

Modelling lactation curves of dairy goats by fitting random regression models using Legendre polynomials or B-splines

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Abstract: A total of 17 356 test-day milk yield (TDMY) records from 642 first lactations of Alpine goats were used to model variations in lactation curve using random regression models (RRM). Orthogonal Legendre polynomials and B-splines were evaluated to obtain adequate and parsimonious models for the estimation of genetic parameters. The analysis was performed using a single-trait RRM, including the additive genetic, permanent environmental, and residual effects. We estimated the mean trend of milk yield, and the additive genetic and permanent environmental covariance functions through random regression using different orders of orthogonal Legendre polynomial (three to six) and B-spline functions (linear, quadratic, and cubic, with three to six knots). This study further evaluated different number of classes of residual variances. The covariance components and the genetic parameters were estimated using the restricted maximum likelihood method. Heritability estimates presented similar trends for both functions. The RRM with a higher number of parameters better described the genetic variation of TDMY throughout the lactation. The most suitable RRM for genetic evaluation of TDMY of Alpine goats is a quadratic B-spline function with six knots, for the mean trend, curves of additive genetic and permanent environmental effects, and five classes of residual variance.

Key words: genetic evaluation, Alpine, milk yield, test day, segmented polynomials.

Résumé : Un total de 17 356 données de production de lait au jour de test (TDMY – « test-day milk yield ») provenant de 642 premières lactations de moutons alpins ont été utilisé pour modéliser les variations de la courbe de lactation au moyen de modèles à régression aléatoire (RRM – « random regression models »). Les polynômes orthogonaux Legendre et les courbes B-splines ont été évaluées pour obtenir des modèles adéquats et parcimonieux pour l'estimation des paramètres génétiques. Les analyses ont été effectuées au moyen d'un RRM à caractéristique unique, incluant les effets génétiques additifs, environnementaux permanents et résiduels. Nous avons estimé la tendance moyenne de production de lait, et les fonctions additives de covariance génétique et environnementale permanente par régression aléatoire utilisant différents ordres de polynôme orthogonal Legendre (trois à six) et fonctions de courbe B-spline (linéaire, quadratique, et cubique, avec trois à six nœuds). Cette étude a évalué plus en détail différents nombres de classes de variance résiduelle. Les composantes de covariance et les paramètres génétiques ont été estimés au moyen de la méthode de maximum de vraisemblance restreint. Les estimations d'héritabilité montraient des tendances similaires pour les deux fonctions. Les RRM ayant un plus grand nombre de paramètres décrivaient mieux la variation génétique des TDMY tout au long de la lactation. Le RRM qui convient le mieux pour l'évaluation génétique des TDMY des moutons alpins est une fonction quadratique à

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courbe B-spline avec six nœuds, pour la tendance moyenne, les courbes d'effets additifs génétiques en environnementaux permanents et cinq classes de variance résiduelle. [Traduit par la Rédaction]

Mots-clés : évaluation génétique, alpin, production de lait, jour de test, polynômes segmentés.

Introduction

The world goat population is around 1.1 billion animals (FAOSTAT, <http://www.fao.org/faostat/>) and the dairy goat industry in particular is under great expansion (Liang and Devendra 2014). To continue expanding and remain competitive with other dairy industries, goat producers need to improve the production efficiency of their herds. Genetic improvement is the most attractive approach to promote permanent gains in livestock species. Milk production is among traits with highest economic relevance for the industry and is a great example of longitudinal traits, characterized by repeated measures in the same individual over time. For the analysis of longitudinal data, random regression models (RRM) have been widely used in various livestock species to analyse a variety of traits (Pereira et al. 2013; Flores and Werf 2015; Sasaki et al. 2015; Englishby et al. 2016; Kheirabadi and Rashidi 2016; Oliveira et al. 2016; Rovadoscki et al. 2016). In RRM, a fixed curve for the population is calculated and individual curves are fitted as deviation from the population curve. The RRM require the use of a function to model the fixed and random curves. Orthogonal Legendre polynomials (LEG) are among the most popular ones (Meyer 2005; Sarmiento et al. 2008; Bignardi et al. 2011; Kheirabadi et al. 2014). However, these models may require higher polynomial degrees and uneven adjustment throughout the lactation curve when compared with other polynomials (Meyer 2005). In addition, LEG may provide implausible parameter estimates for the beginning and the end of the trajectory by overemphasizing observations at the extremes (Meyer 2005). Considering that, B-spline (segmented polynomials) functions have been suggested as an alternative to high degree LEG (Huisman et al. 2002; Silvestre et al. 2006; DeGroot et al. 2007; Bohmanova et al. 2008; Sánchez et al. 2008; Bignardi et al. 2011). However, studies investigating the use of B-splines are still scarce for dairy goats, and therefore, there is a need to investigate these models for modelling lactation curves of dairy goats.

According to Bohmanova et al. (2008), different functions can be used to fit random and fixed regression curves. The first applications used parametric functions and functions of lactation shape such as Ali and Schaeffer (1987) and Wilmink (1987). However, these functions have been replaced with LEG and more recently with B-spline functions. According to Meyer (2005), the use of splines is interesting when a low polynomial degree does not fit well the data. The choice of an appropriate statistical model will allow the application of RRM to genetic evaluations of dairy goats aiming

to improve milk yield over the whole lactation. Therefore, the objective of this study was to investigate the variation in test-day milk production in dairy goats fitting RRM using either orthogonal Legendre polynomials or B-spline functions.

Materials and Methods

Animal care

Animal welfare and use committee approval was not needed for this study as datasets were obtained from pre-existing databases.

Data

A total of 17 356 test-day milk yield (TDMY) records from 642 first lactations of Alpine goats, from a single herd owned by the Universidade Federal de Viçosa (Viçosa, MG, Brazil) were used for this study. Animals were kept in collective stalls under a free stall system and were fed diets based on corn silage and hay, as roughage, and concentrate mixture, available according to the nutritional needs of the animals. Milk control was performed weekly and milking was carried out twice daily. TDMY is the sum of the milk collected in these two periods.

The data editing and consistency analysis were performed using SAS version 9.4 software (SAS Institute Inc. 2014). Only the following records were kept for further analysis: first lactation of does that had their first kidding between 10 and 30 mo of age, lactation length longer than 100 d, type of kidding (one to three kids), days in milk >5, and control intervals shorter than 28 d. Lactations were truncated at 270 d. Pedigree was recorded and the numerator relationship matrix coefficients contained 4767 animals.

Statistical analysis

After data editing, the influence of the following fixed effects on TDMY was investigated: year and season of kidding (years = 2000–2011; season 1, from March to September, and season 2 from October to February), genetic grouping (breed composition), type of kidding (one to three kids), and age of goat at kidding as a covariate, considering linear and quadratic effects. Only animals with the genetic composition of Alpine breed $\geq 50\%$ were kept for further analysis. They were grouped in classes as follows: 1 = 50% of Alpine breed; 2 = >50% and $\leq 75\%$; 3 = >75% and $\leq 93\%$; and 4 = >93%.

