HINAYAH ROJAS DE OLIVEIRA

**COMBINING DIFFERENT FUNCTIONS TO DESCRIBE MILK, FAT AND
PROTEIN YIELD IN GOATS USING BAYESIAN MULTIPLE-TRAIT RANDOM
REGRESSION MODELS**

Dissertation presented to the
Genetics and Breeding Graduate
Program of the Universidade
Federal de Viçosa, in partial
fulfillment of the requirements for
degree of *Magister Scientiae*.

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To all people who have, somehow, contributed to make my dreams come true.

I dedicate.

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“All progress is precarious, and the solution of one problem brings us face to face with another problem.”

Martin Luther King Jr.

“But be not afraid of going slowly, be afraid only of standing still.”

Chinese proverb

BIOGRAPHY

Hinayah Rojas de Oliveira, daughter of Djmir Marques de Oliveira and Sandra Rojas de Oliveira, was born on August 10, 1989, in Bragança Paulista, São Paulo, Brazil. In March 2009, she joined the Animal Science major at the Universidade Federal de Viçosa in the city of Viçosa – MG, where she studied and joined several research groups and projects.

In April 2009, she was admitted as a Trainee at EJZ Consultoria, where in November 2009 she assumed the Human Resources Department and in November 2010 assumed the Presidency. In December 2011 she became advisor in the EJZ Consultoria. From December 2011 to February 2012 she did an English course at the Embassy School, in California-USA. From March 2011 to February 2014 she was granted a scholarship of scientific initiation, under the supervision of Doctor Ricardo Frederico Euclydes and Doctor Robledo de Almeida Torres. In July 2011, she participated of the Projeto Rondon, in the city of Poconé – MT. Since September 2013 she has been writing for a column, the "Gazeta Rural", in the "A Gazeta Regional" newspaper, distributed in the State of São Paulo. From December 2013 to February 2014 she did an internship at the Embrapa Gado de Leite, in the city of Juiz de Fora – MG, under the supervision of Doctor Marcos Vinícius Gualberto Barbosa da Silva.

In November 2011 two of her studies were awarded for its scientific importance at the Simpósio de Integração Acadêmica, at the Universidade Federal de Viçosa, Viçosa-MG. In March 2014 she received an honorable mention of the Centro de Ciências Agrárias of the Universidade Federal de Viçosa, for her excellent performance in the Animal Science major courses, and she started her Masters Course in the area of Genetics and Breeding at the Universidade Federal de Viçosa, under the supervision of Doctor Fabyano Fonseca e Silva.

On July 27, 2015, she submitted to defense committee her dissertation in order to obtain the title of Magister Scientiae in Genetics and Breeding.

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ABSTRACT

OLIVEIRA, Hinayah Rojas de, M.Sc., Universidade Federal de Viçosa, July, 2015. **Combining different functions to describe milk, fat and protein yield in goats using bayesian multiple-trait random regression models.** Adviser: Fabyano Fonseca e Silva. Co-adviser: Robledo de Almeida Torres.

The present study aimed to propose multiple-trait random regression models (multiple-trait RRM) combining different functions to describe milk yield, fat and protein percent in a dairy goats genetic evaluation by using MCMC (Markov Chain Monte Carlo) Bayesian inference. Were analyzed 3,856 milk yield (MY), fat (FP) and protein (PP) percent test-day records from 535 first lactation of Saanen and Alpine goats (including crosses). The initial analyses were performed using single-trait RRM, in which for all effects (average curve, additive genetic and permanent environmental) the following models were considered: third and fifth order Legendre polynomials, linear B-splines with three (at 1, 20 and 40 weeks) and five (at 1, 8, 15, 20 and 40 weeks) knots, Ali and Schaeffer function (Ali and Schaeffer, 1987) and Wilmink function (Wilmink, 1987). Residual variances were modeled by a step function with three classes: 1 to 3, 4 to 8, and 9 to 40 weeks of lactation. After definition of the best single-trait RRM to describe each trait (MY, FP, PP) based on the Deviance Information Criterion (DIC), the functions were combined to compose the multiple-trait RRM. The model based on Ali and Schaeffer function fitted better for MY and PP, while the model based on fifth order Legendre polynomials (Leg5) was the best one for FP. All tested RRM considering the combinations of functions presented lower DIC values, showing the superiority of these models when compared to other multiple-trait RRM based only on one function. Among the combined RRM, those considering Ali and Schaeffer function to describe the MY and PP, and Leg5 to describe the FP, presented the best fit. Estimates of heritability for MY and FP were close until 20 weeks, ranging from 0.25 at 0.54. The estimates of heritability for PP were, in general, higher than the estimates for MY and FP, ranging from 0.35 until 0.51. The genetic correlation between MY and FP and between MY and PP throughout the lactation period were negative, except for the period immediately after lactation peak. The genetic correlation between FP and PP was positive and approximately constant throughout the lactation (about 0.54). We concluded that combining different functions in a unique multiple-trait RRM can be a plausible alternative for joint genetic evaluation of different longitudinal traits.

RESUMO

OLIVEIRA, Hinayah Rojas de, M.Sc., Universidade Federal de Viçosa, julho de 2015. **Modelos de regressão aleatória multicaracterísticos combinando diferentes funções para descrever produção de leite, gordura e proteína em caprinos via inferência bayesiana.** Orientador: Fabyano Fonseca e Silva. Co-orientador: Robledo de Almeida Torres.

O presente estudo objetivou propor modelos de regressão aleatória multicaracterísticos (MRAM) combinando diferentes funções para descrever a produção de leite e a porcentagem de gordura e proteína do leite, em uma avaliação genética de cabras leiteiras via inferência bayesiana. Foram analisados 3.856 registros de produção de leite (MY), porcentagem de gordura (FP) e proteína (PP) no dia do controle da primeira lactação de 535 cabras Alpina e Saanen (incluindo mestiças). As análises iniciais foram realizadas utilizando MRA unicaracterísticos (MRAU), nos quais para todos os efeitos (curva média, genética aditiva e de ambiente permanente), os seguintes modelos foram considerados: terceira e quinta ordem dos polinômios ortogonais de Legendre; B-splines lineares com três (na 1^o, 20^o e 40^o semana) e cinco (na 1^o, 8^o, 15^o, 20^o e 40^o semana) nós, função de Ali e Schaeffer (Ali e Schaeffer, 1897) e função de Wilmink (Wilmink, 1987). As variâncias residuais foram consideradas heterogêneas com três classes: 1 a 3, 4 a 8 e 9 a 40 semanas de lactação. Depois da definição dos melhores MRAU para descrever cada característica (MY, FP e PP), baseado no Critério de Informação da Deviance (DIC), as funções foram combinadas para compor o MRAM (MRAM combinado). O modelo baseado na função de Ali e Schaeffer apresentou melhor ajuste para as características MY e PP, enquanto o modelo baseado nos polinômios ortogonais de Legendre de quinta ordem (Leg5) foi o melhor para descrever FP. Todos os MRA testados considerando a combinação de funções apresentaram menores valores de DIC, demonstrando a superioridade destes modelos quando comparados a outros MRAM baseados somente em uma função. Entre os MRAM combinados, aquele que considerou a função de Ali e Schaeffer para descrever MY e PP e o Leg5 para descrever FP apresentou o melhor ajuste. As estimativas de herdabilidade para MY e FP foram próximas até 20 semanas, e variaram de 0,25 até 0,54. As estimativas de herdabilidade para PP foram, em geral, maiores que as estimativas para MY e FP, variando de 0,35 até 0,51. A correlação genética entre MY e FP e entre MY e PP ao decorrer do período de lactação foram negativas, exceto para o período imediatamente após o pico de lactação. A correlação genética entre FP e PP foi positiva e aproximadamente constante durante a lactação (aproximadamente 0,54). Conclui-se que a combinação de diferentes funções em um único MRAM pode ser uma alternativa plausível para a avaliação genética conjunta de diferentes características longitudinais.

INTRODUCTION

Dairy goats are present in every continent and, according to the Asian-Australasian Dairy Goats Network (AADGN, 2014), currently more than 90% of the 921 million goats existing in the world are raised in developing countries, being an important source of food and income for these populations. Among the generated products, despite the low efficiency, goat milk has won a prominent position, since it is the main raw material used in the production of goat cheese. The yield and quality of the goat cheese depends, however, on the content of milk components, especially the fat and protein percent.

Thus, an alternative to improve the efficiency of milk yield, fat and protein percent in dairy goat herds is through genetic breeding, whose the success also depends on the improvement of statistical methods used for the (co)variance components and breeding values estimation. Among the proposed methods, the multiple-trait random regression models (RRM) have been adequate for the joint analyses of milk yield and milk constituents. Nevertheless, multiple-trait RRM considering these traits in goats have not been reported in the literature, which present only multiple-trait analyses considering different kidding orders as different traits, separately for milk, fat and protein yield (Menéndez-Buxadera et al., 2010). In dairy cattle and buffalos, there are some studies based on multiple-trait RRM considering these traits, however, the majority of them are based on the Legendre orthogonal polynomials (Kheirabadi et al., 2014; Pereira et al., 2013; Borquis et al., 2013).

Under a single-trait RRM, studies about the milk yield of dairy goats using splines (Thepparat et al., 2014; León et al., 2012) and other specific functions to model the lactation curve (González-Peña et al., 2012) have demonstrated equal or better fit than the traditional Legendre polynomial models. In relation to the modeling of milk constituents, the majority of the studies about single-trait RRM have also been based on Legendre polynomials (Andonov et al., 2013), but some studies in cows have shown that splines are better to describe fat and protein yield (Bouallegue et al., 2015).

In this context, the combination of these different models under the multiple-trait RRM framework is an important source of research in the field of animal breeding, since it allows using different functions to describe different traits in a unique model, enabling improve the fit quality in relation to single-trait and multiple-trait RRM considering only one function for all traits. Thus, the present study aimed to propose multiple-trait random regression models combining different functions (Legendre, B-spline, Wilmink and Ali and Schaeffer) to describe milk yield, fat and

protein percent in a dairy goats genetic evaluation by using MCMC (Markov Chain Monte Carlo) Bayesian inference.

GENERAL REVIEW

1. Genetic breeding of dairy goats

Dairy goats produce about 2% of the world total amount of milk produced by livestock species (FAO, 2008), however, only the developing countries produce approximately 83% of the total amount. Thus, most organizations engaged in the genetic breeding of dairy goats are located, currently, in developed countries and are dedicated to milk production (Aziz, 2010).

In Brazil, the first goats were introduced by the Portuguese, French and Dutch settlers around 1535 year (Machado, 1996). Nonetheless, only from the 1970, the interest in the commercial exploration of goats for milking purposes has appeared. Due to this interest, in 1974 it was founded the Associação Brasileira de Criadores de Caprinos (ABCC), later giving rise to the Associação Brasileira de Criadores de Caprinos Leiteiros (CAPRILEITE). Thus, in the 1970 and 1980 the Association was responsible for a cycle of importing that brought to Brazil animals from various breeds specifically for milk production, among them the Saanen and Alpine breeds.

The importation of animals was performed from countries that had structured genetics breeding programs, mainly from European countries and United States of America, and resulted in dependence of other countries for the Brazil improve its herds. However, besides of health problem that such importations generated in Brazil, another problem was the difference between the goal selection between the countries. Among these different goals selection, whereas Brazil had as main objective to increase the amount of milk, European countries aimed mainly to improve the quality of milk produced, targeting the manufacture of the goat cheese, and USA had as main goal the type traits (Aziz, 2010).

From the year 2005 on, the Embrapa Caprinos e Ovinos created the Programa de Melhoramento Genético de Caprinos Leiteiros (Capragene). It has as its main objective to promote the genetics improvement of the dairy goats in Brazil through of the accurate identification of the superior genetically sire for traits such as conformation, milk production and quality, reducing the dependency on animal importation. Thus, nowadays dairy goats in Brazil is an activity potentially profitable, which is being consolidated as an important segment of the national livestock. Then, Brazil is currently the 17th largest producer of goat milk in the world and the largest producer of the American continent (FAO, 2012). However, according to Bispo (2009), the daily milk yield

per animal is around 1 kg/goat/day, and the process of herd improvement has not followed the trend of modernization and intensification of the production system, in general. The intensive dairy goat activity prevails especially in the southern and southeastern regions of the country, due to the better prices paid for goat milk. Importantly, that the goat milk is not paid for its quality in Brazil, nonetheless, as some companies have already paid cow milk in accordance with protein and fat content, there is a tendency that, in a few years, the goat milk is also paid for its content.

In France, currently, the breeding programs have been based on index selection called ICC (Index Combine Caprine), which combine information about total protein, total fat and fat and protein percent, but does not include the amount of milk produced. Recently, type traits as attachment of the udder and the placement of teats has been introduced using a type score. The Spanish selection program for improving goat milk production have been based on milk yield and protein percent. In the USA, genetic evaluation have been based on milk, fat and protein yield and type traits (Aziz, 2010).

According to Wood (1967), the knowledge of the lactation curve is essential to lead the nutritional and reproductive management adopted in the farm, since it allows, from the registrations of incomplete productions, for the evaluation of animals before the end of yielding, saving time and financial resources. The comparison of the shape of the curve between different groups of animals, with different genetic group, ages, herds and other treatments of interest, are of great importance because these comparisons can provide information about the effectiveness of these groups, providing a better production control beyond the selection of those more productive animals.

