

# A Comparison of Some Random Regression Models for First Lactation Test Day Milk Yields in Jersey Cows and Estimating of Genetic Parameters <sup>[1]</sup>

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## Summary

This study was conducted to compare random regression models for third order Ali Schaeffer (AS), Wilmlink (W) and Legendre polynomials (L) on estimation of genetic parameters for first lactation milk yield in Jersey cows. For this aim, data used in this study were 6387 official milk yield records from monthly recording of 686 first lactations between 1996 and 2011 in Karakoy Agricultural State Farm, Samsun (Turkey). In this study, (co)variance components, heritability for first lactation test day milk yields (TDMY) and genetic correlations among these TDMYs were estimated by using DFREML statistical package under DXMRR option. To compare the models, -2LogL, Akaike's information criterion (AIC), Bayesian information criterion (BIC), Residual variances (RV) and Log likelihood values were used. Heritabilities (0.08 to 0.28), additive genetic correlations (0.68 to 0.99) and phenotypic correlations (0.21 to 0.66) were estimated by AS(4,4) random regression model which had the lowest AIC and BIC values. As a result, it was decided that the AS(4,4) random regression model can be used for management decisions and genetic evaluation of Jersey cows for milk production.

**Keywords:** Random regression, Test day milk yield, Jersey, Genetic parameters

## Jersey Sığırlarında İlk Laktasyon Test Günü Süt Verimleri için Bazı Şansa Bağlı Regresyon Modellerinin Karşılaştırılması ve Genetik Parametre Tahminleri

### Özet

Bu çalışma Jersey sığırlarında ilk laktasyon süt verimleri için genetik parametrelerinin tahmini üzerine Ali Schaeffer, Wilmlink ve Legendre polinomlarının 3 farklı uyum sırasında şansa bağlı regresyon modellerini karşılaştırmak için yürütülmüştür. Bu amaçla, çalışmada Samsun Karaköy Tarım İşletmesi'ndeki 1996-2011 yılları arasındaki 686 ilk laktasyonun 6387 adet aylık süt verim kaydı kullanılmıştır. Çalışmada ilk laktasyon test günü süt verimleri (TGSV) için kovaryans bileşenleri, kalıtım dereceleri ve TGSV arasındaki genetik korelasyonlar DFREML istatistik paket programı içerisindeki DXMRR opsiyonu kullanılarak tahmin edilmiştir. Modelleri karşılaştırmak için -2LogL, Akaike bilgi kriteri (AIC), Bayesian bilgi kriteri (BIC), Hata varyansı (RV) ve Log olabilirlik değerleri kullanılmıştır. En küçük AIC ve BIC değerlerine sahip AS(4,4) modeli ile kalıtım derecesi değerleri (0.08 - 0.28), eklemeli genetik korelasyonlar (0.68 - 0.99) ve fenotipik korelasyonlar (0.21 - 0.66) tahmin edilmiştir. Sonuç olarak, AS(4,4) modelinin Jersey sığırlarının genetik değerlendirilmesi ve süt üretimi açısından işletme yönetim kararları için kullanılabilir olduğuna karar verildi.

**Anahtar sözcükler:** Şansa bağlı regresyon, Test günü süt verimi, Jersey, Genetik parametreler

## INTRODUCTION

The objective in breeding is to improve the animal's genotype for the traits of interest (breeding goal).

Breeding values are used as a tool for selecting the best animals. Animals with the most favorable genotype are



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selected to produce the next generation [1]. One of the main incomes is milk production for dairy cattle farms and therefore milk yield records have great deal of importance for dairy herds [2]. Milk yield is a trait where the phenotype of an animal can be represented by a continuous function of time. Thus, this trait is characterized by a trajectory with a theoretically infinite number of measurements [3]. Therefore, an appropriate model is one that considers a complex covariance structure. In the infinite-dimensional approach, the covariance structure is modeled as a Covariance Function (CF) [4]. A useful tool for the estimation of CF is the Random Regression Model (RRM) [5].