To check the influence of environmental effects, analyses of variance for unbalanced data were performed through the generalized least square method

using the procedure GLM of SAS version 9.4 software (SAS Institute Inc. 2014). The model used to explain variation of the traits due to known environmental effects was

$$y_{ijkl} = \mu + T_i + G_j + YS_k + b_1(P_{ijkl} - \bar{P}) + b_2(P_{ijkl} - \bar{P})^2 + \varepsilon_{ijkl}$$

where y_{ijkl} is the observation of the random animal l , with type of kidding i , genetic grouping j , and year-season k ; μ is the overall mean; T_i is the fixed effect of type of kidding i ; G_j is the fixed effect of genetic grouping j ; YS_k is the fixed effect of year-season k ; b_1 and b_2 are the linear and quadratic coefficients of regression of the analyzed trait in terms of age of dam at kidding (ADK, included as covariate), respectively; P_{ijkl} is the age of the dam l at kidding; \bar{P} is the overall mean of ADK; and ε_{ijkl} is the residual term associated to each observation y_{ijkl} .

Orthogonal Legendre polynomials

The single-trait animal model for random regression with LEG is described in a generalized manner as

$$y_{ijk} = FE_k + \sum_{m=0}^{k_b-1} b_m \varnothing_m(t_{ij}) + \sum_{m=0}^{k_a-1} \alpha_{im} \varnothing_m(t_{ij}) + \sum_{m=0}^{k_\gamma-1} \gamma_{im} \varnothing_m(t_{ij}) + \varepsilon_{ij}$$

where y_{ijk} is the milk production on the j control of the i th goat within fixed effects k ; FE_k are the fixed effects, which consisted of genetic grouping (breed composition), year-season of kidding (contemporary group), and type of kidding. ADK was included as a covariable with linear and quadratic effects; b_m is the m th regression coefficient of the TDMY on the LEG for modelling the average curve of the population; α_{im} and γ_{im} are the m th regression coefficient of the additive genetic and permanent environment effects, respectively, for the i th goat; k_b , k_a , and k_γ are the degree of LEG; t_{ij} is the control variable, lactation week of the i th goat standardized for the -1 to 1 interval, as described by Kirkpatrick et al. (1990); $\varnothing_m(t_{ij})$ is the LEG function for parameter m evaluated for age t_{ij} ; and ε_{ij} is the specific effect for each observation that was not explained by the correction factors or the regression of the model. The tested models had combinations of distinct adjustment orders for polynomials of fixed, random genetic, and permanent environmental curves, besides a number of classes for residual variance. The first models evaluated ranged from third to sixth order for curves: fixed, additive genetic, and permanent environment, considering homogeneity of variances. Only functions of the same order of adjustment were considered to allow possibilities of equal variations of both components, as recommended by López-Romero et al. (2004).

After choosing the most suitable model considering homogeneity of residual variance, a total of five

different models considering heterogeneity of residual variance were investigated in this second step: two (from 6 to 160 and 161 to 270 days in milk), three (from 6 to 60, 61 to 150, and 151 to 270 days in milk), four (from 6 to 50, 51 to 100, 101 to 200, and 201 to 270 days in milk), five (from 6 to 30, 31 to 90, 91 to 140, 141 to 200, and 201 to 270 days in milk), and six (from 6 to 30, 31 to 90, 91 to 120, 121 to 160, 161 to 210, and 211 to 270 days in milk) classes. The classes of residual variances were formed based on a graphical inspection of TDMY records.

The notation of the models fitted using LEG follows the pattern: LEGkHx, with k referring to the order of the polynomial curve to model the population mean, the additive genetic and permanent environmental effects, and x is the number of classes of residual variances. For instance, a model with regression of mean curve, additive genetic and permanent environment of order 3, and that had four classes of heterogeneous residual variance was coded as LEG3H4.

B-splines (segmented polynomials)

Analysis was performed using single-trait RRM. For all models, the random effects, additive genetic, and permanent environmental, were included in the analysis. The fixed effects included in the analysis were year-season of kidding (contemporary group), genetic grouping (breed composition), type of kidding, and the linear and quadratic effects of the covariate ADK. The matrix form of the single-trait animal model using random regression was given by

$$y = Xb + Za + Wc + e$$

where y is the vector of observations; b is the vector of fixed effects and coefficients of fixed regression; a is the vector of coefficients of additive genetic regression; c is the vector of coefficients of random permanent environment regression; e is the vector of random residual effect; and X , Z , and W are the incidence matrices of fixed, additive genetic, and permanent environmental effects, respectively.

The assumptions regarding to the components of the model are

$$E \begin{bmatrix} y \\ a \\ c \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \\ 0 \end{bmatrix}, V(a) = K_A \otimes A; V(c) = K_C \otimes I_{ND};$$

$$\text{and } V(e) = R$$

where K_A and K_C are the matrices of (co)variance between the regression coefficients random additive genetic and permanent environmental effects, respectively; A is the numerator relationship matrix; I_{ND} is an identity matrix; and R represents a matrix containing residual variances.

Additive genetic, permanent environmental, and average lactation curves were modeled by B-spline functions (linear, quadratic, and cubic), with equidistant knots. As suggested by Meyer (2005), the B-spline of degree $p = 0$ have values equal to unity for all points (t) at a given interval, and zero otherwise. For the k th segment given for knots T_k and T_{k+1} with $T_k \leq T_{k+1}$:

$$B_{k,0}(t) = \begin{cases} 1, & \text{if } T_k \leq t < T_{k+1} \\ 0, & \text{otherwise} \end{cases}$$

Functions with degree $B_{k,p}$, for $p > 0$, can be represented by

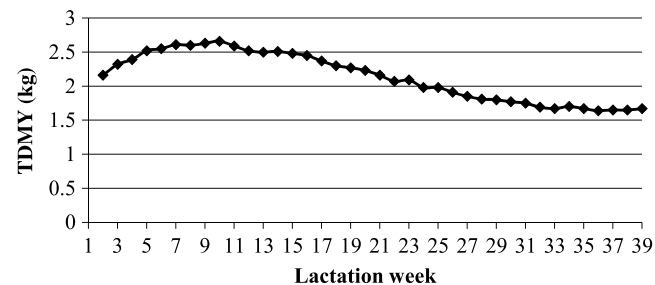
$$B_{k,p}(t) = \frac{t - T_k}{T_{k+p} - T_k} B_{k,p-1}(t) + \frac{T_{k+p+1} - t}{T_{k+p+1} - T_{k+1}} B_{k+1,p-1}(t)$$

The individual segments have been considered as linear (L), quadratic (Q), or cubic (C) order polynomials, with base function of degree $p = 1, 2$, and 3 , joined at knots, which allows the function to become continuous. Polynomials of same degree were considered in the model for the fixed curve, and for additive genetic and permanent environment effects.