There are different mathematical models for studying the lactation curve, as Wood (1967), Ali and Schaeffer (1987) and Wilmink (1987) models (more details about this models on the topic of parametric functions), but not always the parameters used in these models adjust adequately, since many factors can be influencing production. Among the factors that influence the lactation curve of goats are breed, number of offspring, order of kidding, year and season of kidding and potential yield (Silva et al., 2013a). Among the used methodologies, those that consider the random regression models have been proposed as an alternative to model traits that are repetitious in the life of the animal, such as milk yield, fat and protein percent (Borquis et al., 2013).

2. Random regression models

Longitudinal data, such as the milk yield, fat and protein percent test-day, need a special statistical treatment, since the covariance pattern among the repetitive measurements is well structured. Then, an alternative to work this data is through applying random regression models.

The use of random regression models (RRM), also known as infinite dimensions models, was proposed by Henderson Jr. (1982) as an alternative to overcome the problem of overparameterizing in multiple-trait analyses. Thus, in random regression, coefficients for the chosen polynomials are estimated in order to explain the variation of the trait(s) through time.

According to Schaeffer (2004), the RRM must contain a set of fixed curves that describe the phenotypic relation for the various groups of individuals, and random regressions for the additive genetic and the permanent environmental effects. This way, in the RRM the fixed regression describes the average curve of the population, the additive genetic effect describes the curve of each animal as a difference from the genetic average of the population, the permanent environmental random regression describes the non-additive differences, and the variations not explained by the regression are called the residues.

It is important to emphasize that the RRM present a series of advantages in relation to the traditional models, since they do not require a minimum number of records per animal, which means that there is no need to exclude animals with few records of the analysis; consider the relationship matrix for obtaining genetic estimates; allow the estimating of the covariance components among the controls; allow estimating the heritability of the trait and the estimated breeding value of the animals in any given point of the curve; allow to use the phenotypic information without the need of adjustment factors and/or time standards, which means it makes it possible to work with the milk yield data on the same day of the test-day; allow using heterogeneous residual variance; admit the use of random permanent environmental effect; and, mainly, make it possible to estimate a smaller number of parameters than other methodologies, especially when the objective is to obtain genetic parameters among various traits simultaneously analyzed.

Moreover, Andonov et al. (2013), comparing single-trait random regression and repeatability models to predict breeding values for milk yield, fat and protein content test-day records of Norwegian goats, conclude that the genetic merit was predicted more accurate with RRM than with the repeatability model. In bovines, Khanzadeh et al. (2013), working with Holstein cattle, found similar results to the Andonov et al. (2013), when estimated the daughter yield deviations of Iranian Holstein bulls.

The RRM fit implies assuming a determined covariance structure between the records taken over the time. This structure is characterized as a function of covariance and as a result of the covariance among the random regression coefficients (Meyer, 1998). Resende et al. (2001) mention that the RRM and the functions of covariances are able to express in a more realistic way the phenomena associated to longitudinal data, as they assume that the trait in question can continually and gradually change over time.

The possibility of using the milk yield on the day of control instead of the accumulated milk yield (AMY) brings undisputable advantages in terms of animal genetic breeding, since it minimizes the errors in estimating the AMY for the calculation of the breeding values. However, it is still not well defined in the literature the best method for calculating the accuracy of the generated estimates.

The concern about the number of parameters to be estimated is related to the computational demand. In other words, related to difficulties of adequate convergence in terms of computational algorithms. Therefore, the advantage of the RRM becomes even greater when there is the interest in performing multiple-trait analyses of longitudinal data, as in the case of milk yield, protein and fat content, which has become even more essential due the perspective of remuneration related to the quality of the milk.

2.1. Multiple-trait random regression

The use of multiple-trait random regression models (MRRM) for dairy goats is important, since it allows the study of the genetic relations between milk yield and its components during lactation. Thus, it is possible to work with milk yield on test-day along with the protein and fat contents, essential components for the manufacture of milk products. Besides, the multiple-trait random regression assures all the advantages of multiple-trait analyses in relation to single-trait analyses, such the increase in the estimate of additive genetic variance, the reduction of residual variance and the increase of accuracy (Boligon et al., 2011).

However, although it seems to be a sensible choice to work with MRRM in the dairy goats genetic breeding area, few studies have used this methodology. Menéndez-Buxadera et al. (2010), working with Murciano-Granadino goats, compared the genetic parameters and the estimated breeding values obtained with MRRM considering the same trait in different lactations, based on the Legendre orthogonal polynomials, with the ones obtained by the repeatability test-day models (RTDM). The authors have concluded that the estimates obtained by the MRRM are more accurate,

being preferable, since they guarantee a better response for selection programs. Moreover, the authors mention that genetic evaluations based on MRRM have the additional advantage of permitting selection of animals by their lactating curves shape. We have, not found studies based on MRRM considering different traits in dairy goats in the literature.

Borquis et al. (2013), working with Murrah buffalos in a MRRM based on Legendre polynomials for the estimation of genetic parameters for milk, fat, and protein yield, found that the accuracy associated with estimated breeding values obtained using multiple-trait random regression was slightly higher (around 8%) when compared with single-trait random regression. The authors explain this difference to the greater amount of information available per animal, in the MRRM. Muir et al. (2007) and Hammami et al. (2008) found similar results working with dairy cattle.

It is necessary to emphasize, however, that even though the MRRM are more appropriate for studies that involve correlated traits, the multiple-trait random regression analyses are more exigent in computer terms than the single-trait random regression ones, which can mean problems in converging the used algorithms, since the dimensions of the matrices and the vectors are in function of the number of traits analyzed.

The application of RRM has become popular since the use of parametric functions specifically created to model lactating curves, as is the case of Wilmink (1987) and Ali and Schaeffer (1987) functions. However, studies using RRM based on parametric functions are most often found in the literature about goats as a milk-trait analysis. (González-Peña et al., 2012; León et al., 2012).

3. Parametric functions

The first mathematic functions created to represent the pattern of milk yield during lactation were proposed by Brody et al. (1923) and Brody et al. (1924), however, only after the development of the function proposed by Wood (1967) is that the using of parametric functions has become popular. Since then, many researchers have attempted to develop empiric mathematical models to describe the shape of the lactating curve of production animals (Pereira, 2013).

The empiric mathematical models of lactating curves are regular functions $y = f(t)$, defined for positive values of daily milk yield (y) and time of lactation (t). Each function has parameters that are associated to the phases of the curve of lactation, making it possible to estimate the production in any given period. Necessary to pinpoint that although the symbols used to represent

the parameters be similar in different functions, they do not have the same mathematical and/or biological interpretation.

Then, each function presents specific interpretations and unique estimates of its parameters that can describe more or less accurate terms the reality of the data. This way, the usage of a model or function depends on its ability to describe the production, being preferable those with the smallest associated prediction error (Groenewald and Viljoen, 2003), for that posteriorly can be obtained accurate estimates of the breeding values of each animal for the economically interesting traits.

Several mathematics functions, linear and non-linear, have been proposed to describe the shape of the lactation curve. Jamrozik et al. (1997), working with cows, compared many of these functions. Among all, the authors found to be more adequate the RRM based on Ali and Schaeffer (1987) and Wilmink (1987) functions, for after, to be compared to each other. Based on the obtained results, Jamrozik et al. (1997) observed that the RRM based on Wilmink function to describe the shape of the lactation curve required fewer computational resources and less time for analyses, while the RRM base on Ali and Schaeffer function has produced fewer prediction errors. Nonetheless, the authors have also observed that the RRM based on Wilmink and Ali and Schaeffer functions have generated practically the same classification of bulls by predicted genetic values at 305 days, being both of them adequate to describe the curve of milk yield of these animals.

In dairy goats, González-Peña et al. (2012) and Breda et al. (2006), working with Alpine breed, compared diverse mathematical models used to describe the lactation curve, among them the Wilmink (1987), Ali and Schaeffer (1987) and Legendre orthogonal polynomials. Both authors conclude that Ali and Schaeffer and Legendre polynomials models were the best functions to model adequately lactation curves of Alpine goats. However, Breda et al. (2006) comments that the genetic correlation estimates between milk yields in the beginning and in the end of lactation obtained by Ali and Schaeffer function were negative.

It is important to show, however, that although the parametric functions tend to describe better the shape of the lactation curve, the predictions can be not accurate due to not so adequate numeric properties. Thus, it is suggested that these numerical properties can be improved through orthogonalizing the covariance for each given random effect (Nobre et al., 2003).

This way, based on the fact that polynomial regression is appropriate and flexible to adjust linear functions of the averages, it can also be used to adjust covariance structures (Nobre et al.,

2003). It has been prioritized, then, the use of non-parametric functions in the processes of estimating covariance functions, as in the Legendre orthogonal polynomials.

4. Legendre orthogonal polynomials

The Legendre orthogonal polynomials (LOP) are non-parametric functions derived from a transformation made in the independent variable. In the case of milk yield, the transformation of the lactation days (a_i) can be obtained through the equation shown in Kirkpatrick et al. (1990):

$$a_i^* = \frac{2(a_i - a_{\min})}{a_{\max} - a_{\min}} - 1$$

in which $a_{\max}$ and $a_{\min}$ are the highest and the lowest days in lactation that can be found in the data set, respectively.

Also, still according to Kirkpatrick et al. (1990), the j^{th} normalized LOP, ϕ_k , can be defined as follow:

$$\phi_k(a_i^*) = \frac{1}{2^j} \sqrt{\frac{2k+1}{2}} \sum_{m=0}^{[k/2]} (-1)^m \binom{k}{m} \binom{2k-2m}{k} (a_i^*)^{k-2m}$$

where a_i^* is the established day for the range in which the polynomial k is defined as $[-1 \text{ to } +1]$.

One of the biggest advantages of the LOP is that, since they are orthogonal, they reduce the problems of multicollinearity of the data, which means the columns of the matrix referring to the days are independent, preventing the matrix to become non-defined positive. Another important advantage of the LOP is that, as the lactating days become independent after the transformation, new terms can be added to the model without the need to alter the previous estimates, a process that increases the computational efficiency.

However, it is important to remember that very complex polynomials make the convergence of the algorithms more difficult, make the results more difficult to be obtained or the analyses less accurate. In addition, it is possible for the polynomial interpolation to present oscillations in the extremes of the curve of the interpolated interval that tend to the infinite. This effect is commonplace in analyses that use the LOP, being known as “Runge Effect”.

The Runge Effect describes the increase of the error of polynomial approximation due to the increase in the adjustment order, with errors predominantly attributed to oscillations in the curve extremes. López-Romero et al. (2004) comments that such behavior can generate unfeasible estimates of variance components in the extremes of the curve of the control variable and negative correlations between farther control days.

On the other hand, the choice of very simple equations and poorly parameterized makes modelling more difficult, becoming inefficient to explain part of the genetic variations. Therefore, an alternative to reduce the order of the employed functions without compromising the fit of the model is through using segmented polynomials.

Several studies involving single-trait random regression models (SRRM) based on the LOP have already been found in the literature of dairy goats, among them Thepparat et al., 2014; Andonov et al., 2013; Silva et al., 2013b; Sarmiento et al., 2008; Zumbach et al., 2008 and Breda et al., 2006. For multiple-trait random regression analyses based on LOP, however, there are still just a few studies found, being that most of studies considering one trait in different lactations (Menéndez-Buxadera et al., 2010).

5. Segmented Polynomials

The segmented polynomials, also known as splines, can be defined as segments of polynomials of m order that are connected in a way to have continuous derivations of $m-1$ order (Rice, 1969). In essence, what is done is to adjust regression lines in different gaps and to connect them with knots. Therefore, another definition for splines is that these are models with local fits among knots that allow to estimate the functional state of the data.

As with the Legendre orthogonal polynomials, in splines, the independent variable (x) is transformed. However, more than just taking into consideration the knots, in splines calculations the order of the used polynomial is considered since the beginning of the analysis. This way, segmented polynomials do not have the advantage of being possible to add coefficient without altering the other ones, as is the case of Legendre polynomials.

The polynomial order to be used must be defined according to the knowledge of the researcher about the trait, being the number of random regression coefficients to model the trajectory of the functions on linear, square and cubic bases given respectively by N , $N+1$ and $N+2$, considering N the number of internal knots (Brito, 2012).

According to Schenkel (1989), among the advantages of the segmented polynomials, it can be mentioned: the reduction of multicollinearity in analyses, once the independent variable (x) is transformed; the improvement in modeling, given that the behavior of the function that describes the relation of the variables in one region becomes independent from the behavior in other regions; their linearity in terms of parameters; the fact that they have best properties (Best Linear Unbiased Estimators - BLUE); and the increase in the domain of approximation, which means, they are able to provide estimates in a broad spectrum of possible values.

Misztal (2006) comments that since each coefficient of a segmented polynomial affects only a fraction of the trajectory, models with better numerical properties are expected, so that the changes in the extremes of the trajectory are more moderate. Therefore, differently from what happens with LOP, in splines the Runge Effect is not observed.

Furthermore, Misztal (2006) demonstrates that the knots of the segmented polynomials can be chosen in order to correspond to the pattern of changes along the trajectory, which would result in a reduction in the dimension of the model. This way, the knots can be denser in regions of fast changes, and scarcer in regions of slow changes. However, one of the biggest difficulties of working with segmented polynomials is the recognition of the spots where the knots must be inserted. To define the best points, Schenkel (1989) comments that among the known methods are the previous knowledge of the researcher in the area, the use of diagrams and averages for estimating the knots and/or the use of a non-linear model for estimating not only the knots but also the regression coefficients.

