Random Regression Models for Test-day Milk and Fat Yields in Brazilian Gyr Cattle

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Introduction

Nowadays, random regression models (RRM) applied to test-day records have been implemented by most Interbull members for genetic evaluation of dairy cattle. Some benefits attributed to the adoption of RRM are: the use of test day records per animal can be maximized with correspondent increasing in genetic evaluation accuracies (Meyer (2004)); better definition of contemporary groups and quantification of the environmental effects (Visscher and Goddard (1995)); the possibility of calculating persistency of milk yield breeding values as functions of days in milk. Additionally, RRM allow genetic evaluation of animals whose lactation is still ongoing, without projections, which enables more frequent evaluations and decreases generation interval (Swalve (2000)). Orthogonal Legendre polynomials (LP) have been frequently used for modeling the covariance structure of test-day records in dairy cattle. Orthogonal polynomials show low correlations between random regression coefficients and provide covariance matrices estimates that tend to be robust over different data sets (Schaeffer (2004)). The objective of this study was to estimate genetic covariance functions for first lactation milk and fat yields of Brazilian Gyr cows using random regression on orthogonal Legendre polynomials of days in milk.

Material and methods

Data were provided by Embrapa Dairy Cattle (Brazilian Agricultural Research Corporation), comprising 38,268 test-day milk yields (TDMY) and 10,769 test-day fat yields (TDFY) from 5,158 and 1,559 first lactation records of Brazilian Gyr cows. Lactations were recorded in 4,444 (milk) and 467 (fat) herds between 1990 and 2007. Cows with records were daughters of 327 (milk) and 183 (fat) sires. Test day yields from 5 to 305 days of lactation, time interval between successive tests less than 45 days and age of calving between 24 and 60 months were required. Contemporary groups (CG) were defined as herd-year-test month (HTM) and had at least three records. Test day records were grouped in 10 monthly classes (TDC) according to days in milk: 5-30, 31-60, 61-90, 91-120, 121-150, 151-180, 181-210,

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211-240, 241-270 and 271-305. Average and standard deviation of TDMY and TDFY were 9.36 kg (3.87) and 0.45 kg (0.19), respectively. Variance components were estimated by REML using the "Wombat" package (Meyer (2007)). Random regressions on orthogonal Legendre polynomials (LP) of days in milk, for additive genetic and permanent environmental effects, with orders from 4 to 7, were considered. At first, residual variance was assumed constant (homogeneous) throughout the lactation. Latter, residual variances were assumed to be heterogeneous with 4 (1, 2, 3-9 and 10 months of lactation), 6 (1, 2, 3-6, 7-8, 9 and 10 months of lactation), or 10 (1, 2, ..., 10 months of lactation) classes, for TDMY. For fat yield, 4 (1-3, 4-6, 7-9 and 10 months of lactation), 6 (1-3, 4-5, 6, 7-8, 9 and 10 months of lactation), or 10 (1, 2, ..., 10 months of lactation) classes were considered. The models were designated by $k_a k_p r$, where k_a is the order of the additive genetic effect, k_p is the order of the permanent environmental effect and r is the number of residual classes. Then, 456 is a model with polynomial order of 4 for additive genetic effect, 5 for permanent environmental effect, and 6 residual classes. The model included fixed effects of CG, age of cow at calving as covariable (linear and quadratic effects) and a regression on LP of order 4 to taking into account the population average trend. Models were compared by Akaike's (AIC) and Schwarz's Bayesian (BIC) information criteria. Standard multi-trait test-day models were also applied for both, milk (TDMM) and fat yields (TDFM). The models included the same effects as the RRM, excluding the fixed regression on LP of days in milk and including days in milk (linear effect) as covariable.

Results and discussion

Results from AIC and BIC indicated that models with heterogeneous residual variances adjusted the data better than those with homogeneous residual variance. For both, milk and fat yields, a model with 4 classes of residual variances described the changes in residual variances along the lactation best, according to BIC. Thus, for models varying the order of fit for additive genetic and permanent environmental effects, residual variances were modeled with 4 classes.

Results from AIC indicated the model 774, containing 60 parameters, as the most adequate for fitting TDMY (Table 1), while BIC indicated the model 454 (29 parameters) as the best. For TDFY, models 454 (29 parameters) and 444 (24 parameters) were the best according to AIC and BIC results (Table1). Parameter estimates obtained by 774 and 454 models (TDMY) and 454 and 444 models (TDFY) were contrasted. The phenotypic variance estimates obtained with all models were very similar, for both traits. On the other hand, genetic variance estimates obtained with RRM were higher than those estimated by standard TDM, but showed the same trend. Genetic variance estimates were higher in the beginning and at the end of lactation for TDMY, but increased from the beginning to the end of lactation, for TDFY.