Recently, Test-Day Models (TDM) based on different random regression functions have been suggested for the genetic evaluation of dairy cows. TDMs analyzes individual test-day records instead of 305 day milk yields of cows, which are currently used by Ptak and Schaeffer [6], Swalve [7], Jamrozik and Schaeffer [8], Pool and Meuwissen [9], Schaeffer et al. [10], Takma and Akbas [11], Takma and Akbas [12], Bignardi et al. [13], Galic and Kumlu [14].

Moreover, Random Regression Models are able to predict covariance structures among the test day points along a continuous scale [15]. Thus, the (co)variances between records for additive genetic and permanent environmental effects can be described by using different covariance functions as Ali-Schaeffer [16], Wilmink [17] or Legendre polynomials [12].

Several Random Regression Models (e.g Wilmink, Ali-Schaeffer or Legendre polynomial models) were used to estimate the genetic parameters of milk yields and to compare the each other [18-22]. However, it cannot be founded a study on the applications of random regression models for estimating the genetic parameters of Jersey cows. Thus, the aims of this study are to compare of different order Ali-Schaeffer, Wilmink and Legendre polynomial random regression models and to find the best model that provided a good description of the genetic parameters for Jersey herds.

## MATERIAL and METHODS

Data were 6387 first lactation milk yield official records from monthly recording of 686 lactations between 1996 and 2011 (over 15 years) of Jersey cattle herd under pasture-based dry seasonal production system in Karakoy Agricultural State Farm in Samsun (Turkey). Also, each data set was composed of the test days and the total amount of milk at the morning and evening milking of the test days. The lactation had variable length with a minimum of 150 and maximum of 305 days long. The average and standard deviation of test-day milk yields were 12.71 and 3.35 kg, respectively and a coefficient of variation of 26.38%.

In general, Random Regression Models (RRM) include

lactational submodels, frequently using the lactation functions proposed by Ali and Schaeffer [16] and by Wilmink [17]. The first has shown better performance in adjusting observed daily phenotypes. The second, with a good adjustment performance, provides a more parsimonious model. Beside, Legendre polynomials (L(2,2), L(3,3) L(4,4)) were used to describe the (co)variance matrix within a Random Regression Test Day Model. Previous studies suggest that at least a three coefficient polynomial is needed to model the (co)variance structure of the random components of the data for RRM based on Legendre polynomials [21,23,24].

In this study, (co)variance components, heritability for first lactation test day milk yields (TDMY) and genetic correlations among these TDMYs were estimated by derivative-free REML (DFREML) statistical package using a RRM models Ali-Schaeffer, Wilmink functions and Legendre polynomials under DXMRR option [25] with different orders of fit for additive genetic ( $\alpha_{jm}=2,3,4$ ) and permanent environmental effects ( $p_{jm}=2,3,4$ ) [12].

The equation for all the models analyzed can be written in scalar notation as:

$$Y_{ijk} = HTD_i + \sum_{m=1}^{K_B} \beta_m x_{(m)}(t_{ij}) + \sum_{m=1}^{K_A} \alpha_{jm} \varphi_m(t_{ij}) + \sum_{m=1}^{K_P} P_{jm} \varphi_m(t_{ij}) + e_{ijk}$$

Where;

$Y_{ijk}$ :  $k^{\text{th}}$  TDMY of the cow  $j$  obtained at  $i^{\text{th}}$  herd-test day (month)

$HTD_i$ :  $i^{\text{th}}$  herd-test day (month)

$\beta_m$ :  $m^{\text{th}}$  fixed regression coefficients for cow  $j$ ,

$t_{ij}$ :  $i^{\text{th}}$  test day of the cow  $j$

$x_{(m)}(t_{ij})$ :  $m^{\text{th}}$  covariates evaluated at and represented just by the Ali-Schaeffer and Wilmink functions, where  $C = 305$ ,  $X_1 = 1$ ,  $X_2 = \text{DIM}/C$ ,  $X_3 = (X_2)^2$ ,  $X_4 = \ln(C/\text{DIM})$ ,  $X_5 = (X_4)^2$  for Ali-Schaeffer function and  $X_1 = 1$ ,  $X_2 = t$  and  $X_3 = \exp(-0.05t)$  for Wilmink function,