Thepparat et al. (2014) compared covariance functions of milk yield from test-day records among exotic (Saanen, Anglo-Nubian, Toggenburg and Alpine) and crossbred goats (Thai native and exotic breed). Among the tested covariance functions were Wilmink function (1987), second and third order Legendre polynomials, and two models with linear splines with 4 knots (located at 5, 25, 90 and 155 days in milk and 5, 35, 95 and 155 days in milk). The authors concluded that the covariance function had an important impact on (co)variance estimation in RRM and that the RRM based on splines with 4 knots (located at 5, 25, 90 and 155 days in milk) had better fit than all other tested functions. The authors also comments that the model based on linear splines was more appropriate than model based on LOP due to its greater flexibility, offering knots in the shape of fitted curves.

It is necessary to emphasize that there are several types of segmented polynomials. Nonetheless, segmented polynomials of the B type have been preferred in studies related to animal

genetic evaluation, and it is possible to find interesting studies with dairy cows (Bohmanova et al., 2008; Jamrozik et al., 2010; Bignardi et al., 2012). Studies with dairy goats using B-splines are still scarce in literature.

5.1. B-Splines

B-spline functions are local base functions used to implement the spline segments due to their better numerical and computational properties, when compared to other base functions (de Boor, 2001; Schumaker, 2007). According to Meyer (2005), the B-splines functions comprehend a set of overlapped functions, smooth and non-negative, that are single-mode and add up the unit for all time values.

The B-spline segmented polynomials present interesting computational properties, since they reduce the cost per iteration and increase the convergence rate, when compared to models with LOP (Bohmanova et al., 2005; Robbins et al., 2005). Misztal (2006) states that this superiority of the B-splines functions is due to better numerical properties of these functions, since each coefficient affects only a fraction of the trajectory.

Santos et al. (2014), studying the prediction of the genetic values for milk yield from Guzará cows, using random regression models, compared the quality of the fit of the additive genetic and permanent environmental effects modeled by Wilmink function, Ali and Schaeffer function, cubic B-spline and LOP. The authors have concluded that the best fit was provided by the model that used the cubic B-spline function with five coefficients of random regression for the additive genetic and permanent environmental effects. However, the same authors comment that the effects can be modeled using Ali and Schaeffer function and/or the Legendre polynomials, with little variation in the estimates of the generated genetic parameters. Bignardi et al. (2011) compared model variations in test-day milk yield during the first lactation of Brazilian Holstein cows by RRM considering the mean trend of milk yield modeled with a fourth order LOP, and the additive genetic and permanent environmental covariance functions modeled by Ali and Schaeffer, Wilmink and B-spline functions. The authors concluded that the RRM based on B-spline and Legendre polynomials as base functions are the most adequate to describe the covariance structure of the data, however, they comments that B-spline functions were less susceptible to implausible genetic variance estimates at extremes of the trajectory.

In the dairy goat area, studies about RRM based on B-spline are still scarce in the literature. Brito (2012), who compared RRM based on LOP (from 3 to 6 order) and B-splines (linear,

quadratic and cubic, from 3 to 6 knots) to describe the milk yield test-day of Alpine and Saanen goats, concluded that the most suitable RRM for genetic evaluation of milk yield of Alpine and Saanen breeds are a quadratic B-spline function with six knots, and a cubic B-spline function with six knots, respectively.

One of the methodologies used to estimate regression coefficients (either adopting the B-spline segmented polynomials, Legendre polynomials or through parametric functions) is the usage of Bayesian methods.

6. Bayesian Inference

The statistic inference works in the presence of observations (y), being the values initially unknown described by means of a probability distribution $p(y|\theta)$. Thus, the Bayesian theory is based on a theorem proposed by Thomas Bayes in 1761, which proposes that the uncertainty of a parameter must be quantified in terms of probability. The proportionality that represents Bayes Theorem is given by:

$$p(\theta|y) \propto p(y|\theta) p(\theta)$$

where:

$p(\theta)$ is the prior probability density of θ , which reflects the level of accumulated knowledge about the possible values of θ , before data contained in y is obtained;

$p(y|\theta)$ corresponds to likelihood function of y that represents the contribution of the data to the knowledge of the parameter;

$p(\theta|y)$ is the posterior probability density of θ , over which are done the inferences related to some specific parameter of interest.

The Markov Chain Monte Carlo (MCMC) methods constitute a family of iterative processes to approximate the generation of multivariate distribution samples. These methods have become the most important computational tool in Bayesian statistics, since they generate Markov Chains, which means chains whose parameter n depends only on the parameter $n-1$, by means of the iterative Monte Carlo simulation, that generates random values, whose stationary distribution is the own posterior density of interest (Sorensen and Gianola, 2002). This way, the MCMC method avoids the resolution of the complicated integrals that did not allow the use of the Bayesian technique.

Gibbs sampling, a particular case of the algorithm of Metropolis-Hastings of the MCMC method, is presented as a technique for indirectly obtaining the random variables of a marginal distribution without, however, the need to calculate the marginal probability density function (Casela and George, 1992). Geman and Geman (1984) define Gibbs sampling as a method of alternated conditional sampling defined in terms of subvectors of θ . Each iteration in Gibbs sampling consists of simulating values for each subvector de θ , conditionally to values of all the subvectors, totalizing K simulations for each complete iteration of the cycle. This kind of approximation will get better as the number of samples used in the calculations increase. However, successive samples are dependent on one another, which is undesirable and, for this reason, there is a discard of intermediate samples, known as thin. Besides, the stage of heating up of the chain, or in the other words, previous stage to the chain convergence, is also discarded (burn-in). The size of the chain to be generated is related to the easiness for converging the posterior distributions of the parameters, and they should vary according to the data and the functions used in the analyses.

Among the advantages of the Bayesian inference, it is necessary to mention that it provides precise solutions for the problem of finite size samples, since that for each data set there is an exact posterior distribution for inferences; it makes possible to build exact probability intervals for the estimates of the genetic parameters, being the probability of the parameters associated to the quantity and accuracy of the used information; in general, it presents estimates with smaller pattern deviation than the Restricted Maximum Likelihood Method (REML); it permits the use of prior information; and it presents computational advantages, since it does not require solutions for mixed model equations, making analyses easier.

However, when comparing models in Bayesian inference, it is not usual to adopt the Akaike information criteria (AIC) and the Bayesian information criterion (BIC) because the prior act as reducers of the effective number of parameters through its interdependences. Then, when working with Bayesians it is used the Deviation Information Criteria (DIC), proposed by Spiegelhalter et al. (2002), for comparing the models.

The DIC can be describe as follow:

$$DIC = D(\bar{\theta}) + 2p_D ,$$

where $D(\bar{\theta})$ is a point estimate of the deviance obtained by substituting the parameters by their posterior means estimates in the likelihood function; and p_D is the effective number of parameters in the model.

MATERIALS AND METHODS

Phenotypic data and systematic effects

In the present study, 3,856 milk yield, fat and protein percent test-day records from 535 first lactation of Saanen and Alpine goats (including crosses) belong to Universidade Federal de Viçosa, Brazil, were analyzed. The relationship matrix included a total of 1,061 animals, up to 3 previous generations to animals with phenotypic data.

The goats were kept in collective stalls under the free stall system and received feed based on corn silage and hay, in addition to concentrated mixture, provided according to their nutritional requirements. In order to reduce the reproductive seasonality of the animals, the herd adopts the use of hormonal protocols. The kids were separated from their mothers immediately after birth. The goats have kidded between 2000 and 2014 years, and the milk yield records were obtained by mechanical milking. Milk components were estimated monthly at the Milk Quality Laboratory of the Universidade Federal de Viçosa.

Milk yield, fat and protein percent records were considered weekly, varying from 1 (starting subsequently on the fifth day after kidding) to 40 weeks. According to Meyer (2005), RRM using polynomials of high orders require that each animal has more records than the order of the used polynomials to avoid implausible (co)variance component estimates. Thus, only animals with at least five records were included in the analyses. Data considered as outliers ($\mu \pm 3$ standard deviation, inside contemporary group) were discarded.

The systematic effects for all traits were: contemporary group (defined as year and season of kidding, where the season was divided in April to September and October to March. A total of 21 contemporary group were formed, with minimum of 5 and maximum of 57 animals); litter size (formed by 2 groups, one or two kids, where the first group was formed by 176 animals and the second one was formed by 359 animals); and genetic group (formed by 3 groups, Alpine $\geq 90\%$, Saanen $\geq 90\%$, and crossbreed between Alpine and Saanen goats, with minimum of 122 and maximum of 241 animals). The age of the dam at kidding was included as covariate with linear effect for all traits. After data editing, the descriptive statistics of milk yield, fat and protein percent test-day records are shown on Table 1.

Table 1. Descriptive statistics of milk yield, fat and protein percent test-day records.

Statistics	Milk yield (Kg)	Fat percent (%)	Protein percent (%)
N	3,856	3,856	3,856
Mean	2.33	4.51	4.09
SD	0.96	0.86	0.38
Minimum	0.20	1.36	2.14
Maximum	6.30	8.93	6.45

N: number of observations; SD: standard deviation.

Random regression models

The initial analyses were performed using single-trait random regression models (single-trait RRM). These models included the average curve of the population, systematic effects and, the additive genetic, permanent environmental and residual as random effects. To model the average curve, additive genetic and permanent environmental curves, third and fifth order Legendre polynomials, linear B-splines with three (at 1, 8 and 40 weeks) and five (at 1, 8, 15, 20 and 40 weeks) knots, Ali and Schaeffer function (Ali and Schaeffer, 1987) and Wilmink function (Wilmink, 1987) were used. The Ali and Schaeffer function (1) and the Wilmink function (2) can be describe as follow:

$$y_t = a + bf + cf^2 + dw + gw^2, \quad (1)$$

where a, b, c, d and g are the parameters that define the shape of the lactation curve; f is given by (t/t_t) and w is given by $\ln(t_t/t)$, assuming that t is the number of weeks in lactation in which milk yield was registered and t_t is the total time of lactation (in weeks).

$$y_t = a + b \exp(-kt) + ct, \quad (2)$$

where a is a parameter associated to the initial milk yield; b is a parameter associated to the decline rate of milk yield after the lactation peak; c is a parameter associated to the increase rate of milk yield up to the lactation peak; t is the number of weeks in milking in which production was registered; and k is a mathematical constant, assumed herein that $k=0.05$.

Residual variances were modeled by a step function with three classes: 1 to 3, 4 to 8, and 9 to 40 weeks of lactation. These classes were chosen according to preliminary single-trait RRM analyses considering a basic third order Legendre polynomials.

The RRM were compared based on the Deviance Information Criterion (DIC) developed by Spiegelhalter et al. (2002). The DIC can be describe as follow:

$$\text{DIC} = D(\bar{\theta}) + 2p_D ,$$

where $D(\bar{\theta})$ is a point estimate of the deviance obtained by substituting the parameters by their posterior means estimates in the likelihood function; and p_D is the effective number of parameters in the model. In order to facilitate the interpretation of the DIC values in terms of the superiority of one model over another, the model posterior probabilities (MPP) were calculated from DIC using the approximation presented by Silva et al. (2011), which is given by:

$$p(M_t | I) = \exp(-\Delta_t / 2) / \sum_{t=1}^2 \exp(-\Delta_t / 2) ,$$

where $p(M_t | I)$ is the posterior probability of model t ; Δ_t is the DIC difference between model t and the best model (that present smaller DIC).

After definition of the best single-trait RRM to describe each trait (milk yield, fat and protein percent) based on the DIC, the functions were combined to compose the multiple-trait RRM (combined RRM). The coefficients of the functions related to intercept, in the combined RRM, were standardized in order to ensure that the generated estimates by the different functions could be properly scaled. Multiple-trait RRM analyses considering the same function for all traits were also tested.

To choose the best multiple-trait RRM, the spent time per iteration was considered as selection criterion, in addition to DIC and MPP. The general RRM can be described as follow:

$$y_{ijkl} = CG_k + LS_l + GG_o + \sum_{m=0}^{p-1} \beta_m X_m + \sum_{m=0}^{p-1} \alpha_{im} Z_m + \sum_{m=0}^{p-1} \omega_{im} W_m + e_{ijkl} , \quad (3)$$

where y_{ijkl} is the milk yield, fat and/or protein percent in the test-day j for goat i within contemporary group k , litter size l and genetic group o ; CG_k is the contemporary group effect; LS_l is the litter size effect; GG_o is the genetic group effect, β_m are the m fixed regression coefficients; α_{im} and ω_{im} are the m random regression coefficients associated with the additive genetic and permanent environmental effects of animal i , respectively; X_m , Z_m and W_m are the polynomial m for weeks in milk, with order $p-1$; and e_{ijkl} is the random error. In the matrix notation, the model in (3) can be described as:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{a} + \mathbf{W}\mathbf{p} + \mathbf{e} ,$$

where: $\mathbf{y}$ is the vector of phenotypic record(s); $\boldsymbol{\beta}$, $\mathbf{a}$, $\mathbf{p}$ and $\mathbf{e}$ are, respectively, the vectors of systematic effects, additive genetic coefficients, permanent environmental coefficients and residual effects; $\mathbf{X}$, $\mathbf{Z}$ and $\mathbf{W}$ are incidence matrices of $\boldsymbol{\beta}$, $\mathbf{a}$ and $\mathbf{p}$, respectively.

