13305.03. The highest change was observed in the L(3,3) model, while the least change was observed in the L(6,6) model.

Table 3 presents eigenvalues and their proportions in the

Fig 1. Estimation of additive genetic effects for TDMY from different order Legendre models

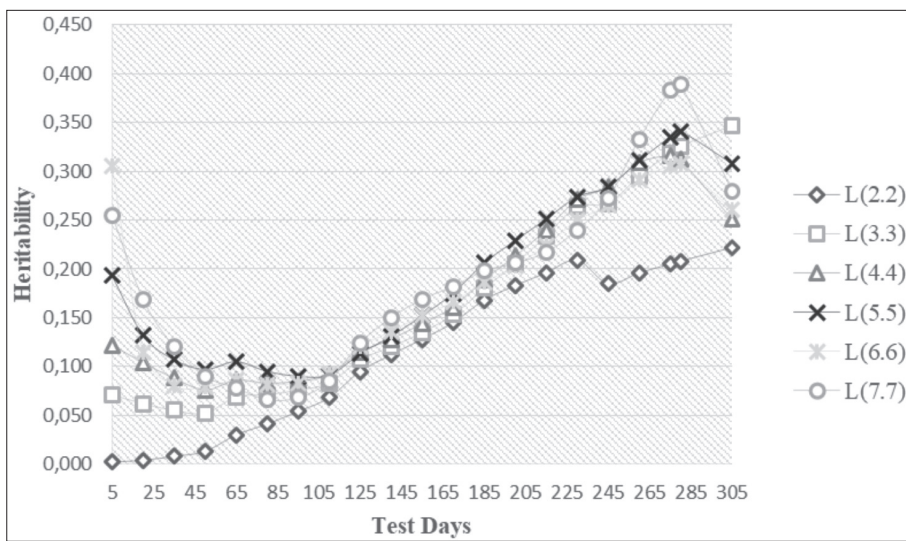Fig 2. Estimation of permanent environmental effects for TDMY from different order Legendre models

Fig 3. Estimation of heritability values for TDMY from different order Legendre models

Table 1. *Findings of the criteria used for comparing different order Legendre models*

Models	Number of Parameters	-2LogL	AIC	BIC	RV1	RV2	RV3	RV4	RV5
L(2.2)	11	28334.16	28356.16	28432,05	30.32	13.46	9.15	7.63	15.37
L(3.3)	17	27677.92	27711.92	27829.18	23.62	12.91	7.99	7.05	11.27
L(4.4)	25	27034.55	27084.55	27257.00	18.13	11.45	7.58	6.04	8.67
L(5.5)	35	26817,78	26887.78	27129.21	16.22	10.82	7.09	5.80	8.06
L(6.6)	47	26721.68	26815.68	27139.89	14.81	10.64	6.82	5.49	7.60
L(7.7)	61	26610.07	26732.07	27152.83	13.91	10.17	6.56	5.09	7.06

Table 2. *LogL values and the changes in LogL for different order models*

Models	Number of Parameters	LogL	Changes in LogL	Changes in LogL (%)	Chi-Square
L (2,2)	11	-14167.08	-	-	-
L (3,3)	17	-13838.96	328.12**	2,37	16.81
L (4,4)	25	-13517.27	321.69**	2,38	20.09
L (5,5)	35	-13408.89	108.38**	0,81	23.21
L (6,6)	47	-13360.84	48.05**	0,36	26.22
L (7,7)	61	-13305.03	55.81**	0,42	29.14

** $P<0.01$

Table 3. *Eigenvalues and their proportions in the total variance for the (co) variance of the additive genetic effect estimated from different models*

Models	1	2	3	4	5	6	7
L (2,2)	9.88 (99.99)	0.000 (0.01)					
L (3,3)	13.19 (97.07)	0.40 (2.93)	0.00 (0.00)				
L (4,4)	13.64 (94.52)	0.69 (4.81)	0.10 (0.67)	0.00 (0.00)			
L (5,5)	13.88 (91.65)	0.090 (5.94)	0.36 (2.40)	0.00 (0.01)	0.00 (0.00)		
L (6,6)	12.44 (89.75)	0.85 (6.12)	0.46 (3.28)	0.12 (0.84)	0.00 (0.01)	0.00 (0.00)	
L (7,7)	13.65 (89.75)	1.01 (6.67)	0.46 (3.02)	0.08 (0.50)	0.01 (0.04)	0.00 (0.01)	0.00 (0.00)

Table 4. *Eigenvalues and their proportions in the total variance for the (co) variance of the permanent environmental effect estimated from different order models*