First, we evaluated the B-spline functions for all curves considering the homogeneity of residual variances. In possession of the most suitable model under homogeneity of residual variances, two forms of residual variance structures were evaluated: residual variance constant throughout lactation or residual variance constant within lactation, but varying among classes of days in milk. If heterogeneous, we considered the same classes as specified for LEG. The m knots were chosen to divide weeks of lactation in $m - 1$ equidistant intervals and external knots were located on the 6th and 270th days in milk for all models. The same number of knots was adjusted for all effects. The number of random regression coefficients for modelling the trajectory of linear, quadratic, and cubic base functions was given by $m, m + 1$, and $m + 2$, respectively. The extremity knots do not interfere in the number of parameters of the model.

The B-spline RRM were coded as follows: "BSXkHy", where $X = L, Q$, or C , are the degrees of the linear, quadratic, or cubic polynomial segments, respectively; k is the number of knots of the fixed curve, additive genetic and permanent environmental effects; and y is the number of classes of residual variances. Therefore, as illustration, a model with the following representation BSL3H2 is a linear B-spline function, considering two classes of residual variances, three knots for all effects, and two segments ($k - 1$).

Fig. 1. Test-day milk yield (TDMY) per week for Alpine goats.



Variance components, model comparison, and genetic parameter estimates

Variance components were estimated via restricted maximum likelihood (REML) approach, using WOMBAT software (Meyer 2007). The results obtained when fitting RRM using B-spline functions were also compared with the best model obtained using LEG. Criteria for choosing models in this study were Logarithm of the REML function (LogL), Akaike's information criterion (AIC) (Akaike 1998) and Bayesian information criterion (BIC) (Schwarz 1978). The information criteria AIC and BIC can be described as $AIC = -2\log L + 2p$ and $BIC = -2\log L + p\log(N - r)$, where p is the number of parameters in the model; N is the total number of observations; and r is the rank of the incidence matrix of fixed effects in the model. Lower values for AIC and BIC and greater values for LogL indicate better model fit. For comparison between full and reduced models, we also used the likelihood ratio test (LRT; Wolfinger 1993), at 1% of probability.

The components of (co)variance and genetic parameters estimated over the lactation curve obtained by the models that provided better adjustments were also investigated. In addition, monitoring was done to verify the occurrence of convergence problems or estimates that were not consistent with the biology of the trait.

Results and Discussion

Analysis of fixed effects

All fixed effects (genetic grouping, year-season of kidding, ADK with linear and quadratic effect, and type of kidding) were significant at 1% level of significance and therefore were included in the final model for the study of TDMY. The average number of observations per test day was 456 ± 91 . Figure 1 shows the TDMY as a function of the lactation week. Milk production varied accordingly to a standard lactation curve for specialized dairy goat breeds, starting with 2.16 kg in the first milk control, increasing to 2.66 kg in the 10th week after kidding and gradually reducing in subsequent milk recordings until 1.67 in the 39th week of lactation.

Table 1. Models, number of parameters (*p*), logarithm of the restricted maximum likelihood function (*LogL*), Akaike's information criterion (AIC), Bayesian information criterion (BIC), and likelihood ratio test (LRT) for orthogonal Legendre polynomials (LEG).

Model ^a	<i>p</i>	<i>LogL</i>	AIC	BIC	LRT
LEG3H1	13	2374.138	-4722.276	-4621.400	**
LEG4H1	21	2714.039	-5386.076	-5223.122	**
LEG5H1	31	2941.077	-5820.154	-5579.608	**
LEG6H1	43	3050.944	-6015.888	-5682.228	Full model
LEG6H2	44	3142.035	-6196.070	-5854.652	**
LEG6H3	45	3155.987	-6221.974	-5872.796	**
LEG6H4	46	3153.432	-6214.864	-5857.928	**
LEG6H5^b	47	3179.123	-6264.246	-5899.548	NS
LEG6H6	48	3182.000	-6268.000	-5895.544	Full model

Note: **, *P* < 0.01; NS, no significant difference; Full model, model containing all the highest level of the effects.

^aLEG_xH_y, where *x* is the polynomial order for the fixed curve and for the additive genetic and permanent environmental effects, and *y* is the number of residual variance classes.

^bValues in boldface type indicate the best model based on *LogL*, AIC, BIC, and LRT criteria.

Fit and model comparison

Orthogonal Legendre polynomials

Table 1 shows the RRM fitted by LEG considering homogeneity of residual variances and model comparison. It was observed that values of *LogL*, AIC, and BIC improved with higher polynomial orders (Table 1). In accordance with LRT, there were significant differences (*P* < 0.01) between the full and reduced models. In general, higher values for the *LogL* criteria will always be expected for the more parameterized models because they are more flexible. However, it is important to use other comparison criteria that provide a choice of more parsimonious models, such as the AIC and BIC criteria. The LEG6H1 model was the one that best fitted the data according to all criteria. Nevertheless, it is important to evaluate the need to consider heterogeneity of residual variances throughout lactation, as there may be improvements in the partition of the total variation and consequently, generate better estimates of genetic parameters (Olori et al. 1999).

For greater number of classes there are more parameters to be estimated in the maximization of the likelihood function. More parameterized models may have bigger problems of convergence and estimation. It can hamper the use of RRM for genetic evaluations using large datasets. Therefore, it is important to use more parsimonious models without losing quality of fit of the random effects included in the model. The results of the models considering heterogeneity of residual variances are shown in Table 1. The model that considered

homogeneity of residual variance attained the worst fit, which is in agreement with other studies (Assis et al. 2006; Breda et al. 2006; Menezes et al. 2011; Silva et al. 2013). The residual variance is influenced by many factors which may vary throughout lactation. For instance, the effect of scale of production that is greater in the early stage of lactation than in the lactation end. This can be verified by the result of the division into only two classes of residual variances, which has provided a large reduction in the values of AIC and BIC, indicating better fit. In addition, the increase in number of classes considerably improved the modelling of random effects included in the analysis. These results are in agreement with those presented by Breda et al. (2006) and Silva et al. (2013) for Alpine goats, where a similar trend of fit improvement with increased number of residual variance classes was reported. The LEG6H6 model best fit based on AIC and *LogL*. However, it presented a slightly smaller BIC value compared with LEG6H5. This can be explained by the fact that BIC criterion applies a greater penalty to more parameterized models (Vrieze 2012), and LEG6H6 has one more parameter than the previous model. Furthermore, no significant differences based on the LRT were observed between these two models. As a greater number of parameters generate greater computational demand, more issues with convergence of algorithms can be expected for higher parameterized models. Therefore, the model that considered five classes of residual variances (LEG6H5) seemed to be the most suitable model.