In this context, $\mathbf{y} \sim N(\mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{a} + \mathbf{W}\mathbf{p}, \mathbf{R} \otimes \mathbf{I})$, $\boldsymbol{\beta}_1$, $\boldsymbol{\beta}_2$ and $\boldsymbol{\beta}_3$ follow independent uniform distributions. For the vectors $\mathbf{a} = [\mathbf{a}_1 \ \mathbf{a}_2 \ \mathbf{a}_3]'$ and $\mathbf{p} = [\mathbf{p}_1 \ \mathbf{p}_2 \ \mathbf{p}_3]'$, were assumed, respectively, $\mathbf{a} \sim N(\mathbf{0}, \mathbf{G} \otimes \mathbf{A})$ and $\mathbf{p} \sim N(\mathbf{0}, \mathbf{R}_p \otimes \mathbf{I})$, in which $\mathbf{G}$ and $\mathbf{R}_p$ are the covariance matrices. For the residual vector it was assumed that $\mathbf{e} \sim N(\mathbf{0}, \mathbf{R} \otimes \mathbf{I})$. Uniform prior distributions were assumed for the systematic effects, Gaussian distributions for genetic and permanent environmental coefficients, and the inverse Wishart distribution for the (co)variance matrices. Details about the multiple-trait RRM, including $\mathbf{G}$, $\mathbf{R}_p$ and $\mathbf{R}$ matrix, are shown in Appendix I. All analyses were executed using a computer Intel Core i7-2600 (8M Cache, up to 3.80 GHz) and 8.00 GB RAM. The operating system used was Windows 7. The (co)variance components were estimated by Bayesian inference using the GIBBS3F90 software (Misztal, 2010).

A chain length of 250,000 cycles, considering a burn-in period of 50,000 cycles, and a sampling interval (thin) of 5 cycles was established for all analyses. The convergence criterion was based on graphical analysis and Geweke criterion (Geweke, 1992) available in the package Bayesian Output Analysis (Smith, 2007) of the R software (R Core Team, 2015).

The posterior marginal distribution samples for heritability throughout the lactation curve for each trait were obtained by:

$$h_{qj}^2 = \frac{\hat{\sigma}_{a_j(q)}^2}{\hat{\sigma}_{a_j(q)}^2 + \hat{\sigma}_{p_j(q)}^2 + \hat{\sigma}_{e(q)}^2},$$

where: h_{qj}^2 is the heritability estimate for trait q at test-day j , $\hat{\sigma}_{a_j(q)}^2$ is the additive genetic variance for trait q at test-day j (on the Σ matrix, in Appendix I), $\hat{\sigma}_{p_j(q)}^2$ is the permanent environmental variance for trait q at test-day j (on the Φ matrix, in Appendix I), and $\hat{\sigma}_{e(q)}^2$ is the residual variance for trait q , that depends on the residual variance classes mentioned earlier (if week in lactation ≤ 3 ; $3 < \text{week} \leq 8$ and if the week in lactation > 8).

The posterior marginal distribution samples for correlation between traits throughout the lactation curve were obtained by:

$$r_{q,q'} = \frac{\hat{\sigma}_{aj(q,q')}}{\sqrt{\hat{\sigma}_{a_j(q)}^2 \cdot \hat{\sigma}_{a_j(q')}^2}},$$

where: $r_{q,q'j}$ is the correlation between traits q and q' at test-day j , $\hat{\sigma}_{aj(q,q')}$ is the genetic covariance between q and q' at test-day j (on the Σ matrix, in Appendix I), $\hat{\sigma}_{aj(q)}^2$ is the additive genetic variance for trait q at test-day j and $\hat{\sigma}_{aj(q')}^2$ is the additive genetic variance for trait q' at test-day j (on the Σ matrix, in Appendix I).

The breeding values for each animal i were estimated for accumulated milk yield at 40 weeks (MY), and for fat (FP) and protein (PP) percent of milk using the posterior mean of the estimated random regression coefficients, as follow:

$$\widehat{EBV}_{MY_i} = \sum_1^{40} \widehat{EBV}_{ij(MY)} \quad \widehat{EBV}_{FP_i} = (\sum_1^{40} \widehat{EBV}_{ij(FP)}) / 40 \quad \widehat{EBV}_{PP_i} = (\sum_1^{40} \widehat{EBV}_{ij(PP)}) / 40$$

where $\widehat{EBV}_{ij}$ of animal i at test-day j is provided by multiplying the vector of (co)variables for animal i related to the function used (Legendre, B-spline, Wilmink or Ali and Schaeffer) by the vector with breeding values for covariance function coefficients (details in Appendix I).

After estimating the breeding values for each trait (MY, FP or PP), the breeding values were standardized and the animals were ranking based on the index selection, calculated by:

$$\hat{I}_i = 0.50 * \widehat{EBV}_{MY_i} + 0.25 * \widehat{EBV}_{FP_i} + 0.25 * \widehat{EBV}_{PP_i}$$

where $\hat{I}_i$ is the index selection of the animal i . The Pearson correlation for the index selection and the Kendall rank correlation were obtained using the function `cor`, in the R software (R Core Team, 2015), for all animals in the pedigree and for the sires with more than 10 daughters each. Percentages of selected individuals in common between different RRM were obtained considering 2%, 5%, 10%, 20% and 50% of the best individuals.

The animals were clustered by the additive genetic curves estimated by the combined RRM considering the Euclidean distance, using the `NbClust` package (Charrad et al., 2014) available in the R software (R Core Team, 2015). Total milk yield, total fat yield and total protein yield for each group were calculated as the sum of the milk, fat and protein mensal yield estimated, respectively.

RESULTS

The Deviance Information Criterion (DIC) and the model posterior probabilities (MPP) calculated for the comparison between the single-trait RRM for MY, FP and PP, based on third and fifth order Legendre polynomials (Leg3 and Leg5), linear B-splines with three and five knots

(Bspn3 and Bspn5), Ali and Schaeffer function (Ali) and Wilmink function (Wil) are shown in Table 2.

Table 2. Deviance Information Criterion (DIC) and the model posterior probabilities (MPP) estimated for the single-trait random regression tested models.

Milk yield (MY)			Fat percent (FP)			Protein percent (PP)		
Model	DIC	MPP	Model	DIC	MPP	Model	DIC	MPP
Ali	6165.48	≈ 1.00	Leg5	8144.93	≈ 0.91	Ali	962.60	≈ 0.58
Leg5	6273.24	≈ 0.00	Ali	8149.64	≈ 0.09	Leg5	963.23	≈ 0.42
Bspn5	6275.53	≈ 0.00	Bspn5	8187.79	≈ 0.00	Bspn5	979.14	≈ 0.00
Wil	6759.78	≈ 0.00	Wil	8299.88	≈ 0.00	Wil	1175.74	≈ 0.00
Bspn3	6790.29	≈ 0.00	Leg3	8324.83	≈ 0.00	Leg3	1253.82	≈ 0.00
Leg3	6809.16	≈ 0.00	Bspn3	8439.99	≈ 0.00	Bspn3	1456.79	≈ 0.00

Ali: Ali and Schaeffer function; Leg5 and Leg3: fifth and third order Legendre polynomials, respectively; Bspn5 and Bspn3: linear B-spline with five and three knots, respectively; Wil: Wilmink function.

The model based on Ali and Schaeffer function fitted better for MY and PP, while the model based on fifth order Legendre polynomials was the best for FP. These single-trait results were used to define the following combined multiple-trait RRM: Ali_Ali_Leg5, Ali_Leg5_Ali and Ali_Leg5_Leg5; where the first name (before the underline) refers to the function used to describe the MY, the second one the FP and the third one the PP. The spent time per iteration (Time), DIC and the MPP calculated for the simple and combined multiple-trait RRM are shown in Table 3.

Table 3. Spent time per iteration (Time), Deviance Information Criterion (DIC) and the model posterior probabilities (MPP) estimated for the multiple-trait random regression models.

Model	Time	DIC	MPP
Ali_Leg5_Ali	0.1728	808.4021	≈ 1.00
Ali_Ali_Leg5	0.1742	830.8451	≈ 0.00
Ali_Leg5_Leg5	0.1787	848.6646	≈ 0.00
Leg5_Leg5_Leg5	0.1050	884.9908	≈ 0.00
Ali_Ali_Ali	0.0632	933.3734	≈ 0.00
Bspn5_Bspn5_Bspn5	0.1267	989.2999	≈ 0.00
Wil_Wil_Wil	0.0270	1497.0308	≈ 0.00
Leg3_Leg3_Leg3	0.0275	1649.0182	≈ 0.00
Bspn3_Bspn3_Bspn3	0.0348	2431.1232	≈ 0.00

Symbol models: The first name (before the underline) refers to the function used to describe the MY, the second one the FP and the third one the PP. Ali: Ali and Schaeffer function; Leg5 and Leg3: fifth and third order Legendre polynomials, respectively; Bspn5 and Bspn3: linear B-spline with five and three knots, respectively; Wil: Wilmink function.

Time was higher for the models considering the combinations of functions (Ali_Ali_Leg5, Ali_Leg5_Ali and Ali_Leg5_Leg5) due to greater complexity of these analyzes. However, all combined RRM presented lower DIC values, showing the superiority of these models when compared to other multiple-trait models based on one function (Leg5_Leg5_Leg5, Ali_Ali_Ali, Bspn5_Bspn5_Bspn5, Wil_Wil_Wil, Leg3_Leg3_Leg3 and Bspn3_Bspn3_Bspn3). Among the combined models, the model that presented the best fit to the data was the model considering Ali to describe the MY and PP, and Leg5 to describe the FP, similar to that found in the single-trait analysis.

The used function have influence on the variance components estimates, thus, we compared the variances obtained using the combined RRM (Ali_Leg5_Ali) with the variances estimated by two multiple-trait RRM considering the same function to all traits (Ali_Ali_Ali and Leg5_Leg5_Leg5). These variances from multiple-trait models were also compared with the estimates generated by three single-trait RRM: two based on Ali (to describe MY and PP) and one based on Leg5 (to describe FP).

In general, the additive genetic variance ($\hat{\sigma}_a^2$) and permanent environmental variances ($\hat{\sigma}_{pe}^2$) estimated by the combined RRM, by the simple multiple-trait RRM and by the single-trait RRM,

followed the same pattern for each trait, but, the σ_a^2 were smaller in the single-trait RRM when compared to multiple-trait models (Figure 1).

Figure 1. Additive genetic variance (—) and permanent environmental variance (---) estimated by the combined multiple-trait random regression model (a, b, c), multiple-trait random regression model based on fifth order Legendre polynomials (d, e, f), multiple-trait random regression model based on Ali and Schaeffer function (g, h, i) and by the single-trait random regression model (j, k, l); for milk yield (MY, left), fat percent (FP, middle) and protein percent (PP, right).

The σ_a^2 estimated for MY by the combined RRM and by the multiple-trait RRM based on Ali were very similar, nonetheless, the σ_{pe}^2 estimated by the combined RRM was a little higher than the others multiple-trait RRM. The σ_a^2 and σ_{pe}^2 estimated for FP by combined RRM was higher than those estimated by two simple multiple-trait models and by single-trait RRM, mainly by the

ending of lactation (after 35 weeks). The variances estimated for PP by the different models were approximately the same.

In all tested models, the residual variances (σ_e^2) were smaller for the combined RRM and for the simple multiple-trait RRM when compared to single-trait RRM (Table 4).

Table 4. Posterior mean and 95% highest posterior density interval (LL: low limit and HL: high limit) for residual variance for milk yield, fat and protein percent from each assumed class (1-3, 4-8 and 9-40 weeks), using the combined multiple-trait (Ali_Leg5_Ali), multiple-trait based on fifth order Legendre polynomials (Leg5_Leg5_Leg5), multiple-trait based on Ali and Schaeffer function (Ali_Ali_Ali) and single-trait (Ali for MY and PP, and Leg5 for FP) random regression models.

Model	Classes	Milk yield (MY)			Fat percent (FP)			Protein percent (PP)		
		Mean	LL	HL	Mean	LL	HL	Mean	LL	HL
Combined RRM	1-3	0.1603	0.1095	0.2124	0.5498	0.4373	0.6803	0.0889	0.0662	0.1117
	4-8	0.3255	0.2641	0.3896	0.3977	0.3307	0.4897	0.0469	0.0380	0.0566
	9-40	0.2016	0.1884	0.2151	0.3355	0.3138	0.3585	0.0555	0.0521	0.0590
Multiple by Leg5	1-3	0.1620	0.1110	0.2150	0.5492	0.4248	0.6736	0.0929	0.0708	0.1167
	4-8	0.3240	0.2622	0.3880	0.3686	0.2955	0.4416	0.0507	0.0415	0.0604
	9-40	0.2032	0.1902	0.2173	0.3662	0.343	0.3894	0.0539	0.0505	0.0575
Multiple by Ali	1-3	0.1620	0.1090	0.2150	0.6152	0.4912	0.7452	0.0890	0.0661	0.1118
	4-8	0.3240	0.2607	0.3874	0.4126	0.3382	0.4888	0.0467	0.0372	0.0562
	9-40	0.2032	0.1897	0.2167	0.3529	0.3296	0.3761	0.0556	0.0521	0.0591
Single-trait	1-3	0.1880	0.1294	0.2504	0.6861	0.5633	0.8147	0.0933	0.0718	0.1162
	4-8	0.3250	0.2650	0.3891	0.4358	0.3630	0.5155	0.0474	0.0383	0.0566
	9-40	0.2104	0.1967	0.2246	0.3711	0.3476	0.3964	0.0572	0.0536	0.0609

Figure 2 shows the change of the heritability and genetic correlation between the traits over 40 weeks in milk, estimated by the combined RRM. Estimates of heritability for MY and FP were close until 20 weeks, and they ranged from 0.25 at 0.54. The estimates of heritability for PP were, in general, higher than the estimates for MY and FP, ranging from 0.35 until 0.51. The genetic correlation between MY and FP and between MY and PP throughout the lactation period were negative, except for the period immediately after lactation peak. The genetic correlation between FP and PP was positive and approximately constant throughout the lactation.