$\alpha_{jm}$ :  $m^{\text{th}}$  additive genetic random regression coefficients for cow  $j$ ,

$P_{jm}$ :  $m^{\text{th}}$  permanent environmental random regression coefficients for cow  $j$ ,

$\varphi_m$ :  $m^{\text{th}}$  polynomial evaluated for the age  $t_{ij}$ ,

$K_B$ ,  $K_A$  and  $K_P$  are the order of fitted fixed, random additive and random permanent regression coefficients,

$e_{ijk}$ : random residual effect for  $Y_{ijk}$ .

The RRM were compared using the Akaike's (AIC) and Schwarz's Bayesian (BIC) information criteria [26], as well as by the exam of the variance components, the eigenvalues of the covariance functions and correlation estimates between milk yields on different test-days. The AIC and BIC

allow the comparison between non-hierarchical models and penalize those models that contain a larger number of parameters, with the BIC attributing a more rigorous penalty [27]. AIC was computed as:

$$AIC = -2\log L + 2k$$

where  $k$  is the number of free parameters in the model. The model with the minimum AIC is chosen as the best approximating model, i.e. the closest one to the real and unknown process that generated the observed data [24,28]. BIC was computed by the expression:

$$BIC = -2\log L + k \log(\lambda)$$

where  $k$  is as in AIC criteria, and, using REML,  $\lambda = n - r(X)$ ,  $n$  being equal to the number of test day records and  $r(X)$  equal to the rank of the systematic effects incidence matrix. The lowest BIC specifies the best fitting model [24]. Significant differences in the fit of Legendre polynomials with order from  $k=2$  to  $k=4$  were tested using a chi-square ( $\chi^2$ ) test of the likelihood [11].

## RESULTS

In the present study we used Ali Schaeffer, Wilmink and Legendre polynomials of different orders to model genetic and permanent environmental variations during lactation. Estimated the logarithm of the likelihood function ( $-2\log L$ ), Akaike's Information Criterion (AIC), Bayesian Information Criterion (BIC) and Residual Variance (RV) for used models were given in [Table 1](#). In studied models, the number of parameters ranged from 7 to 21. Values of the AIC, BIC and  $-2\log L$  were changed between 14213.06 and 16694.53.

The maximum log likelihood values and changes in the log likelihoods from the models with different orders of fit were presented in [Table 2](#). While  $-2\log L$  values were increased, AIC, BIC and RV values were decreased with increasing order of model. The most change in the estimated log likelihood values for order of fit estimated by Ali-Schaeffer, Wilmink and Legendre polynomials have been found to be significant ( $P < 0.05$ ).

**Table 1.** Criteria used for comparison of the models

**Tablo 1.** Modellerin karşılaştırılmasında kullanılan kriterler

Models	Number of Parameters	-2LogL	AIC	BIC	RV
AS (2,2)	7	15496.82	14559.28	14606.37	2.38
AS (3,3)	13	15686.70	14285.40	14372.75	2.03
AS (4,4)	21	16074.12	14213.06	14354.31	1.85
W (2,2)	7	16180.67	15243.14	15290.25	2.63
W (3,3)	13	16337.22	14935.92	15023.41	2.19
W (4,4)	21	16694.53	14833.56	14974.89	2.00
L (2,2)	7	15954.84	15017.31	15064.40	2.61
L (3,3)	13	15843.62	14442.32	14529.77	2.09
L (4,4)	21	16172.05	14310.98	14452.25	1.89

*-2LogL: logarithm of the likelihood function, AIC: Akaike's information criterion, BIC: Bayesian information criterion, RV: residual variance*

**Table 2.** Maximum log likelihood values and changes in the log likelihoods from the models with different orders of fit