Sarmiento et al. (2006), also working with data from Alpine goats, indicated the model of fifth order for the additive genetic effect and seventh order for the permanent environmental effect as the best option. However, they suggested that the use of a lower parameterized model of fourth order for the additive genetic effect and sixth order for the permanent environmental effects would give similar results. Silva et al. (2013) investigating orthogonal Legendre polynomials reported that the most suitable model for genetic evaluation of TDMY in dairy goats was the one that considered the fixed curve of order 4, the curve of additive genetic effects of order 2, the curve of permanent environmental effects of order 7, and at least five classes of residual variances.

After choosing the best model using LEG, the variance components and heritability for all points of lactation and genetic correlations among milk yield on days 6, 39, 71, 104, 137, 170, 203, 236, and 270 were investigated. The highest values of additive genetic and residual variance were observed in the stage of production peak, which occurred around 40 d after kidding (Figs. 2a, 2b). A possible explanation could be the effect of production scale, since at that stage it was observed the largest milk yields of the lactation. These results differ from those found by Silva et al. (2013), that observed increasing genetic variance along the lactation curve.

Fig. 2. (a) Estimates of variances obtained for the LEG6H5 (Legendre polynomial of order 6 and 5 classes of residual variance) model. (b) Variance estimates for the BSQ6H5 (quadratic B-spline model of polynomial order 6 and 5 classes of residual variance) model.

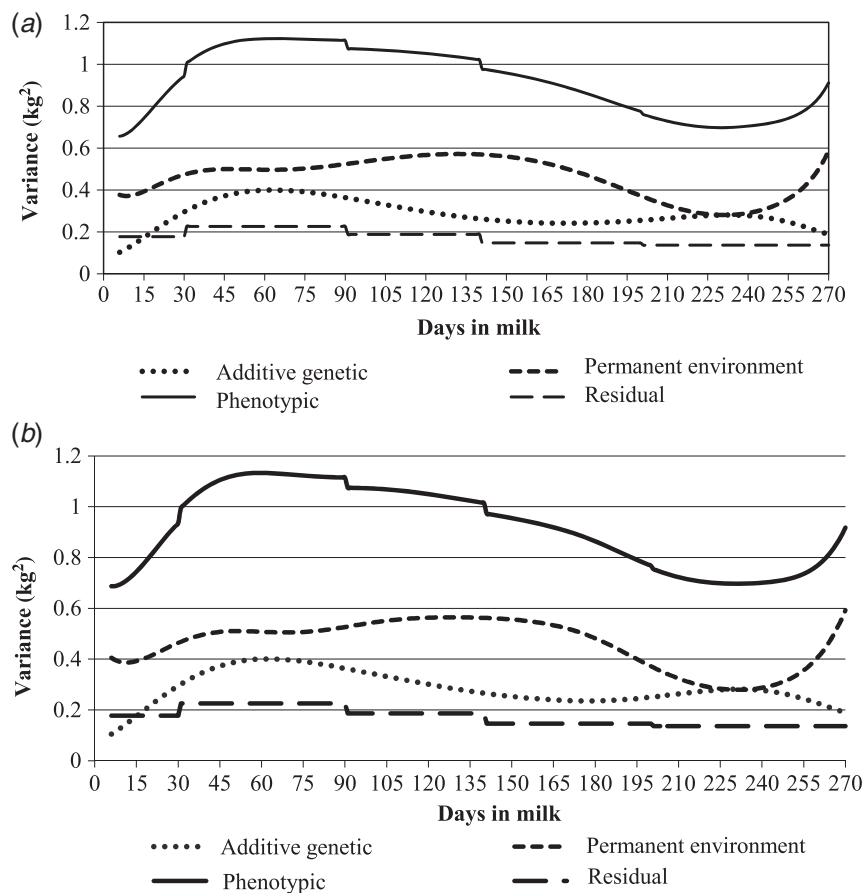
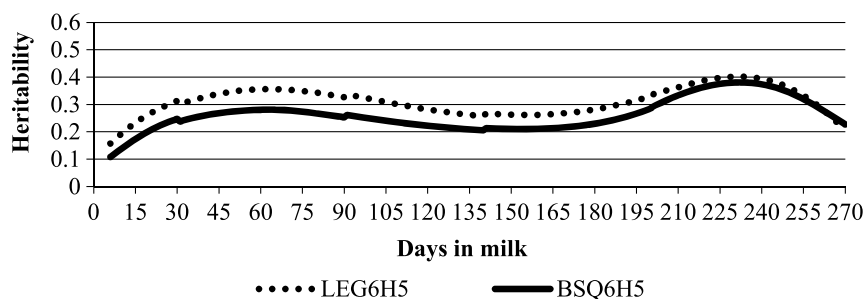


Fig. 3. Heritability estimates for test-day milk yield over the lactation for the models LEG6H5 (Legendre polynomial of order 6 and 5 classes of residual variance) and BSQ6H5 (quadratic B-spline model of polynomial order 6 and 5 classes of residual variance).



The phenotypic and permanent environmental variances were lower in early lactation and increased at the end of lactation compared with the other lactation stages. This may be due to the smaller number of records at the beginning and end of lactation, which does not represent major problems for the prediction of breeding values as RRM were used. However, missing data in the beginning or end of lactation will require extrapolations to predict values associated to permanent environmental effects of animals in those lactation

stages. As shown in Figs. 2a and 2b, the estimates of variances in the final period seemed worse than the estimates of the onset of lactation, which was expected as there was a greater reduction in the number of records at the end of the lactation. Menezes et al. (2011) also found higher estimates of permanent environmental effects at the end of lactation. Heritability estimates ranged from 0.15 to 0.40 throughout the lactation (Fig. 3). It was observed that the heritability estimates were lower in early and late lactation. This was possibly

Table 2. Estimates of genetic correlations for test-day milk yield (TDMY) obtained for the model LEG6H5^a (above diagonal) and for BSQ6H5^b (below diagonal).

TDMY	6	39	71	104	137	170	203	236	270
6	—	0.97	0.95	0.88	0.84	0.76	0.71	0.43	0.25
39	0.98	—	0.97	0.90	0.88	0.80	0.74	0.45	0.29
71	0.96	0.97	—	0.95	0.94	0.84	0.75	0.51	0.21
104	0.90	0.92	0.96	—	0.95	0.87	0.84	0.49	0.33
137	0.86	0.89	0.94	0.96	—	0.92	0.88	0.54	0.40
170	0.77	0.79	0.84	0.91	0.93	—	0.91	0.63	0.51
203	0.68	0.72	0.74	0.83	0.87	0.89	—	0.84	0.78
236	0.43	0.45	0.47	0.56	0.61	0.71	0.76	—	0.83
270	0.19	0.21	0.18	0.33	0.35	0.70	0.75	0.83	—

^aLegendre polynomial of order 6 and 5 classes of residual variance.