Figure 2. Heritability (a) for milk yield (—), fat percent (— · —) and protein percent (— — —), and genetic correlation (b) between milk yield and fat percent (—▲—), milk yield and protein percent (—●—) and between fat and protein percent (—■—) estimated by the combined multiple-trait random regression model (Ali_Leg5_Ali).

How the animal model was used in this study, EBVs were available for kids, dams and sires. However, individual goat EBVs are subject to systematic errors by management practices, usually not accounted by statistical methods. Thus, main target for breeding organizations would be estimate breeding values of sires for daughter yield and therefore it is of major interest to show how sire rankings are also affected by the functions used in the RRM. The index selection is an alternative to combining EBVs from different traits of the same animal in a unique value, making that several useful traits can be selected simultaneously. EBVs originated in different RRM can be highly different, what can change the index selection of the animal and consequently, change the position of the animal in the ranking. Thus, index selection for sires that had more than 10 daughters (total of 21 sires) were selected for comparison, in addition to comparison of index selection for all animals in the pedigree.

The standard deviations and range of the index selection are given for all animals and only for sires, in Table 5. These statistics are shown for combined RRM, multiple-trait RRM based on Leg5, multiple-trait RRM based on Ali and for single-trait RRM analyses.

Table 5. Standard deviations and range of the index selection provided by combined multiple-trait (Ali_Leg5_Ali), multiple-trait based on fifth order Legendre polynomials (Leg5_Leg5_Leg5), multiple-trait based on Ali and Schaeffer function (Ali_Ali_Ali) and from single-trait (Ali for MY and PP, and Leg5 for FP) random regression model analyses, based on 1,061 animals in the pedigree (All animals) or only on 21 sires with more than 10 daughters each (Only sires).

	All animals				Only sires			
	Combined RRM	Multiple by Leg5	Multiple by Ali	Single-trait	Combined RRM	Multiple by Leg5	Multiple by Ali	Single-trait
SD	0.6824	0.6725	0.6845	0.5574	0.8137	0.7749	0.8425	0.6135
Min	-2.1328	-2.3329	-1.5891	-2.0735	-1.1035	-1.0470	-1.5891	-1.3460
Max	2.9569	3.2382	2.5411	2.0736	2.0770	2.2438	1.7458	0.6891

SD: Standard deviations; Min: Minimum; Max: Maximum.

In Table 6, the rankings are presented for the 2% best animals (All animals) and for the 21 sires with more than 10 daughters each (Only sires), based on index selection calculated according to the combined RRM, multiple-trait RRM based on Leg5 and Ali, and single-trait RRM analyses.

Table 6. Ranking of the 2% best animals (All animals) and of the 21 sires with more than 10 daughters each (Only sires), based on the index selection provided by combined multiple-trait (Ali_Leg5_Ali), multiple-trait based on fifth order Legendre polynomials (Leg5_Leg5_Leg5), multiple-trait based on Ali and Schaeffer function (Ali_Ali_Ali) and from single-trait (Ali for MY and PP, and Leg5 for FP) random regression model analyses.

Ranking	All animals				Only sires			
	Combined RRM	Multiple by Leg5	Multiple by Ali	Single-trait	Combined RRM	Multiple by Leg5	Multiple by Ali	Single-trait
1°	67	67	1	114	545	545	545	644
2°	41	545	484	516	604	604	644	622
3°	115	41	401	153	746	817	746	604
4°	105	115	340	401	644	746	604	746
5°	262	262	56	4	817	598	817	545
6°	340	105	310	115	540	644	540	540
7°	274	578	129	351	598	540	622	598
8°	484	401	274	380	694	714	613	826
9°	1	205	291	507	613	622	694	714
10°	545	153	115	309	714	569	714	616
11°	219	1	41	501	622	694	826	569
12°	401	389	355	355	601	601	598	717
13°	205	225	409	686	569	616	616	794
14°	129	707	225	216	616	613	794	694
15°	153	219	124	67	826	717	601	817
16°	452	629	89	225	559	794	734	613
17°	1061	484	501	484	717	826	569	601
18°	82	129	77	123	794	609	537	559
19°	486	404	774	434	609	559	717	609
20°	96	23	4	274	734	537	609	537
21°	185	234	7	205	537	734	559	734

Four different index selection were available for each animal, one provided by the combined RRM, two provided by the multiple-trait RRM (based on Leg5 and Ali) and one provided by single-trait RRM. Correlations between these four genetic evaluations were computed using the index selection for all animals and only for sires. The index selection correlation and rank correlation are shown in Table 7 and Table 8, respectively.

Table 7: Person correlation between index selection provided by the combined multiple-trait (Ali_Leg5_Ali), multiple-trait based on fifth order Legendre polynomials (Leg5_Leg5_Leg5), multiple-trait based on Ali and Schaeffer function (Ali_Ali_Ali) and from single-trait (Ali for MY and PP, and Leg5 for FP) random regression model, for all animals in the pedigree (below of diagonal) and only for sires with more than 10 daughters each (above of diagonal).

	Combined RRM	Multiple by Leg5	Multiple by Ali	Single-trait
Combined RRM		0.9595	0.8704	0.7311
Multiple by Leg5	0.8768		0.8049	0.7058
Multiple by Ali	0.8060	0.6515		0.7520
Single-trait	0.6945	0.6080	0.6785	

Table 8: Kendall rank correlation based on index selection provided by the combined multiple-trait (Ali_Leg5_Ali), multiple-trait based on fifth order Legendre polynomials (Leg5_Leg5_Leg5), multiple-trait based on Ali and Schaeffer function (Ali_Ali_Ali) and from single-trait (Ali for MY and PP, and Leg5 for FP) random regression model, for all animals in the pedigree (below of diagonal) and only for sires with more than 10 daughters each (above of diagonal).

	Combined RRM	Multiple by Leg5	Multiple by Ali	Single-trait
Combined RRM		0.0762	0.1619	-0.1524
Multiple by Leg5	0.0455		-0.0190	0.2190
Multiple by Ali	0.0917	0.0550		-0.1143
Single-trait	0.0693	0.0519	0.0564	

The percentage of selected individuals in common increased according to increase the percentage of selected animals, and were higher between the combined RRM and the multiple-trait RRM based on fifth order Legendre polynomials (Table 9).

Table 9: Percentage of selected individuals in common, in increasing levels, based on rankings provided by the combined multiple-trait (Ali_Leg5_Ali), multiple-trait based on fifth order Legendre polynomials (Leg5_Leg5_Leg5), multiple-trait based on Ali and Schaeffer function (Ali_Ali_Ali) and from single-trait (Ali for MY and PP, and Leg5 for FP) random regression model, for all animals in the pedigree.

Compared models	Percentage of selected individuals in common				
	2%	5%	10%	20%	50%
Combined RRM and Multiple by Leg5	0.6190	0.6481	0.7358	0.7264	0.8396
Combined RRM and Multiple by Ali	0.3810	0.5185	0.6321	0.6651	0.7981
Combined RRM and Single-trait	0.3333	0.4630	0.5283	0.5519	0.7377
Multiple by Leg5 and Multiple by Ali	0.3333	0.3148	0.4717	0.5613	0.7151
Multiple by Leg5 and Single-trait	0.3333	0.3889	0.4811	0.5425	0.7075
Multiple by Ali and Single-trait	0.3810	0.3889	0.5189	0.5613	0.7245

To compare the different RRM, XY scatter plots, with X-axis being the animal index selection provided by one RRM and the Y-axis being the animal index selection provided by other RRM, were used (Figure 3). Deviations of observations from the straight line indicate difference in the index selection or change in the rank.

Figure 3: Differences between the index selections estimated based on combined RRM and multiple-trait RRM based on Legendre polynomials (a), combined RRM and multiple-trait RRM based on Ali and Schaeffer function (b), combined RRM and single-trait RRM (c), multiple-trait RRM based on Legendre polynomials and multiple-trait RRM based on Ali and Schaeffer function (d), multiple-trait RRM based on Legendre polynomials and single-trait RRM (e) and multiple-trait RRM based on Ali and Schaeffer function and single-trait (f), for all animals in the pedigree, as XY scatter plot.

The animals were clustered according to additive genetic curves estimated by the combined RRM (Ali_Leg5_Ali). In total, five groups, with 255, 91, 706, 2 and 7 animals respectively, were

formed. The first group brought together the animals that had smaller total milk production, with delayed production peak, low persistency of lactation and FP and PP curves similar to average of the FP and PP curves of the population. The second, grouped the animals that had early production peak, high persistency of lactation and more PP in milk than the average of PP of the population. The third group is associated with the animals that had the lactation curve, FP and PP curve similar to average curves of the population. The fourth and fifth groups clustered the best animals of the ranking estimated according to the combined RRM, which showed, in general, higher MY, FP and PP. The fourth group, however, presented less total milk yield, with delayed production peak, lower persistency of lactation and lesser PP in milk than the fifth group. Table 10 show the mean and standard deviation for total milk yield, total fat yield and total protein yield by each group, and the Figure 4 show the behavior of daily milk yield, daily fat percent and daily protein percent, by each formed group.

Table 10. Number of observations, mean and standard deviation for total milk yield, total fat yield and total protein yield, by formed group.

Group	N	Total milk yield (Kg)		Total fat yield (Kg)		Total protein yield (Kg)	
		Mean	SD	Mean	SD	Mean	SD
1	255	191.40	64.21	8.14	2.86	6.49	3.95
2	91	238.80	52.71	9.75	2.20	8.91	3.30
3	706	208.60	44.23	8.61	1.92	7.13	2.59
4	2	267.04	84.19	11.68	4.35	9.70	3.97
5	7	276.70	48.29	13.25	1.95	10.90	1.17

N: number of observations; SD: standard deviation.

Figure 4. Average of additive genetic curves for milk yield (—), fat percent (— · —) and protein percent (— —) estimated by the combined multiple-trait random regression model for the first (a), second (b), third (c), fourth (d) and fifth (e) groups.

DISCUSSION

According to DIC values estimated for the single-trait RRM (Table 2), the more parameterized models were best to describe the data. Thus, the improvement in the quality of the fit compensated the increased in the models complexity. The single-trait RRM based on Leg5 and Ali were adequate, respectively, to describe FP and PP, however, for MY data, the best one was the Ali model. Results of González-Peña et al. (2012) also indicate that Ali was one of the best functions for to model lactation curves of dairy goats in genetic evaluations. To date, the only study that we found in the literature that considered FP and PP in dairy goats was of Andonov et al. (2013), who tested exclusively the order (first to third) of Legendre polynomials for the additive genetic and permanent environmental effects. In dairy cattle, however, Bouallegue et al. (2015) modelling individual lactation curves for MY, FP and PP using parametric, orthogonal and spline models found that the regression splines (quadratic and cubic spline models with three knots), high orders Legendre polynomial and Ali model showed better fitting performances compared with the three-parameter models (Wood and Wilmink models) and with the lower order polynomial models. The authors also commented that Ali model was more preferred for PP than for FP.

In general, single-trait RRM based on B-spline functions (Bspn3 and Bspn5) and simple multiple-trait RRM based on B-spline functions (Bspn3_Bspn3_Bspn3 and Bspn5_Bspn5_Bspn5) presented worst fit (Table 2 and Table 3) when compared to other models considering the same number of parameters. Meyer (2005) comments that, despite the several advantages of using B-splines functions as basis functions, models based on these functions tended to involve more coefficients than corresponding analyses with polynomial basis functions, as Legendre polynomials. Thus, since in this work the number of coefficients of the models was fixed, models based on Legendre polynomials and models based on parametric functions (Ali and Wil) presented, in general, better fit. These results corroborate with those obtained by Bignardi et al. (2011), working with Holstein cows.

Specifically about the multiple-trait models, the spent time per iteration (Table 3) was higher for all combined RRM due to greater complexity of these analyzes, however, the greater complexity did not prevent the convergence of the chains considering the same number of iterations and the same size of burn-in considered in the simple multiple-trait RRM analyzes. Thus, despite of the combined RRM increasing the complexity of the models, there was no convergence problems for these models, demonstrating that the combined RRM can be a feasible alternative. Analyzes considering models based on parametric functions (Ali and Wil), were faster than

analyzes considering Legendre polynomials and linear B-splines, possibly due to the fact that these functions are specific to model the lactation curve and thus, show higher correlations between the parameters of the curve when compared to existing correlations between the coefficients of Legendre polynomials and between the knots of the linear B-spline functions.

All combined RRM presented lower DIC than the multiple-trait RRM considering the same function for all traits (Table 3). Thus, these combinations of functions in a unique model provided the increase of the fit quality in relation to the simple multiple-trait RRM, since it allows to consider simultaneously different functions, and its respective advantages in the same model. However, when choosing the functions to compose the combined RRM, they need to be adequate to modeling the traits in study, otherwise, if the functions were chosen wrongly, the combined RRM may presented poor fit to the data and consequently, increase the DIC value, because the complexity of the combined RRM will be higher and there will be no gains in the fit quality.