**Tablo 2.** Farklı uyum sıraları ile modellerden elde edilen log olabilirlikteki değişimler ve maksimum log olabilirlik değerleri

Models	Number of Parameters	Log Likelihood	Changes in Log Likelihood	Changes in Log Likelihood (%)	$\chi^2$
AS (2. 2)	7	-7272.64	-	-	-
AS (3. 3)	13	-7129.70	142.94*	2.00	12.59
AS (4. 4)	21	-7085.53	44.17*	0.62	15.51
W (2. 2)	7	-7614.57	-	-	-
W (3. 3)	13	-7454.96	159.61*	2.14	12.59
W (4. 4)	21	-7395.78	59.18*	0.80	15.51
L (2. 2)	7	-7501.65	-	-	-
L (3. 3)	13	-7208.16	293.49*	4.07	12.59
L (4. 4)	21	-7134.49	73.67*	1.03	15.51

\* Significant change ( $P < 0.05$ )

In *Table 3*, first three eigenvalues of the additive genetic (co)variance matrix and their relative proportions (in parenthesis) estimated by Ali-Schaeffer, Wilmlink and Legendre polynomial random regression models were given. The fourth eigenvalue had negligible proportions.

Eigenvalues of the estimated permanent environmental (co)variance matrix and their relative proportions (in parenthesis) were given in *Table 4* for different order of fit with Ali-Schaeffer, Wilmlink and Legendre polynomial models.

**Table 3.** Eigenvalues of the additive genetic (co)variance matrix and the proportion of total variance (%) estimated from Ali-Schaeffer, Wilmlink functions and Legendre polynomials

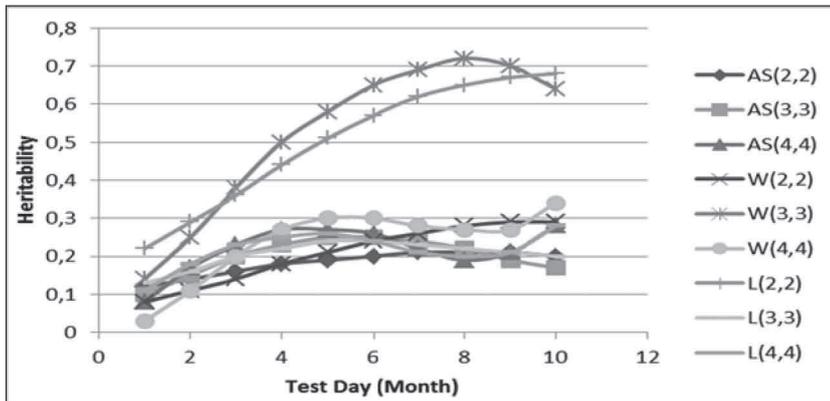
**Tablo 3.** Ali-Schaeffer, Wilmlink fonksiyonları ve Legendre polinomiyallerden tahmin edilen eklemeli genetik (ko)varyans matrislerinin özdeğerleri ve toplam varyanstaki payı (%)

Eigenvalues			
Models	First	Second	Third
AS (2,2)	2.09786 (98.81)	0.02524 (1.19)	-
AS (3,3)	2.24101 (93.94)	0.04168 (1.75)	0.10286 (4.31)
AS (4,4)	2.36989 (94.00)	0.03752 (1.49)	0.11365 (4.51)
W (2,2)	2.75402 (99.99)	0.00011 (0.01)	-
W (3,3)	8.06202 (97.97)	0.00019 (0.01)	0.16641 (2.02)
W (4,4)	2.89087 (94.27)	0.01239 (0.40)	0.16331 (5.33)
L (2,2)	7.09811 (99.62)	0.02685 (0.38)	-
L (3,3)	2.23548 (93.06)	0.05556 (2.31)	0.11128 (4.63)
L (4,4)	2.34273 (93.76)	0.05293 (2.12)	0.10287 (4.12)