^bQuadratic B-spline model of polynomial order 6 and 5 classes of residual variance.

due to the greater influence of environmental effects on these stages and (or) proportionally lower additive genetic variance on this stages. For instance, in early lactation, first parity goats are usually not well adapted to the milking process and they have a deep postpartum stress due to negative energy balance. On the other hand, in late lactation many of them are in advanced stage of pregnancy, which can justify the decrease at this stage. Furthermore, as already mentioned, in these two extremes there was a greater amount of missing records, which can also cause errors in the estimation of variance components. Similar results were reported by Sarmiento et al. (2008). However, Silva et al. (2013) found higher estimates in the final third of lactation and Menezes et al. (2011) found higher values at the beginning of the lactation.

Table 2 presents the estimates of genetic correlations obtained by LEG6H5 model among milk production on days 6, 39, 71, 104, 137, 170, 203, 236, and 270. Genetic correlations in this study, obtained by LEG6H5 model, ranged from 0.21 to 0.95. Silva et al. (2013) found estimates of genetic correlations ranging from 0.98 to 1.00. Genetic correlations were smaller as the intervals among TDMYs increased. This result was consistent with Oliveira et al. (2016), who also found higher estimates of genetic correlations for shorter TDMY intervals in Alpine and Saanen goats. One possible explanation is that gene groups and the expression of genes related to milk production varies throughout lactation, and this expression is more similar to adjacent TDMY. However, other studies in this field are still needed (Strucken et al. 2015). Despite the smaller genetic correlations among more distant TDMYs, all estimates were positive, indicating that the selection of animals for milk production on any given day of lactation will bring positive responses to all other points on the curve. However, for the points where the genetic correlations were small (even if favorable), it is important to include additional curve points in the selection index to make progress in the whole pattern of the lactation curve.

B-splines

The models that were tested considering homogeneity of residual variances are shown in Table 3. The WOMBAT software (Meyer 2007) does not allow evaluation of models BSC3 (three knots and cubic order), as it is expected to have at least one parameter influencing the dependent variable in all three segments. Therefore, at least four knots are needed to be evaluated for cubic order B-splines. Regardless of the B-spline functions used (linear, quadratic, or cubic), when we increased the number of knots, AIC and the BIC showed higher absolute values indicating better fit (Table 3). Considering only the number of knots, the values of AIC and BIC were always higher in models for second-degree polynomial (quadratic), indicating that these polynomials fitted better to the data. Among B-spline functions considering homogeneity of residual variances, the model that best fit the data was BSQ6H5 (quadratic B-spline model of polynomial order 6 and 5 classes of residual variance). However, the criteria LRT does not allow comparisons between the BSQ6H1 and the other B-spline models with one class of residual variance (BSL6H1 and BSC6H1). This happened because there is no sufficient degrees of freedom for this comparison, since the number of parameters in the three models was the same (i.e., 43). Thus, different numbers of classes for the residual variances of B-splines of degrees 1, 2, and 3 (BSL6, BSQ6, and BSC6) were also investigated. Among the models with the same number of parameters, but with different degrees of the B-spline function (linear, quadratic, and cubic), those using a quadratic B-spline fitted better in accordance with the adopted comparison criteria (Table 4). Moreover, for all polynomial orders evaluated, the most parsimonious B-spline model that better fitted the data had five residual variance classes, similarly to the best model adjusted for orthogonal Legendre polynomials (i.e., LEG6H5). These findings indicate that five is actually the most suitable number of residual variance classes to be used in analyzes of TDMY for Alpine goats. The most appropriate division of classes of residual variance also influence the number of classes to be used.

Table 3. Models, number of parameters (p), logarithm of the restricted maximum likelihood function ($\text{Log}L$), Akaike's information criterion (AIC), Bayesian information criterion (BIC), and likelihood ratio test (LRT) for B-splines considering homogeneity of residual variances.

Model ^a	p	$\text{Log}L$	AIC	BIC	LRT
BSL3H1	13	2201.291	-4376.582	-4275.706	**
BSL4H1	21	2631.513	-5221.026	-5058.074	**
BSL5H1	31	2876.156	-5690.312	-5449.766	**
BSL6H1^b	43	3066.300	-6046.600	-5712.942	Full model
BSQ3H1	13	2339.923	-4653.846	-4552.978	**
BSQ4H1	21	2711.716	-5381.432	-5218.480	**
BSQ5H1	31	2952.442	-5842.884	-5610.338	**
BSQ6H1^b	43	3092.906	-6099.812	-5766.154	Full model
BSC4H1	21	2717.819	-5393.638	-5230.686	**
BSC5H1	31	2958.138	-5852.276	-5611.728	**
BSC6H1^b	43	3079.741	-6073.482	-5739.824	Full model

Note: **, $P < 0.01$. Full model, model containing all the highest level of the effects.

^aBSXkHy, where X = L, Q, and C represents the degree of linear, quadratic, and cubic polynomials, respectively; k is the polynomial order for the fixed curve and for the additive genetic and permanent environmental effects; and y is the number of residual variance classes.

^bValues in boldface type indicate the best model based on $\text{Log}L$, AIC, BIC, and LRT criteria.

Among all the models evaluated using B-splines, BSQ6H5 was the one that better fitted the data according to the comparison criteria used. The fact that the model BSQ6H5 has fitted the data better than the BSL6H5 and BSC6H5 models may be due to how each of them considers the points that influence the parameters of each knot, as shown by Meyer (2005). Models using linear B-splines ignore the estimation of the influence of a curve point in more distant points, while the cubic B-spline functions take into consideration the influence of more distant points. The linear B-spline functions require a smaller number of points (records) to estimate the coefficients, and therefore, have less multicollinearity issues. In the case of cubic B-spline functions, more points are used to estimate the coefficients (Meyer 2005). However, besides the higher multicollinearity, late lactation records may influence the early lactation records and vice-versa. This is not desirable, as genes that influence peak production, lactation length, and lactation persistence may not be the same (Strucken et al. 2015). In this study, quadratic B-spline functions seem to have better balanced the advantages and disadvantages of each order.

The results of Tables 1 and 4 show that the models that considered homogeneous residual variances presented the worst adjustments to the data according to the

Table 4. Models, number of parameters (p), logarithm of the restricted maximum likelihood function ($\text{Log}L$), Akaike's information criterion (AIC), Bayesian information criterion (BIC), and likelihood ratio test (LRT) B-splines considering heterogeneity of residual variances.