The σ_a^2 and σ_{pe}^2 estimates for all traits by using the combined RRM (Ali_Leg5_Ali), the simple multiple-trait RRM (Leg5_Leg5_Leg5 and Ali_Ali_Ali) and by the single-trait RRM (Ali for MY and PP, and Leg5 for FP), followed the same pattern (Figure 1). Nonetheless, higher σ_a^2 and smaller σ_e^2 were obtained using the multiple-trait models, when compared to estimates obtained from single-trait RRM (Figure 1 and Table 4). These differences between the estimate variances are due to the fact that multiple-trait RRM present more information available simultaneously to estimate the (co)variance components, providing a complete structure of correlation between the traits. This feature of multiple-trait RRM is maintained in the combined RRM.

According to Hammami et al. (2008), for studies based on milk test-days records are expected σ_a^2 estimates curves with lower values in the extremes because they are high influenced by environmental factors. Nevertheless, in this study were observed for MY that at the beginning and at the ending of the lactation the σ_a^2 were inflated in all tested multiple-trait models (Figure 1). Bignardi et al. (2011) also reported these inflated genetic variances estimated by Ali and Schaeffer function and Legendre polynomials for MY in dairy cattle. The σ_{pe}^2 estimated for MY have high values at the beginning, peak and ending of the lactation for all models (Figure 1), demonstrating that in these phases the permanent environmental effects are higher. However, the σ_e^2 estimated for MY (Table 4) was higher for second class (4 to 8 weeks, referent to lactation peak) than for first and third one, probably because in this period the MY is higher than in other lactation phases, generating a scale effect.

The σ_a^2 and σ_{pe}^2 estimates for FP were very similar for all tested models (Figure 1), however, at the extremes of the curves, the obtained estimates were higher for the combined RRM and for the multiple-trait RRM based on Leg5 than for other models. Misztal (2006) attributed this poor fit in the extremes to the Legendre polynomials, thus, the Runge Effect may be influencing in the estimates generated at the extremes of the curve in this models. Andonov et al. (2013) obtained similar pattern of the variances, working with FP in a RRM based on third order Legendre polynomials. The σ_a^2 and σ_{pe}^2 estimated for PP were approximately constant for all weeks in all tested models (Figure 1), contrasting with the results presented by Andonov et al. (2013), who also found high estimates in the extremes of the curve for PP, using Legendre polynomials. The σ_e^2 estimated for FP and PP (Table 4) were higher in the first class (1 to 3 weeks), probably due to stress resulting from kidding. Borquis et al. (2013), working with buffalos, found higher σ_e^2 values for fat yield at the ending of the lactation (9 and 10 months) and for protein yield at the beginning of the lactation (first month).

All traits showed fluctuations in the pattern of the heritability over the lactation curve (Figure 2), which could be related to some artifact associated with the use of Legendre polynomial and Ali function. The heritability estimates obtained in this work were slightly higher than those reported by Zumbach et al. (2008), Menéndez-Buxadera et al. (2010) and Silva et al. (2013b) for MY; and by Andonov et al. (2013), for MY, FP and PP. These high estimates may probably be explained by the smaller number of animals in the considered population when compared with the mentioned studies in dairy goats. In general, the heritability estimates for PP was higher than the heritabilities estimated for MY and FP, demonstrating that the PP is less affected by the environment than MY and FP. Thus, especially the insertion of PP trait in the breeding programs can provide satisfactory results, mainly when cheese production is the aim of the production system. At lactation peak (4 to 8 weeks), the heritability estimates for MY were lower than those obtained at other points of the curve, indicating that at this stage the MY receive strong influence of the environment. For FP, disregarding the effect that the Legendre polynomials exert in the curve extremes, the heritabilities estimates were approximately constant over all lactation period, except before the fifth week and after the 25th week, when it tends to increase. For PP, the heritability estimated was high along all lactation, except in the ending (after 28 weeks), where the heritabilities decrease.

To date, genetic correlations between MY, FP and PP along lactation in dairy goats are scarce in literature. However, in dairy cattle, higher genetic correlations between milk and protein

yield than between milk and fat yield was reported (Hammami et al., 2008). In this study, correlations between FP and PP (Figure 2) was positive and had medium values (0.37 to 0.64), indicating that the selection in one of these traits can assist in the selection of another one. This correlation, was lower in the middle of the lactation curve (15 to 25 weeks), possibly because in this phase the MY is decreasing quickly. The correlation between MY and FP (-0.58 to 0.03) and between MY and PP (-0.46 to 0.12) were medium and negative, except for the lactation peak, where the correlations were lower, become slightly positive. A selection scheme focusing only on milk yield could lead to a decrease in fat and protein percent and to deterioration of cheese yield and quality. This is an extra reason to also consider fat and protein as selection target.

The wide range of index selection for all RRM (Table 5) suggests the existence of genetic variation between animals. In general, standard deviations of the index selection provided by the multiple-trait RRM were higher than the standard deviations provided by the single-trait RRM analyzes, probably because the multiple-trait RRM provide a complete structure of correlation between the traits, revealing more genetic variation. The minimum and maximum index selection found in the different RRM analyzes are similar, however, when we compared the minimum and maximum values estimated by the different RRM for all animal in the pedigree with the estimated values only for sires, the range found for sires was lower, showing the existence of young animals genetically superior to their parents in the herd.

The ranking of the 2% best animals and of the 21 sires with more 10 daughters each, presented according to combined RRM (Ali_Leg5_Ali), multiple-trait RRM based on Leg5 and Ali, and single trait RRM (Ali for MY and PP, and Leg5 for FP) analyses, showed that few sires are present in the ranking of the 2% best animals of the herd (Table 6).

The index selection correlations (Table 7) were higher between the combined RRM and the multiple-trait RRM by Leg5. This bigger similarity can be explained by the fact that the coefficients of Legendre polynomials are more flexible than the parameters of the Ali and Schaeffer function, making the MY and PP could be better fit by Legendre polynomials than the FP by Ali and Schaeffer function. This best fit considering the multiple-trait RRM based on Leg5 can also be observed when we compare the DIC value estimated for the multiple-trait by Leg5 with the DIC value estimated for the multiple-trait by Ali (Table 3), and when we compare the σ_e^2 estimated for this models (Table 4). In general, the multiple-trait RRM had low correlation with the single-trait RRM, showing that the selection of animals to more than one trait based on single-trait analysis could compromise the genetic breeding. Correlations estimated only for sires are higher than

correlations estimated for all animals in pedigree due the lower number of animals and due the lower range of the index selection for sires.

Kendall rank correlation (Table 8) showed that, although the Person correlation between index selection are of medium to high magnitude, the number of concordant pairs between the rankings provided by the different models were few. The percentage of selected individuals in common increased according to increase the percentage of selected animals (Table 9), indicating that how higher the intensity selection applied to the herd, greater the need of using an appropriate model. Figure 3 shows difference in the index selection or change in the rank, based on combined RRM, multiple-trait RRM based on Leg5, multiple-trait RRM based on Ali and single-trait RRM. These results, in general, allow us to observe how many animals would be not correctly selected using the simple multiple-trait RRM and single-trait RRM.

Genetic differences between animal groups (Figure 3 and Table 6) can be easily identified when the animals are clustered according to additive genetic curves. In this work, five groups based on MY, FP and PP of the milk were formed. The groups differ mainly for MY and FP, since the PP was approximately constant among groups. There was a large difference in the lactation peak phase and persistency of lactation between the groups, indicating that some animals are genetically preferable to intensive production systems (animals with high peak of the production and shorter lactations) and others preferable to extensive production systems (animals with high persistency of the lactation).

CONCLUSIONS

Random regression models based on Ali and Schaffer function are the most adequate to describe the milk yield and protein percent, and models based on fifth order Legendre polynomials were better for describe fat percent. The combined RRM can be a plausible alternative to fit different longitudinal traits and its importance increase according to increase the difference of the genetic behavior of the traits.

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APPENDIX I

Multiple-trait random regression models

Considering the general multiple-trait random regression model:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{a} + \mathbf{W}\mathbf{p} + \mathbf{e}$$

a three-trait random regression model can be defined as follow:

$$\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \\ \mathbf{y}_3 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & 0 & 0 \\ 0 & \mathbf{X}_2 & 0 \\ 0 & 0 & \mathbf{X}_3 \end{bmatrix} \cdot \begin{bmatrix} \boldsymbol{\beta}_1 \\ \boldsymbol{\beta}_2 \\ \boldsymbol{\beta}_3 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_1 & 0 & 0 \\ 0 & \mathbf{Z}_2 & 0 \\ 0 & 0 & \mathbf{Z}_3 \end{bmatrix} \cdot \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \\ \mathbf{a}_3 \end{bmatrix} + \begin{bmatrix} \mathbf{W}_1 & 0 & 0 \\ 0 & \mathbf{W}_2 & 0 \\ 0 & 0 & \mathbf{W}_3 \end{bmatrix} \cdot \begin{bmatrix} \mathbf{p}_1 \\ \mathbf{p}_2 \\ \mathbf{p}_3 \end{bmatrix} + \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \\ \mathbf{e}_3 \end{bmatrix},$$

where:

$\mathbf{y}$ is the vector of phenotypic records with $\mathbf{y}_1$, $\mathbf{y}_2$ and $\mathbf{y}_3$ referring to milk yield, fat and protein percent, distributed as $N(\mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{a} + \mathbf{W}\mathbf{p}, \mathbf{R} \otimes \mathbf{I})$;

$\boldsymbol{\beta}$ is the vector of systematic effects with $\boldsymbol{\beta}_1$, $\boldsymbol{\beta}_2$ and $\boldsymbol{\beta}_3$ referring to the systematic effects attributed, respectively, to milk yield, fat and protein percent, and have independent uniform distributions;

$\mathbf{a}$ is the vector of additive genetic coefficients with $\mathbf{a}_1$, $\mathbf{a}_2$ and $\mathbf{a}_3$ referring to the additive genetic coefficients attributed, respectively, to milk yield, fat and protein percent, distributed as $N(\mathbf{0}, \mathbf{G} \otimes \mathbf{A})$;

$\mathbf{p}$ is the vector of permanent environmental coefficients with $\mathbf{p}_1$, $\mathbf{p}_2$ and $\mathbf{p}_3$ referring to the permanent environmental coefficients attributed, respectively, to milk yield, fat and protein percent, distributed as $N(\mathbf{0}, \mathbf{R}_p \otimes \mathbf{I})$;

$\mathbf{X}$, $\mathbf{Z}$ and $\mathbf{W}$ are the incidence matrices of $\boldsymbol{\beta}$, $\mathbf{a}$ and $\mathbf{p}$, respectively;

$\mathbf{e}$ is the vector of residual coefficients with $\mathbf{e}_1$, $\mathbf{e}_2$ and $\mathbf{e}_3$ referring to the residual coefficients attributed, respectively, to milk yield, fat and protein percent, and distribution $N(\mathbf{0}, \mathbf{R} \otimes \mathbf{I})$.

The $\mathbf{G}$, $\mathbf{R}_p$ and $\mathbf{R}$ matrices can be describe as follow:

$$\mathbf{G} = \begin{bmatrix}
\sigma_{a_{l(1)}}^2 & \sigma_{a_{1,2(1)}} & \cdots & \sigma_{a_{1,K(1)}} & \sigma_{a_{1,l(1,2)}} & \sigma_{a_{1,2(1,2)}} & \cdots & \sigma_{a_{1,L(1,2)}} & \sigma_{a_{1,l(1,3)}} & \sigma_{a_{1,2(1,3)}} & \cdots & \sigma_{a_{1,M(1,3)}} \\
& \sigma_{a_{2(1)}}^2 & \cdots & \sigma_{a_{2,K(1)}} & & \sigma_{a_{2,2(1,2)}} & \cdots & \sigma_{a_{2,L(1,2)}} & & \sigma_{a_{2,2(1,3)}} & \cdots & \sigma_{a_{2,M(1,3)}} \\
& & \ddots & \vdots & & & \ddots & \vdots & & & \ddots & \vdots \\
& & & \sigma_{a_{K(1)}}^2 & \text{Symmetric} & & & \sigma_{a_{K,L(1,2)}} & \text{Symmetric} & & & \sigma_{a_{K,M(1,3)}} \\
\hline
& & & & \sigma_{a_{l(2)}}^2 & \sigma_{a_{1,2(2)}} & \cdots & \sigma_{a_{1,L(2)}} & \sigma_{a_{1,l(2,3)}} & \sigma_{a_{1,2(2,3)}} & \cdots & \sigma_{a_{1,M(2,3)}} \\
& & & & & \sigma_{a_{2(2)}}^2 & \cdots & \sigma_{a_{2,L(2)}} & & \sigma_{a_{2,2(2,3)}} & \cdots & \sigma_{a_{2,M(2,3)}} \\
& & & & & & \ddots & \vdots & & & \ddots & \vdots \\
& & & & & & & \sigma_{a_{L(2)}}^2 & \text{Symmetric} & & & \sigma_{a_{L,M(2,3)}} \\
\hline
& & & & & & & & \sigma_{a_{l(3)}}^2 & \sigma_{a_{1,2(3)}} & \cdots & \sigma_{a_{1,M(3)}} \\
& & & & & & & & & \sigma_{a_{2(3)}}^2 & \cdots & \sigma_{a_{2,M(3)}} \\
& & & & & & & & & & \ddots & \vdots \\
& & & & & & & & & & & \sigma_{a_{M(3)}}^2
\end{bmatrix}$$

where $k=1,2,\dots,K$; $l=1,2,\dots,L$ and $m=1,2,\dots,M$. $\sigma_{a_{1(1)}}^2$ is the additive genetic variance for the first coefficient “1” of first trait “(1)”; $\sigma_{a_{1,2(1)}}$ is the additive genetic covariance between the first and second coefficient “1,2” of first trait “(1)” and $\sigma_{a_{1,2(1,2)}}$ is the additive genetic covariance between the first coefficient of first trait and the second coefficient of the second trait “1,2(1,2)”, and so on.