**Table 4.** Eigenvalues of the permanent environmental (co)variance matrix and the proportion of total variance (%) estimated from Ali-Schaeffer, Wilmlink functions and Legendre polynomials

**Tablo 4.** Ali-Schaeffer, Wilmlink fonksiyonları ve Legendre polinomiyallerden tahmin edilen kalıcı çevre (ko)varyans matrislerinin özdeğerleri ve toplam varyanstaki payı (%)

Eigenvalues				
Models	First	Second	Third	Fourth
AS (2,2)	3.53207 (77.87)	1.00352 (22.13)	-	-
AS (3,3)	3.57297 (73.27)	0.99176 (20.34)	0.31201 (6.39)	-
AS (4,4)	3.50227 (69.14)	1.11461 (22.00)	0.33763 (6.67)	0.11079 (2.19)
W (2,2)	3.84564 (78.21)	1.07157 (21.79)	-	-
W (3,3)	0.00002 (0.00)	1.87079 (84.42)	0.34528 (15.58)	-
W (4,4)	3.91735 (69.22)	1.26276 (22.31)	0.37336 (6.60)	0.10586 (1.87)
L (2,2)	0.00002 (0.01)	1.37299 (99.99)	-	-
L (3,3)	3.59741 (73.26)	1.00259 (20.42)	0.31061 (6.32)	-
L (4,4)	3.56877 (69.72)	1.10422 (21.58)	0.33405 (6.53)	0.11091 (2.17)



**Fig 1.** Changes of heritability for TDMYs during lactation estimated from Ali-Schaeffer, Wilmlink and Legendre polynomial models

**Şekil 1.** Ali-Schaeffer, Wilmlink Legendre polinomiyallerinden tahmin edilen test günü süt verimleri için kalıtım derecesi değişimleri

**Table 5.** Heritability (diagonal), additive genetic (above diagonal) and phenotypic (below diagonal) correlations among test day milk yields estimated from AS (4,4) models**Table 5.** AS (4,4) modelinden elde edilen test günü süt verimleri arasındaki kalıtım derecesi (köşegen), eklemeli genetik (köşegen üstü) ve fenotipik korelasyonlar (köşegen altı)

Test Day (TD) (months)	TD1	TD2	TD3	TD4	TD5	TD6	TD7	TD8	TD9	TD10
TD1	0.08	0.94	0.87	0.81	0.76	0.73	0.73	0.77	0.82	0.78
TD2	0.60	0.17	0.98	0.95	0.93	0.91	0.91	0.94	0.93	0.82
TD3	0.46	0.61	0.23	0.99	0.98	0.97	0.97	0.98	0.93	0.78
TD4	0.37	0.55	0.63	0.26	0.99	0.99	0.99	0.98	0.91	0.74
TD5	0.32	0.49	0.59	0.64	0.27	0.99	0.99	0.98	0.89	0.70
TD6	0.29	0.43	0.53	0.59	0.65	0.26	0.99	0.98	0.88	0.68
TD7	0.27	0.37	0.45	0.53	0.61	0.66	0.22	0.98	0.90	0.72
TD8	0.26	0.33	0.39	0.47	0.55	0.62	0.66	0.19	0.96	0.82
TD9	0.25	0.29	0.34	0.40	0.48	0.55	0.61	0.66	0.21	0.95
TD10	0.21	0.27	0.30	0.33	0.37	0.41	0.46	0.54	0.64	0.28

Heritabilities for TDMYs during lactation estimated from Ali-Schaeffer, Wilmlink and Legendre polynomials were given in [Fig. 1](#). The values were changed from 0.03 to 0.68.

Heritability, additive genetic and phenotypic correlations between TDMYs estimated from AS(4,4) models were given in [Table 5](#).