Model ^a	p	$\text{Log}L$	AIC	BIC	LRT
BSL6H1	43	3066.300	-6046.600	-5712.942	**
BSL6H2	44	3155.888	-6223.776	-5882.358	**
BSL6H3	45	3192.276	-6294.552	-5945.374	**
BSL6H4	46	3184.473	-6276.946	-5920.010	**
BSL6H5	47	3209.369	-6324.738	-5960.042	NS
BSL6H6	48	3208.161	-6320.322	-5947.866	Full model
BSQ6H1	43	3092.906	-6099.812	-5766.154	**
BSQ6H2	44	3185.676	-6283.352	-5941.934	**
BSQ6H3	45	3202.330	-6314.660	-5965.482	**
BSQ6H4	46	3197.208	-6302.416	-5945.478	**
BSQ6H5^b	47	3223.592	-6353.184	-5988.488	NS
BSQ6H6	48	3224.676	-6353.352	-5980.896	Full model
BSC6H1	43	3079.741	-6073.482	-5739.824	**
BSC6H2	44	3171.470	-6254.940	-5913.522	**
BSC6H3	45	3185.888	-6281.776	-5932.598	**
BSC6H4	46	3182.311	-6272.622	-5915.684	**
BSC6H5	47	3208.625	-6323.250	-5958.554	NS
BSC6H6	48	3210.447	-6324.894	-5952.438	Full model

Note: **, $P < 0.01$; NS, no significant difference; Full model, model containing all the highest level of the effects.

^aBSXkHy, where X = L, Q, and C represents the degree of linear, quadratic, and cubic polynomials, respectively; k is the polynomial order for the fixed curve and for the additive genetic and permanent environmental effects; and y is the number of residual variance classes.

^bValues in boldface type indicate the best model based on $\text{Log}L$, AIC, BIC, and LRT criteria.

comparison criteria used. This highlights the need to consider a heterogeneous structure of residual variances, because the variances tend to differ along the lactation. Similar results were obtained by Bignardi et al. (2011), when evaluating models for adjustments of lactation curves of Holstein cows and the authors concluded, according to the AIC and BIC criteria, that models containing homogeneous residual variances provided worst fits, regardless of the function used to model the random effects.

After choosing the best model using B-splines, variance components were investigated (i.e., heritability for all points throughout the lactation and genetic correlations among milk yield on days 6, 39, 71, 104, 137, 170, 203, 236, and 270). The largest variance estimates were observed for additive genetic and residual for the production peak stage, which occurs around 40 d after birth (Fig. 2b). It could be due to a scale effect since the highest TDMYs were observed in that lactation stage. The residual variance was greatest in the lactation peak and

gradually reduced until the end of the lactation. The phenotypic and permanent environment variances seemed to be underestimated in the early stage of lactation and overestimated at the end. This may be due to the smaller number of records available at the beginning and especially at the end of lactation, as a consequence of the proximity of the goat dry-period and the fact that several goats are already in advanced pregnancy stage.

The random effect of permanent environment ranged along the lactation curve. This demonstrates that adjusting the coefficients for heterogeneity of residual variances allowed separating more efficiently the nongenetic term from the genetic variation, reflecting in more accurate heritability estimates. The heritability estimates were higher in late lactation, which is consistent with the dairy cattle literature (e.g., Cobuci et al. 2005; Costa et al. 2008). However, especially for dairy goats this pattern was not reported in the literature yet, because in late lactation a decrease in heritability has been observed in other studies (Assis et al. 2006; Sarmiento et al. 2008; Oliveira et al. 2016). Heritability estimates obtained by BSQ6H5 model were smaller in the extremities of the lactation curve (Fig. 3). This can be explained by the lower additive genetic variances in those stages. Table 2 presents the genetic correlations for TDMY among days 6, 39, 71, 104, 137, 170, 203, 236, and 270, obtained using BSQ6H5 model. Estimates of genetic correlations were positive and larger between adjacent TDMY and reduced to the extent that increased the interval among milking controls. For points where the genetic correlations have shown small magnitude, it is important to include additional curve points in the selection index to make progress in the whole lactation curve. These results were very similar to those observed for LEG6H5 model.

Comparison among models using orthogonal Legendre polynomials and B-splines

The best models using LEG or B-splines were compared to make a recommendation of the best model to be used in genetic evaluations of dairy goats. In general, more parameterized models tend to be more penalized, as parsimonious models are desirable (Vrieze 2012). In this study, the two best models have the same number of parameters. BSQ6H5 presented greater LogL value compared with LEG6H5 model, indicating better fit. This was possibly due to the similar number of parameters in both models. However, major multicollinearity issues are expected when using high degree LEG. It may happen due to the fact that dependency problems of parameter estimates from the beginning to the end of the regression are reduced when using B-splines.

The phenotypic, additive genetic, permanent environmental, and residual obtained by the two models (LEG6H5 and BSQ6H5) were very similar and showed the same trend throughout lactation (Figs. 2a, 2b). The number of residual variance classes was the same for both models (five). Furthermore, both models yielded

higher estimates of the variance of permanent environmental effects in the end of the lactation curve, possibly due to the smaller number of records. Meyer (2005) stated that RRM using B-splines tend to be less susceptible to problems of erratic estimates at the extremes of the curve, a problem often observed when using LEG.

The heritability estimates obtained by LEG6H5 model were high throughout almost the entire lactation when compared with BSQ6H5 model (Fig. 3). However, it showed the same trend of variation throughout lactation, indicating that periods with higher heritability coincided for both models. Heritability estimates obtained by the two models suggest that there was enough genetic variability to make genetic progress for TDMY in dairy goats. According to LogL criteria, the model that best fitted the data was BSQ6H5. In addition, this model contained individual segments of polynomials of smaller degrees, which allows better control of the overall influence of individual observations and tend to provide better genetic parameter estimates. In agreement with our results, León et al. (2012) and Thepparat et al. (2015), working with Muricano-Granadina and Thailand goats, respectively, reported better fits when using spline functions. The findings obtained in this study indicate that there is enough genetic variability to make genetic progress for TDMY in dairy goats and it will be of great relevance to the implementation of genetic evaluations in dairy goats.

Conclusions

For the genetic evaluation of dairy goats aiming to improve TDMY, we recommend to fit a RRM using B-splines of degree 2 (quadratic) for the curves: fixed of the population, additive genetic, and permanent environment, with five segments (six knots) and five classes of residual variances.

Heritability estimates obtained for the lactation curve were moderate to high, indicating that there is enough genetic variability to make genetic progress for TDMY in dairy goats.

References

- Akaike, H. 1998. Information theory and an extension of the maximum likelihood principle. Pages 199–213 in E. Parzen, K. Tanabe, and G. Kitagawa, eds. Selected papers of Hirotugu Akaike. Springer, New York, NY, USA.
- Ali, T., and Schaeffer, L. 1987. Accounting for covariances among test day milk yields in dairy cows. *Can. J. Anim. Sci.* **67**: 637–644. doi:10.4141/cjas87-067.
- Assis, G.M.L.D., Albuquerque, L.G.D., Sarmiento, J.L.R., Carneiro Júnior, J.M., Lopes, P.S., and Rodrigues, M.T. 2006. Estimação de parâmetros genéticos em caprinos leiteiros por meio de análise de regressão aleatória utilizando-se a Amostragem de Gibbs. *Rev. Bras. Zootec.* **35**: 706–714. doi:10.1590/S1516-35982006000300011 [in Portuguese, English abstract].
- Bignardi, A., El Faro, L., Torres Júnior, R., Cardoso, V., Machado, P., and Albuquerque, L.G.D. 2011. Random regression models using different functions to model test-day milk yield of Brazilian Holstein cows. *Genet. Mol. Res.* **10**: 3565–3575. doi:10.4238/2011.October.31.4. PMID:22057992.