$$\mathbf{R}_p = \begin{bmatrix}
\sigma_{p_{l(1)}}^2 & \sigma_{p_{1,2(1)}} & \cdots & \sigma_{p_{1,K(1)}} & \sigma_{p_{1,l(1,2)}} & \sigma_{p_{1,2(1,2)}} & \cdots & \sigma_{p_{1,L(1,2)}} & \sigma_{p_{1,l(1,3)}} & \sigma_{p_{1,2(1,3)}} & \cdots & \sigma_{p_{1,M(1,3)}} \\
& \sigma_{p_{2(1)}}^2 & \cdots & \sigma_{p_{2,K(1)}} & & \sigma_{p_{2,2(1,2)}} & \cdots & \sigma_{p_{2,L(1,2)}} & & \sigma_{p_{2,2(1,3)}} & \cdots & \sigma_{p_{2,M(1,3)}} \\
& & \ddots & \vdots & & & \ddots & \vdots & & & \ddots & \vdots \\
& & & \sigma_{p_{K(1)}}^2 & \text{Symmetric} & & & \sigma_{p_{K,L(1,2)}} & \text{Symmetric} & & & \sigma_{p_{K,M(1,3)}} \\
\hline
& & & & \sigma_{p_{l(2)}}^2 & \sigma_{p_{1,2(2)}} & \cdots & \sigma_{p_{1,L(2)}} & \sigma_{p_{1,l(2,3)}} & \sigma_{p_{1,2(2,3)}} & \cdots & \sigma_{p_{1,M(2,3)}} \\
& & & & & \sigma_{p_{2(2)}}^2 & \cdots & \sigma_{p_{2,L(2)}} & & \sigma_{p_{2,2(2,3)}} & \cdots & \sigma_{p_{2,M(2,3)}} \\
& & & & & & \ddots & \vdots & & & \ddots & \vdots \\
& & & & & & & \sigma_{p_{L(2)}}^2 & \text{Symmetric} & & & \sigma_{p_{L,M(2,3)}} \\
\hline
& & & & & & & & \sigma_{p_{l(3)}}^2 & \sigma_{p_{1,2(3)}} & \cdots & \sigma_{p_{1,M(3)}} \\
& & & & & & & & & \sigma_{p_{2(3)}}^2 & \cdots & \sigma_{p_{2,M(3)}} \\
& & & & & & & & & & \ddots & \vdots \\
& & & & & & & & & & & \sigma_{p_{M(3)}}^2
\end{bmatrix}$$

where $k=1,2,\dots,K$; $l=1,2,\dots,L$ and $m=1,2,\dots,M$. $\sigma_{p_{1(1)}}^2$ is the permanent environmental variance for the first coefficient “1” of first trait “(1)”; $\sigma_{p_{1,2(1)}}$ is the permanent environmental covariance between the first and the second coefficient “1,2” of first trait “(1)” and $\sigma_{p_{1,2(1,2)}}$ is the covariance between the first coefficient of first trait and the second coefficient of second trait, and so on.

where $\sigma_{e_{1(1)}}^2$ is the residual variance for the first trait “(1)”, based on the first residual variance class “1” and $\sigma_{e_{1(1,2)}}$ is the covariance between the first and the second trait “(1,2)”, based on the first residual variance class “1”, and so on. The number of columns with similar variances depends on the number of weeks in each residual variance class, thus, in this study we had 3 columns referents to $\sigma_{e_1}^2$, 5 columns referents to $\sigma_{e_2}^2$ and 32 columns referents to $\sigma_{e_3}^2$. The covariances were different of zero between traits in the same residual variance class.

The general matrix of genetic covariance can be defined as follow:

$$\Sigma = \mathbf{T}_i \cdot \mathbf{G} \cdot \mathbf{T}_i'$$

where $\mathbf{G}_{((k+l+m) \times (k+l+m))}$ has been defined previously, and $\mathbf{T}_{i(120 \times (k+l+m))}$ can be defined by:

$$\mathbf{T}_i = \begin{bmatrix} \begin{array}{cccc|ccc|ccc} T_{0(1)1} & T_{1(1)1} & \cdots & T_{K(1)1} & & & & & & \\ T_{0(1)2} & T_{1(1)2} & \cdots & T_{K(1)2} & & & & & & \\ \vdots & \vdots & \ddots & \vdots & & & & & & \\ T_{0(1)40} & T_{1(1)40} & \cdots & T_{K(1)40} & & & & & & \\ \hline & & & & T_{0(2)1} & T_{1(2)1} & \cdots & T_{L(2)1} & & \\ & & & & T_{0(2)2} & T_{1(2)2} & \cdots & T_{L(2)2} & & \\ & & & & \vdots & \vdots & \ddots & \vdots & & \\ & & & & T_{0(2)40} & T_{1(2)40} & \cdots & T_{L(2)40} & & \\ \hline & & & & & & & & T_{0(3)1} & T_{1(3)1} & \cdots & T_{M(3)1} \\ & & & & & & & & T_{0(3)2} & T_{1(3)2} & \cdots & T_{M(3)2} \\ & & & & & & & & \vdots & \vdots & \ddots & \vdots \\ & & & & & & & & T_{0(3)40} & T_{1(3)40} & \cdots & T_{M(3)40} \end{array} \end{bmatrix}$$

where $T_{0(1)1}$ is the first coefficient (relating to intercept – “ T_0 ”) of the used function, in the time “1”, for the trait “(1)”. K, L and M depends on the coefficients number of the used function.

Thus, the $\Sigma_{(120 \times 120)}$ matrix is defined as:

$$\Sigma = \begin{bmatrix} \sigma_{a_1(1)}^2 & \sigma_{a_{1,2}(1)} & \dots & \sigma_{a_{1,40}(1)} & \sigma_{a_{1,1}(1,2)} & \sigma_{a_{1,2}(1,2)} & \dots & \sigma_{a_{1,40}(1,2)} & \sigma_{a_{1,1}(1,3)} & \sigma_{a_{1,2}(1,3)} & \dots & \sigma_{a_{1,40}(1,3)} \\ & \sigma_{a_2(1)}^2 & \dots & \sigma_{a_{2,40}(1)} & & \sigma_{a_{2,2}(1,2)} & \dots & \sigma_{a_{2,40}(1,2)} & & \sigma_{a_{2,2}(1,3)} & \dots & \sigma_{a_{2,40}(1,3)} \\ & & \ddots & \vdots & & & \ddots & \vdots & & & \ddots & \vdots \\ & & & \sigma_{a_{40}(1)}^2 & \text{Symmetric} & & & \sigma_{a_{40,40}(1,2)} & \text{Symmetric} & & & \sigma_{a_{40,40}(1,3)} \\ \hline & & & & \sigma_{a_1(2)}^2 & \sigma_{a_{1,2}(2)} & \dots & \sigma_{a_{1,40}(2)} & \sigma_{a_{1,1}(2,3)} & \sigma_{a_{1,2}(2,3)} & \dots & \sigma_{a_{1,40}(2,3)} \\ & & & & & \sigma_{a_2(2)}^2 & \dots & \sigma_{a_{2,40}(2)} & & \sigma_{a_{2,2}(2,3)} & \dots & \sigma_{a_{2,40}(2,3)} \\ & & & & & & \ddots & \vdots & & & \ddots & \vdots \\ & & & & & & & \sigma_{a_{40}(2)}^2 & \text{Symmetric} & & & \sigma_{a_{40,40}(2,3)} \\ \hline & & & & & & & & & \sigma_{a_1(3)}^2 & \sigma_{a_{1,2}(3)} & \dots & \sigma_{a_{1,40}(3)} \\ & & & & & & & & & & \sigma_{a_2(3)}^2 & \dots & \sigma_{a_{2,40}(3)} \\ & & & & & & & & & & & \ddots & \vdots \\ & & & & & & & & & & & & \sigma_{a_{40}(3)}^2 \\ \text{Symmetric} & & & & & & & & & & & & \end{bmatrix}$$

where $\sigma_{a_1(1)}^2$ is the additive genetic variance for the first trait “(1)” at test-day “1”; $\sigma_{a_{1,2}(1)}$ is the additive genetic covariance between the first and the second test-day “1,2” of the first trait “(1)” and $\sigma_{a_{1,2}(1,2)}$ is the additive genetic covariance between the first test-day of the first trait and the second test-day of the second trait “1,2(1,2)”, and so on.

The general matrix of permanent environmental covariance can be defined as follow:

$$\Phi = \mathbf{T}_i \cdot \mathbf{R}_p \cdot \mathbf{T}_i'$$

where $\mathbf{R}_p((k+l+m) \times (k+l+m))$ and $\mathbf{T}_i(120 \times (k+l+m))$ have been defined previously. Thus, the Φ matrix can be describe as follow:

$$\Phi = \begin{bmatrix} \sigma_{p_{i(1)}}^2 & \sigma_{p_{1,2(1)}} & \cdots & \sigma_{p_{1,40(1)}} & \sigma_{p_{1,1(1,2)}} & \sigma_{p_{1,2(1,2)}} & \cdots & \sigma_{p_{1,40(1,2)}} & \sigma_{p_{1,1(1,3)}} & \sigma_{p_{1,2(1,3)}} & \cdots & \sigma_{p_{1,40(1,3)}} \\ & \sigma_{p_{2(1)}}^2 & \cdots & \sigma_{p_{2,40(1)}} & & \sigma_{p_{2,2(1,2)}} & \cdots & \sigma_{p_{2,40(1,2)}} & & \sigma_{p_{2,2(1,3)}} & \cdots & \sigma_{p_{2,40(1,3)}} \\ & & \ddots & \vdots & & & \ddots & \vdots & & & \ddots & \vdots \\ & & & \sigma_{p_{40(1)}}^2 & \text{Symmetric} & & & \sigma_{p_{40,40(1,2)}} & \text{Symmetric} & & & \sigma_{p_{40,40(1,3)}} \\ \hline & & & & \sigma_{p_{i(2)}}^2 & \sigma_{p_{1,2(2)}} & \cdots & \sigma_{p_{1,40(2)}} & \sigma_{p_{1,1(2,3)}} & \sigma_{p_{1,2(2,3)}} & \cdots & \sigma_{p_{1,40(2,3)}} \\ & & & & & \sigma_{p_{2(2)}}^2 & \cdots & \sigma_{p_{2,40(2)}} & & \sigma_{p_{2,2(2,3)}} & \cdots & \sigma_{p_{2,40(2,3)}} \\ & & & & & & \ddots & \vdots & & & \ddots & \vdots \\ & & & & & & & \sigma_{p_{40(2)}}^2 & \text{Symmetric} & & & \sigma_{p_{40,40(2,3)}} \\ \hline & & & & & & & & & \sigma_{p_{i(3)}}^2 & \sigma_{p_{1,2(3)}} & \cdots & \sigma_{p_{1,40(3)}} \\ & & & & & & & & & & \sigma_{p_{2(3)}}^2 & \cdots & \sigma_{p_{2,40(3)}} \\ & & & & & & & & & & & \ddots & \vdots \\ & & & & & & & & & & & & \sigma_{p_{40(3)}}^2 \\ \hline & & & & & & & & & & & & \text{Symmetric} \end{bmatrix}$$

where $\sigma_{p_{1(1)}}^2$ is the permanent environmental variance for the first trait “(1)” at test-day “1”; $\sigma_{p_{1,2(1)}}$ is the permanent environmental covariance between the first and the second test-day “1,2” of the first trait “(1)” and $\sigma_{p_{1,2(1,2)}}$ is the permanent environmental covariance between the first test-day of the first trait and the second test-day of the second trait “1,2(1,2)”, and so on.

The breeding value ($\widehat{\mathbf{EBV}}_{ij}$) of the animal i at test-day j can be obtained as follow:

$$\widehat{\mathbf{EBV}}_{ij} = \mathbf{T}_i \cdot \hat{\mathbf{a}}_i$$

where $\hat{\mathbf{a}}_i$ is a vector of breeding values for covariance function coefficients for the animal i ; and $\mathbf{T}_i$ is a matrix of covariables associated with the function used for the animal i , has been defined previously. Thus, the resultant $\widehat{\mathbf{EBV}}'_{ij}$ vector is given by:

$$\widehat{\mathbf{EBV}}'_{ij} = \left[\widehat{\mathbf{EBV}}_{i(1)} \quad \widehat{\mathbf{EBV}}_{i(2)} \quad \cdots \quad \widehat{\mathbf{EBV}}_{i(1)} \quad \vdots \quad \widehat{\mathbf{EBV}}_{i(2)} \quad \widehat{\mathbf{EBV}}_{i(2)} \quad \cdots \quad \widehat{\mathbf{EBV}}_{i(2)} \quad \vdots \quad \widehat{\mathbf{EBV}}_{i(3)} \quad \widehat{\mathbf{EBV}}_{i(3)} \quad \cdots \quad \widehat{\mathbf{EBV}}_{i(3)} \right]$$

where “ i ” is referent to animal, “ j ” is referent to test-day and “(1), (2) and (3)” are referent to traits: milk yield, fat and protein percent, respectively.