## DISCUSSION

Choice of best model partly depends on the criteria's (-2LogL, AIC, BIC and RV values). The W(2,2) models had the highest values for AIC, BIC and RV (15243.14, 15290.25, 2.63 respectively), while the W(4,4) models had the highest values for -2LogL (16694.53) ([Table 1](#)). According to estimated AIC and BIC by using the Ali-Schaeffer and Legendre polynomials were better than the finding of Wilmlink function. Similar results have been reported by Takma and Akbas <sup>[12]</sup>, Bignardi et al. <sup>[13]</sup> and Costa et al. <sup>[22]</sup>. While the AS(4,4) models had lowest AIC, BIC and RV values, the AS(2,2) models had lowest -2LogL values. Also, AIC, BIC and RV values were decreased while -2LogL values were increased with increasing order of model.

Although the L(3,3) model had the largest change (4.07%) of Log likelihood values, the Ali-Schaeffer and Legendre polynomial models which had the lowest AIC and BIC values was better than the Wilmlink model in terms of Log likelihood values ([Table 2](#)). So, the AS(4,4) model showed a good fit than other models ([Table 1](#) and [Table 2](#)). At the same time, the L(4,4) model have nearly similar values with AS(4,4) model.

For estimated values by Ali-Schaeffer, Wilmlink and Legendre polynomial models, first eigenvalues belonging to additive genetic effect account for over 95% of total variation ([Table 3](#)).

For estimated values by Ali-Schaeffer, Wilmlink and Legendre polynomial models, first and second eigenvalues belonging to permanent environmental effect account for over 90% of total variation. But second and third eigenvalues of W(3,3) models for permanent environmental effect account for over 90% of total variation. Also, the second eigenvalues for the L(2,2) model was account for 99% of total variation ([Table 4](#)).

The heritability estimates for TDMYs from W(3,3) model and L(2,2) model showed higher variability from other models ([Fig. 1](#)). This figure showed that the estimates of heritability for W(4,4) model was similar at early part of lactation and was higher from other models in the rest of the lactation. Additionally, for estimates the Ali-Schaeffer and Legendre Polynomials models were determined to be better than Wilmlink model. Also, the estimates of heritability with AS(4,4), W(2,2), W(4,4) and L(4,4) models showed higher in the middle and at the end of lactation. In there, the W(4,4) model and L(4,4) model were estimated nearly similar heritability values. While the estimates of heritability increased in the middle of lactation was similar to the study by Takma and Akbas <sup>[12]</sup>, increased at the end of lactation was not similar to the studies by Takma and Akbas <sup>[11]</sup> and Cobuci et al. <sup>[29]</sup>.

The additive genetic correlations were higher than the phenotypic correlations for AS(4,4) model ([Table 5](#)). These findings were similar with other studies <sup>[11,14]</sup>. While additive genetic correlations were changed from 0.68 to 0.99, the phenotypic correlations for TDMYs estimated from AS(4,4) model varied from 0.21 to 0.66. Both additive genetic correlations and phenotypic correlations were a decline, due to the increased distance between the periods. Heritability estimates were altered from 0.08 to 0.28. In addition, heritability estimates from AS(4,4) model was reached the point of peak at the middle and last part of lactation ([Table 5](#)).

In our study, the AS(4,4) models was a better performance than others for estimating the genetic parameters of Jersey cows under pasture-based dry seasonal production system in Karakoy Agricultural State Farm in Samsun (Turkey). Also, some studies have found the same performance with Ali-Schaeffer function for Holstein Friesian cows<sup>[12-14]</sup>. Due to the fact that there has no studies comparing different order of fit (L(2.3), L(2.4), ..., L(5.6), L(6.6)) Ali-Schaeffer, Wilmink and Legendre polynomial random regression model for Jersey cows in first lactation, it can be apparently declared that the AS(4,4) models can be used for management decisions and genetic evaluation of Jersey cows for milk production.

It seems that there is no consensus in literature for Jersey cows about the best order of fit Ali-Schaeffer, Wilmink and Legendre polynomials models to be used to model of TDMY with RRM. So, several RRM obtained with these models have been compared for fitting performance and estimated genetic parameters for TDMY with the AS(4,4) models that fits best. As a result, this study would be helpful to give the literature for estimating the genetic parameters of Jersey cows with RRM.

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