- Bohmanova, J., Miglior, F., Jamrozik, J., Misztal, I., and Sullivan, P. 2008. Comparison of random regression models with Legendre polynomials and linear splines for production traits and somatic cell score of Canadian Holstein cows. *J. Dairy Sci.* **91**: 3627–3638. doi:[10.3168/jds.2007-0945](https://doi.org/10.3168/jds.2007-0945). PMID:[18765621](https://pubmed.ncbi.nlm.nih.gov/18765621/).
- Breda, F.C., Albuquerque, L.G., Yamaki, M., Reis Filho, J.C., Sarmiento, J.L.R., Lopes, P.S., and Rodrigues, M.T. 2006. Estimaco de parâmetros genéticos para produo de leite de cabras da raa Alpina. *Rev. Bras. Zootec.* **35**: 396–404. doi:[10.1590/S1516-35982006000200009](https://doi.org/10.1590/S1516-35982006000200009) [in Portuguese, English abstract].
- Cobuci, J.A., Euclides, R.F., Lopes, P.S., Costa, C.N., Torres, R.D.A., and Pereira, C.S. 2005. Estimation of genetic parameters for test-day milk yield in Holstein cows using a random regression model. *Genet. Mol. Biol.* **28**: 75–83. doi:[10.1590/S1415-47572005000100013](https://doi.org/10.1590/S1415-47572005000100013).
- Costa, C.N., Melo, C.M.R.D., Packer, I.U., Freitas, A.F.D., Teixeira, N.M., and Cobuci, J.A. 2008. Genetic parameters for test day milk yield of first lactation Holstein cows estimated by random regression using Legendre polynomials. *Rev. Bras. Zootec.* **37**: 602–608. doi:[10.1590/S1516-35982008000400003](https://doi.org/10.1590/S1516-35982008000400003).
- DeGroot, B., Keown, J.F., Van Vleck, L.D., and Kachman, S.D. 2007. Estimates of genetic parameters for Holstein cows for test-day yield traits with a random regression cubic spline model. *Genet. Mol. Res.* **6**: 434–444. PMID:[17952867](https://pubmed.ncbi.nlm.nih.gov/17952867/).
- Englishby, T., Banos, G., Moore, K., Coffey, M., Evans, R., and Berry, D. 2016. Genetic analysis of carcass traits in beef cattle using random regression models. *J. Anim. Sci.* **94**: 1354–1364. doi:[10.2527/jas.2015-0246](https://doi.org/10.2527/jas.2015-0246). PMID:[27135995](https://pubmed.ncbi.nlm.nih.gov/27135995/).
- Flores, E., and Werf, J. 2015. Random regression test day models to estimate genetic parameters for milk yield and milk components in Philippine dairy buffaloes. *J. Anim. Breed. Genet.* **132**: 289–300. doi:[10.1111/jbgi.12133](https://doi.org/10.1111/jbgi.12133). PMID:[25727642](https://pubmed.ncbi.nlm.nih.gov/25727642/).
- Huisman, A., Veerkamp, R., and Van Arendonk, J. 2002. Genetic parameters for various random regression models to describe the weight data of pigs. *J. Anim. Sci.* **80**: 575–582. doi:[10.2527/2002.803575x](https://doi.org/10.2527/2002.803575x). PMID:[11892676](https://pubmed.ncbi.nlm.nih.gov/11892676/).
- Kheirabadi, K., and Rashidi, A. 2016. Genetic description of growth traits in Markhoz goat using random regression models. *Small Rumin. Res.* **144**: 305–312. doi:[10.1016/j.smallrumres.2016.10.003](https://doi.org/10.1016/j.smallrumres.2016.10.003).
- Kheirabadi, K., Rashidi, A., Alijani, S., and Imumorin, I. 2014. Modeling lactation curves and estimation of genetic parameters in Holstein cows using multiple-trait random regression models. *Anim. Sci. J.* **85**: 925–934. doi:[10.1111/asj.12185](https://doi.org/10.1111/asj.12185). PMID:[25228285](https://pubmed.ncbi.nlm.nih.gov/25228285/).
- Kirkpatrick, M., Lofsvold, D., and Bulmer, M. 1990. Analysis of the inheritance, selection and evolution of growth trajectories. *Genetics*, **124**: 979–993. PMID:[2323560](https://pubmed.ncbi.nlm.nih.gov/2323560/).
- León, J.M., Macciotta, N.P.P., Gama, L.T., Barba, C., and Delgado, J.V. 2012. Characterization of the lactation curve in Murciano-Granadina dairy goats. *Small Rumin. Res.* **107**: 76–84. doi:[10.1016/j.smallrumres.2012.05.012](https://doi.org/10.1016/j.smallrumres.2012.05.012).
- Liang, J., and Devendra, C. 2014. Expanding the contribution of dairy goats in efficient and sustainable production systems. *Anim. Prod. Sci.* **54**: 1198–1203.
- López-Romero, P., Rekaya, R., and Carabano, M. 2004. Bayesian comparison of test-day models under different assumptions of heterogeneity for the residual variance: the change point technique versus arbitrary intervals. *J. Anim. Breed. Genet.* **121**: 14–25. doi:[10.1046/j.0931-2668.2003.00409.x](https://doi.org/10.1046/j.0931-2668.2003.00409.x).
- Menezes, G.R.D.O., Torres, R.D.A., Sarmiento, J.L.R., Rodrigues, M.T., Brito, L.F., Lopes, P.S., and Silva, F.G.D. 2011. Random regression models in the milk yield evaluation in Saanen goats. *Rev. Bras. Zootec.* **40**: 1526–1532. doi:[10.1590/S1516-35982011000700018](https://doi.org/10.1590/S1516-35982011000700018).
- Meyer, K. 2005. Random regression analyses using B-splines to model growth of Australian Angus cattle. *Genet. Sel. Evol.* **37**: 473–500. doi:[10.1186/1297-9686-37-141](https://doi.org/10.1186/1297-9686-37-141). PMID:[16093011](https://pubmed.ncbi.nlm.nih.gov/16093011/).
- Meyer, K. 2007. WOMBAT — a tool for mixed model analyses in quantitative genetics by restricted maximum likelihood (REML). *J. Zhejiang Univ. Sci. B*, **8**: 815–821. doi:[10.1631/jzus.2007.B0815](https://doi.org/10.1631/jzus.2007.B0815). PMID:[17973343](https://pubmed.ncbi.nlm.nih.gov/17973343/).
- Oliveira, H.R.D., Silva, F., Siqueira, O., Souza, N., Junqueira, V., Resende, M., Borquis, R., and Rodrigues, M.T. 2016. Combining different functions to describe milk, fat, and protein yield in goats using Bayesian multiple-trait random regression models. *J. Anim. Sci.* **94**: 1865–1874. doi:[10.2527/jas.2015-0150](https://doi.org/10.2527/jas.2015-0150). PMID:[27285684](https://pubmed.ncbi.nlm.nih.gov/27285684/).
- Olori, V., Hill, W., McGuirk, B., and Brotherstone, S. 1999. Estimating variance components for test day milk records by restricted maximum likelihood with a random regression animal model. *Livest. Prod. Sci.* **61**: 53–63. doi:[10.1016/S0301-6226\(99\)00052-4](https://doi.org/10.1016/S0301-6226(99)00052-4).
- Pereira, R., Bignardi, A., El Faro, L., Verneque, R., Vercesi Filho, A., and Albuquerque, L. 2013. Random regression models using Legendre polynomials or linear splines for test-day milk yield of dairy Gyr (*Bos indicus*) cattle. *J. Dairy Sci.* **96**: 565–574. doi:[10.3168/jds.2011-5051](https://doi.org/10.3168/jds.2011-5051). PMID:[23084890](https://pubmed.ncbi.nlm.nih.gov/23084890/).
- Rovadoscki, G.A., Petrini, J., Ramirez-Diaz, J., Pertile, S.F., Pertille, F., Salvian, M., Iung, L.H., Rodriguez, M.A.P., Zampar, A., Gaya, L.G., Carvalho, R.S., Coelho, A.A., Savino, V.J., Coutinho, L.L., and Mourão, G.B. 2016. Genetic parameters for growth characteristics of free-range chickens under univariate random regression models. *Poult. Sci.* **95**: 1989–1998. doi:[10.3382/ps/pew167](https://doi.org/10.3382/ps/pew167). PMID:[27208151](https://pubmed.ncbi.nlm.nih.gov/27208151/).
- Sánchez, J., Misztal, I., Aguilar, I., and Bertrand, J. 2008. Genetic evaluation of growth in a multibreed beef cattle population using random regression-linear spline models. *J. Anim. Sci.* **86**: 267–277. doi:[10.2527/jas.2007-0064](https://doi.org/10.2527/jas.2007-0064).
- Sarmiento, J.L.R., Albuquerque, L.G.D., Torres, R.D.A., Rodrigues, M.T., Lopes, P.S., and Reis Filho, J.C. 2008. Comparison of random regression models for the estimation of genetic parameters in dairy goats. *Rev. Bras. Zootec.* **37**: 1788–1796. doi:[10.1590/S1516-35982008001000011](https://doi.org/10.1590/S1516-35982008001000011).
- Sarmiento, J.L.R., Reis Filho, J.C., Albuquerque, L.G.D., Lopes, P.S., and Rodrigues, M.T. 2006. Genetic evaluation of Alpine goats using test day milk yield. *Rev. Bras. Zootec.* **35**: 443–451. doi:[10.1590/S1516-35982006000200015](https://doi.org/10.1590/S1516-35982006000200015).
- SAS Institute Inc. 2014. Base SAS 9.4 procedures guide. SAS Institute Inc., Cary, NC, USA.
- Sasaki, O., Aihara, M., Nishiura, A., Takeda, H., and Satoh, M. 2015. Genetic analysis of the cumulative pseudo-survival rate during lactation of Holstein cattle in Japan by using random regression models. *J. Dairy Sci.* **98**: 5781–5795. doi:[10.3168/jds.2014-9152](https://doi.org/10.3168/jds.2014-9152). PMID:[26004830](https://pubmed.ncbi.nlm.nih.gov/26004830/).
- Schwarz, G. 1978. Estimating the dimension of a model. *Ann. Stat.* **6**: 461–464. doi:[10.1214/aos/1176344136](https://doi.org/10.1214/aos/1176344136).
- Silva, F.G., Torres, R.A., Brito, L.F., Euclides, R.F., Melo, A.L., Souza, N.O., Ribeiro, J.L., Jr., and Rodrigues, M.T. 2013. Random regression models using Legendre orthogonal polynomials to evaluate the milk production of Alpine goats. *Genet. Mol. Res.* **12**: 6502–6511. doi:[10.4238/2013.December.11.1](https://doi.org/10.4238/2013.December.11.1). PMID:[24390996](https://pubmed.ncbi.nlm.nih.gov/24390996/).
- Silvestre, A., Petim-Batista, F., and Colaco, J. 2006. The accuracy of seven mathematical functions in modeling dairy cattle lactation curves based on test-day records from varying sample schemes. *J. Dairy Sci.* **89**: 1813–1821. doi:[10.3168/jds.S0022-0302\(06\)72250-0](https://doi.org/10.3168/jds.S0022-0302(06)72250-0). PMID:[16606753](https://pubmed.ncbi.nlm.nih.gov/16606753/).
- Strucken, E.M., Laurenson, Y.C., and Brockmann, G.A. 2015. Go with the flow — biology and genetics of the lactation cycle. *Front. Genet.* **6**: 118. doi:[10.3389/fgene.2015.00118](https://doi.org/10.3389/fgene.2015.00118). PMID:[25859260](https://pubmed.ncbi.nlm.nih.gov/25859260/).