Models	1	2	3	4	5	6	7
L (2,2)	36.16 (86.80)	5.50 (13.20)					
L (3,3)	30.99 (79.69)	5.60 (14.40)	2.30 (5.92)				
L (4,4)	30.46 (72.83)	7.15 (17.09)	3.29 (7.88)	0.92 (2.20)			
L (5,5)	30.10 (74.06)	5.93 (15.58)	3.13 (7.70)	1.30 (3.19)	0.19 (0.47)		
L (6,6)	31.31 (73.37)	6.28 (14.73)	3.17 (7.42)	1.47 (3.45)	0.32 (0.75)	0.12 (0.28)	
L (7,7)	30.47 (72.21)	6.01 (14.25)	3.29 (7.81)	1.53 (3.62)	0.65 (1.54)	0.18 (0.42)	0.07 (0.16)

total variance for the (co)variance of the additive genetic effect estimated from different models. One of the additive genetic effects in L(2,2), L(3,3), L(4,4) and L(5,5) models constitutes more than 90% of total eigenvalues. However, 2 of the additive genetic effects in the L(6,6) and L(7,7) models constitute more than 90% of the total eigenvalues.

The eigenvalues calculated in the (co)variance matrices of the permanent environmental effects and the proportions of these eigenvalues in the total eigenvalues estimated from different models are given in *Table 4*. For the permanent environmental effect, at least 2 eigenvalues in L(2,2) and L (3,3) models constitute more than 90% of the total eigenvalue. In other models, at least 3 eigenvalues constitute more than 90% of the total eigenvalue.

DISCUSSION

Different methods are used in modeling repeated measurements in animals. These models explain how the feature in question changes over time. The important point on repeated measurements is the relationships between the test day yields. For this reason, the (co)variance structure between test days is important in the analysis of repeated measurements.

The random regression approach, which is suitable for repeated records and allows model-specific effects for each measurement, is the most appropriate approach to this type of information [27].

At the beginning of lactation, additive genetic effect estimates for TGSV range from 0.09 to 20.10. Other models show similar trends, except for the L(7,7) model excluding the last test days. Obtained results were found similar to the works of Takma and Akbaş [5], Peixoto et al.[16], López-Romero and Carabaño [25], Bignardi et al.[28].

Estimates of the permanent environmental effects of TDMY from the Legendre models have changed between 10.49 and 48.65. When the permanent environmental effect value is analyzed, the trend obtained from the LEG65_10

model found by Behzadi and Mehrpoor [15] were similar to this study result except L(4,4) model result. But, it is the opposite of the tendency found by Takma and Akbaş [5] study. When the results of the heritability values obtained from the study were examined, the heritability values obtained from different models varied between 0.002 and 0.305 on the first test day and the other test days it was found between 0.004 and 0.389. Takma and Akbaş [5] found their heritability estimates in the range of 0.26 to 0.57. Galiç and Kumlu [29] found between 0.12 and 0.15. Prakash et al.[17] estimated between 0.007 and 0.088 with homogeneous residual variance. Behzadi and Mehrpoor [15] estimated between 0.13 and 0.66 with the LEG65_10 model. Naderi [30] estimated heritability between 0.45 and 0.60 with RRM for milk yield. According to these studies, it can be said that the heritability estimates obtained are in a similar range except Naderi [30] study results. Meyer [14] reported that there may be erratic and implausible estimates of variance components and genetic parameters using RRM using cubic, quartic or higher-order polynomials, especially in data sets that contain fewer or less recent records than polynomial order [31]. In the study, there is a situation arising from the variation at the beginning of lactation on the first test day. It is believed that an unreasonable prediction is not encountered on other test days except the last. This situation is thought to arise from the heterogeneous error variance.

The values of -2LogL (between 28334.16 and 26610.07), AIC (between 28356.16 and 27152.83) and BIC (between 28432.05 and 27129.21) obtained from the study result decreased as the model order increased except BIC. These values were found higher than the works of Takma and Akbas [24] and Naderi [30] and lower than the works of Behzadi and Mehrpoor [15], Takma and Akbas [32] and Haiduck Padilha et al.[19].

The magnitude of eigenvalues calculated in additive genetic effects (co) variance matrices and the share of these eigenvalues in total eigenvalues, at least 1 eigenvalue in L(2,2), L(3,3), L(4,4) and L(5,5) models, in other models at

least 2 eigenvalues constitute more than 90% of the total eigenvalues. For the permanent environmental effect, at least two eigenvalues in models L(2,2) and L(3,3) and 3 eigenvalues in others constitute more than 90% of the total eigenvalues. According to the obtained findings, it was determined that the 3rd degree Legendre polynomial model can provide sufficient compliance. These findings were similar to those obtained from the works of Takma and Akbas [24]. Behzadi and Mehrpoor [15] suggested the L6,5_RV10 model. However, when looking at the values for -2LogL, AIC and heterogeneous RV, it was determined that the L(7,7) model fits well according to other models.

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CONFLICT OF INTEREST

The author declares that he has no conflict of interests.

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