APPENDIX II

Gibbs3f90

In this study, the (co)variance components were estimated by Bayesian inference using the GIBBS3F90 software (Misztal, 2010). Herein, we going to show how to modify the parameter file (renf90.par) for combining different functions under a multiple-trait random regression model.

We consider, by way of example, that there are 500 animals with observations and 1000 animals in the Relationship matrix. The combined RRM added two functions, where Wilmlink function will fit the first trait (milk yield, for example) and the third order Legendre polynomials will fit the second one (fat percent, for example). For simplicity, we assume that the systematic effect was contemporary group (with 5 levels) for all traits, and that the average curve, additive genetic and permanent environmental curves were fitted by the same models. The residual variances, in this example, were modeled by a step function with two classes: 1 to 20 and 21 to 40 weeks of lactation. Thus, an example of Data file (renf90.dat), considering just the first five animals, after of the use of Renumf90.exe, can be describe as follow:

3.10	3.37	1	1	15	0.4723665530	0.7071067810	-0.3674234610	-0.5771156730	1	188	188
2.30	4.16	1	1	21	0.3499377490	0.7071067810	0.0000000000	-0.7905694150	2	188	188
2.30	3.31	1	1	25	0.2865047970	0.7071067810	0.2449489740	-0.6957010850	2	188	188
1.60	2.74	1	1	27	0.2592402610	0.7071067810	0.3674234610	-0.5771156730	2	188	188
1.40	2.96	1	1	35	0.1737739430	0.7071067810	0.8573214100	0.3715676250	2	188	188
1.90	3.73	1	1	39	0.1422740720	0.7071067810	1.1022703840	1.1305142640	2	188	188
2.40	2.51	1	1	40	0.1353352830	0.7071067810	1.1635076280	1.3498972760	2	188	188
3.40	3.08	2	1	4	0.8187307530	0.7071067810	-1.0410331410	0.9229897920	1	235	235
3.00	3.75	2	1	8	0.6703200460	0.7071067810	-0.7960841660	0.2114773190	1	235	235
4.00	3.44	2	1	10	0.6065306600	0.7071067810	-0.6736096790	-0.0731276710	1	235	235
2.70	2.06	2	1	18	0.4065696600	0.7071067810	-0.1837117310	-0.7372059800	1	235	235
2.70	2.99	2	1	22	0.3328710840	0.7071067810	0.0612372440	-0.7846401440	2	235	235
1.30	2.37	2	1	23	0.3166367690	0.7071067810	0.1224744870	-0.7668523330	2	235	235
0.70	3.47	2	1	29	0.2345702880	0.7071067810	0.4898979490	-0.4110960960	2	235	235
3.20	3.46	2	1	13	0.5220457770	0.7071067810	-0.4898979490	-0.4110960960	1	279	279
2.00	4.69	2	1	19	0.3867410230	0.7071067810	-0.1224744870	-0.7668523330	1	279	279
2.30	3.36	2	1	23	0.3166367690	0.7071067810	0.1224744870	-0.7668523330	2	279	279
2.00	3.84	2	1	25	0.2865047970	0.7071067810	0.2449489740	-0.6957010850	2	279	279
1.10	2.15	2	1	33	0.1920499090	0.7071067810	0.7348469230	0.0632455530	2	279	279
0.60	2.45	2	1	36	0.1652988880	0.7071067810	0.9185586540	0.5435164730	2	279	279
0.50	2.18	2	1	37	0.1572371660	0.7071067810	0.9797958970	0.7273238620	2	279	279
0.80	4.10	2	1	38	0.1495686190	0.7071067810	1.0410331410	0.9229897920	2	279	279
1.40	4.55	4	1	2	0.9048374180	0.7071067810	-1.1635076280	1.3498972760	1	354	354
3.70	1.89	4	1	3	0.8607079760	0.7071067810	-1.1022703840	1.1305142640	1	354	354
3.00	4.55	4	1	6	0.7408182210	0.7071067810	-0.9185586540	0.5435164730	1	354	354

3.50	1.89	4	1	8	0.6703200460	0.7071067810	-0.7960841660	0.2114773190	1	354	354
3.50	2.50	4	1	11	0.5769498100	0.7071067810	-0.6123724360	-0.1976423540	1	354	354
2.80	3.32	4	1	17	0.4274149320	0.7071067810	-0.2449489740	-0.6957010850	1	354	354
2.50	2.93	4	1	21	0.3499377490	0.7071067810	0.0000000000	-0.7905694150	2	354	354
2.30	2.03	4	1	23	0.3166367690	0.7071067810	0.1224744870	-0.7668523330	2	354	354
2.50	1.88	4	1	31	0.2122479740	0.7071067810	0.6123724360	-0.1976423540	2	354	354
2.80	3.21	4	1	35	0.1737739430	0.7071067810	0.8573214100	0.3715676250	2	354	354
2.40	1.67	4	1	36	0.1652988880	0.7071067810	0.9185586540	0.5435164730	2	354	354
3.60	4.35	5	1	4	0.8187307530	0.7071067810	-1.0410331410	0.9229897920	1	369	369
3.30	3.98	5	1	6	0.7408182210	0.7071067810	-0.9185586540	0.5435164730	1	369	369
3.70	3.24	5	1	7	0.7046880900	0.7071067810	-0.8573214100	0.3715676250	1	369	369
3.70	3.37	5	1	10	0.6065306600	0.7071067810	-0.6736096790	-0.0731276710	1	369	369
4.00	3.46	5	1	12	0.5488116360	0.7071067810	-0.5511351920	-0.3102984950	1	369	369
3.10	2.71	5	1	20	0.3678794410	0.7071067810	-0.0612372440	-0.7846401440	1	369	369
3.10	2.44	5	1	24	0.3011942120	0.7071067810	0.1837117310	-0.7372059800	2	369	369
2.30	2.26	5	1	25	0.2865047970	0.7071067810	0.2449489740	-0.6957010850	2	369	369
2.00	2.89	5	1	31	0.2122479740	0.7071067810	0.6123724360	-0.1976423540	2	369	369
2.50	2.96	5	1	33	0.1920499090	0.7071067810	0.7348469230	0.0632455530	2	369	369
1.40	2.66	5	1	39	0.1422740720	0.7071067810	1.1022703840	1.1305142640	2	369	369

where the first column refers to the first trait (milk yield); the second one refers to the second trait (fat percent); the third refers to the contemporary group; the fourth, fifth and sixth columns refers to the coefficients of Wilmink function; the seventh, eighth and ninth one refers to the coefficients of Legendre polynomials; the tenth column refers to the step function of the residual variances; and the eleventh and twelfth columns refers to the additive genetic and permanent environmental effects, respectively.

It is important to say that, depending on the used functions, the parameter relative to the intercept must be standardized, for erroneous estimates will not be generated.

For this data, the parameter file created by Renumf90.exe (renf90.par) will be modify and describe as follow:

```
# BLUPF90 parameter file created by RENF90
DATAFILE
renf90.dat
NUMBER_OF_TRAITS
2
NUMBER_OF_EFFECTS
19
```

```

OBSERVATION(S)
  1  2
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE  NUMBER_OF_LEVELS  TYPE_OF_EFFECT  [EFFECT
NESTED]
3  3  5 cross          #1- Contemporary group
4  0  1 cov           #2- Parameter a of Wilmink function (Fixed)
5  0  1 cov           #3- Parameter b of Wilmink function (Fixed)
6  0  1 cov           #4- Parameter c of Wilmink function (Fixed)
0  7  1 cov           #5- First coefficient of Legendre polynomials (Fixed)
0  8  1 cov           #6- Second coefficient of Legendre polynomials (Fixed)
0  9  1 cov           #7- Third coefficient of Legendre polynomials (Fixed)
4  0  1000 cov 11 11  #8- Parameter a of Wilmink function (additive genetic)
5  0  1000 cov 11 11  #9- Parameter b of Wilmink function (additive genetic)
6  0  1000 cov 11 11  #10- Parameter c of Wilmink function (additive genetic)
0  7  1000 cov 11 11  #11- First coefficient of Legendre polynomials (additive genetic)
0  8  1000 cov 11 11  #12- Second coefficient of Legendre polynomials (additive genetic)
0  9  1000 cov 11 11  #13- Third coefficient of Legendre polynomials (additive genetic)
4  0  500 cov 12 12   #14- Parameter a of Wilmink function (permanent environmental)
5  0  500 cov 12 12   #15- Parameter b of Wilmink function (permanent environmental)
6  0  500 cov 12 12   #16- Parameter c of Wilmink function (permanent environmental)
0  7  500 cov 12 12   #17- First coefficient of Legendre polynomials (permanent environmental)
0  8  500 cov 12 12   #18- Second coefficient of Legendre polynomials (permanent
environmental)
0  9  500 cov 12 12   #19- Third coefficient of Legendre polynomials (permanent environmental)

RANDOM_RESIDUAL_VALUES
8.940852090  0.158555690
0.158555690  8.833510400

RANDOM_GROUP
8 9 10 11 12 13

RANDOM_TYPE
add_animal

FILE
renadd1.ped

```

(CO)VARIANCES

5.0505	0.7308	0.8064	0.9001	0.3509	0.1049	0.1424	0.2187	-0.5507	-1.2924	0.2142	-0.0217
0.7308	3.8460	0.5363	0.5946	0.2258	0.2412	0.3475	0.4784	0.1066	0.0110	0.1601	-0.0001
0.8064	0.5363	2.6839	0.5094	0.1930	0.2198	0.3171	0.4354	0.1273	0.0756	0.1386	0.0010
0.9001	0.5946	0.5094	2.7512	0.2138	0.2440	0.3520	0.4834	0.1423	0.0861	0.1536	0.0011
0.3509	0.2258	0.1930	0.2138	2.1152	0.0932	0.1344	0.1845	0.0559	0.0362	0.0583	0.0005
0.1049	0.2412	0.2198	0.2440	0.0932	4.8998	0.1216	0.1687	0.0048	-0.0670	0.0642	-0.0012
0.1424	0.3475	0.3171	0.3520	0.1344	0.1216	5.0290	0.2421	0.0052	-0.1000	0.0925	-0.0018
0.2187	0.4784	0.4354	0.4834	0.1845	0.1687	0.2421	5.1155	0.0117	-0.1288	0.1272	-0.0024
-0.5507	0.1066	0.1273	0.1423	0.0559	0.0048	0.0052	0.0117	7.8460	-0.2636	0.0326	-0.0044
-1.2924	0.0110	0.0756	0.0861	0.0362	-0.0670	-0.1000	-0.1288	-0.2636	9.0636	0.0122	-0.0084
0.2142	0.1601	0.1386	0.1536	0.0583	0.0642	0.0925	0.1272	0.0326	0.0122	2.8334	0.0001
-0.0217	-0.0001	0.0010	0.0011	0.0005	-0.0012	-0.0018	-0.0024	-0.0044	-0.0084	0.0001	9.7754

RANDOM_GROUP

14 15 16 17 18 19

RANDOM_TYPE

diagonal

FILE

(CO)VARIANCES

5.0290	0.2421	0.0052	-0.1000	0.0925	-0.0018	-0.0148	-0.0133	0.3418	0.2940	0.1132	0.0003
0.2421	5.1155	0.0117	-0.1288	0.1272	-0.0024	-0.0187	-0.0124	0.4687	0.4059	0.1605	0.0005
0.0052	0.0117	7.8460	-0.2636	0.0326	-0.0044	-0.0478	-0.1585	0.1558	0.0624	-0.0902	-0.0037
-0.1000	-0.1288	-0.2636	9.0636	0.0122	-0.0084	-0.0948	-0.3375	0.1220	-0.0513	-0.2690	-0.0083
0.0925	0.1272	0.0326	0.0122	2.8334	0.0001	0.0040	0.0325	0.1447	0.1424	0.0834	0.0011
-0.0018	-0.0024	-0.0044	-0.0084	0.0001	9.7754	-0.0016	-0.0056	0.0017	-0.0011	-0.0046	-0.0001
-0.0148	-0.0187	-0.0478	-0.0948	0.0040	-0.0016	9.1843	-0.0615	0.0287	-0.0037	-0.0467	-0.0015
-0.0133	-0.0124	-0.1585	-0.3375	0.0325	-0.0056	-0.0615	8.1095	0.1668	0.0486	-0.1325	-0.0050
0.3418	0.4687	0.1558	0.1220	0.1447	0.0017	0.0287	0.1668	1.9233	0.5104	0.3357	0.0051
0.2940	0.4059	0.0624	-0.0513	0.1424	-0.0011	-0.0037	0.0486	0.5104	4.4135	0.2327	0.0022
0.1132	0.1605	-0.0902	-0.2690	0.0834	-0.0046	-0.0467	-0.1325	0.3357	0.2327	6.4656	-0.0027
0.0003	0.0005	-0.0037	-0.0083	0.0011	-0.0001	-0.0015	-0.0050	0.0051	0.0022	-0.0027	7.8859

OPTION hetres_int 10 2