- Thepparat, M., Boonkum, W., Duangjinda, M., Tumwasorn, S., Nakavisut, S., and Thongchumroon, T. 2015. Genetic evaluation using random regression models with different covariance functions for test-day milk yield in an admixture population of Thailand goats. *Anim. Sci. J.* **86**: 655–660. doi:[10.1111/asj.12349](https://doi.org/10.1111/asj.12349). PMID:[25494881](https://pubmed.ncbi.nlm.nih.gov/25494881/).
- Vrieze, S.I. 2012. Model selection and psychological theory: a discussion of the differences between the Akaike information criterion (AIC) and the Bayesian information criterion (BIC). *Psychol. Methods*, **17**(2): 228–243. doi:[10.1037/a0027127](https://doi.org/10.1037/a0027127). PMID:[22309957](https://pubmed.ncbi.nlm.nih.gov/22309957/).
- Wilmink, J. 1987. Adjustment of test-day milk, fat and protein yield for age, season and stage of lactation. *Livest. Prod. Sci.* **16**: 335–348. doi:[10.1016/0301-6226\(87\)90003-0](https://doi.org/10.1016/0301-6226(87)90003-0).
- Wolfinger, R. 1993. Covariance structure selection in general mixed models. *Commun. Stat. Simul. Comput.* **22**: 1079–1106. doi:[10.1080/03610919308813143](https://doi.org/10.1080/03610919308813143).