For milk yield, heritability estimates obtained with 774 and 454 models were similar (Figure 1) and showed the same tend as the genetic variance estimates. With 454 model, heritability estimates varied from 0.24 to 0.36, and with 774 model, from 0.23 to 0.36. Estimates of similar magnitude were described by Herrera *et al.* (2008) using Ali and Schaeffer's logarithmic function to modeling both fixed and random effects for Gyr milk yield.

However, their estimates decreased from the beginning (0.33) to the end (0.21) of lactation. Also working with Gyr data, Pereira *et al.* (2009), using Wilmink or Ali and Schaeffer functions, obtained lower heritability estimates than in the present work, with values ranging from 0.12 to 0.32. Trends for fat yield heritability estimates were very similar for both models (454 and 444). Fat yield heritability estimates were lower at the beginning of lactation and increased with days in milk (0.07 to 0.29). Heritability estimates were lower for fat than for milk yield. Similar results were found by Strabel and Jamrozik (2006) for Polish Black and White, and Jakobsen *et al.* (2002) for the Danish population.

Table 1: Number of parameters (p), number of residual classes (r), log likelihood function (-2 Log L), Akaike's Information Criterion (AIC) and Schwarz's Bayesian Information Criterion (BIC)

				Test-day milk yield			Test-day fat yield		
k_a[1]	k_p[2]	p	r	-2LogL	AIC	BIC	-2LogL	AIC	BIC
4	4	21	1	72482	72524	72701	-34711	-34669	-34517
4	4	24	4	72132	72180	72383	-34751	-34703	-34529*
4	4	26	6	72119	72171	72390	-34754	-34702	-34513
4	4	30	10	72108	72168	72421	-34757	-34697	-34479
4	5	29	4	71958	72016	72260*	-34762	-34704*	-34494
4	6	35	4	71897	71967	72262	-34773	-34703	-34450
4	7	42	4	71871	71955	72309	-34784	-34700	-34396
5	5	34	4	71948	72016	72303	-34766	-34698	-34452
5	6	40	4	71888	71968	72305	-34778	-34698	-34408
5	7	47	4	71862	71956	72352	-34789	-34695	-34355
6	6	46	4	71813	71905	72293	-34780	-34688	-34355
6	7	53	4	71788	71894	72341	-34792	-34686	-34302
7	7	60	4	71750	71870*	72375	-34791	-34671	-34237

[*] Indicates the best model, [1] k_a: order for additive genetic effect; [2] k_p: order for permanent environmental effect

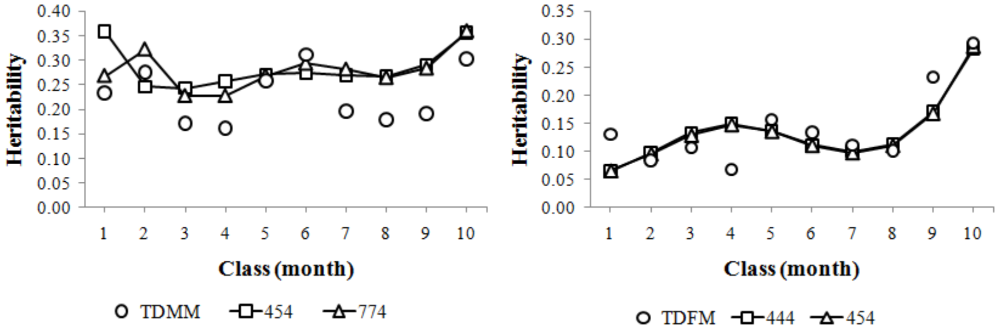

Figure 1: Heritability estimates for test-day milk (left) and fat (right) yields from multi-trait analyses (TDMM and TDFM) and random regressions analyses ($k_a k_p r$).

Phenotypic correlations estimated by all models, for both traits, showed similar surfaces. Estimates were high (0.90) between adjacent yields and small (0.20) between yields at the extremes of the lactation curve. Same pattern was observed for genetic correlation estimates. The genetic correlation estimates between adjacent yields were nearly 0.90, declining to 0.10 between the beginning and the end of lactation. These results agree with those from Herrera *et al.* (2008) and Pereira *et al.* (2009).

Conclusion

Heterogeneity of residual variances has to be considered for test-day milk and fat yields genetic evaluations applying random regression models.

A model considering a fourth order Legendre polynomial for the additive genetic effect, fifth order for the permanent environmental effect and four classes of residual variances is parsimonious and fits Gyr cows test-day milk records adequately. For test-day fat yield, a model with a fourth order Legendre polynomial for the additive genetic and permanent environmental effects and four classes of residual variances would be the best. These models could be used for genetic evaluation of Gyr cattle in Brazil.

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