

Random regressions models to describe the genetic variation of milk yield over multiple parities in Buffaloes

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ABSTRACT: The objectives of this study were to estimate (co)variance functions for additive genetic and permanent environmental effects, as well as the genetic parameters for milk yield over multiple parities, using random regressions models (RRM). Records of 4,757 complete lactations of Murrah breed buffaloes from 12 herds were analyzed. Ages at calving were between 2 and 11 years. The model included the additive genetic and permanent environmental random effects and the fixed effects of contemporary groups (herd, year and calving season) and milking frequency (1 or 2). A cubic regression on Legendre orthogonal polynomials of ages was used to model the mean trend. The additive genetic and permanent environmental effects were modeled by Legendre orthogonal polynomials. Residual variances were considered homogenous or heterogeneous, modeled through variance functions or step functions with 5, 7 or 10 classes. Results from Akaike's and Schwarz's Bayesian information criterion indicated that a RRM considering a third order polynomial for the additive genetic and permanent environmental effects and a step function with 5 classes for residual variances fitted best. Heritability estimates obtained by this model varied from 0.10 to 0.28. Genetic correlations were high between consecutive ages, but decreased when intervals between ages increased

Key words: Genetic parameters, Legendre polynomials, Milk yield.

INTRODUCTION - In general, the milk yields over multiple parities of a cow are considered as the same trait with repeated records. For these traits, repeatability models are normally applied, assuming homogeneity of variances and that the genetic correlations between lactations are equal to unit. However, Aamand et al. (1999) found heterogeneity of variances for milk yield in different lactations and in different days in milk. Repeated traits can be analyzed by a multi-trait model, which allows genetic correlations to differ between records on the same individual. But, an unstructured (co)variance matrix is assumed in

this type of analysis. When many traits are included in the analyses the model will be over-parameterized. Random regression models (RRM) have been proposed as an alternative to model traits that are recorded repeatedly during the animal's life. RRM describe, in a continuous form, the structure of (co)variance along time and allows predicting the breeding values for total milk yield or for specific periods of lactation, while multi-trait models only give predictions for classes of days in milk. The objectives of this study were to estimate (co)variance functions for additive genetic and permanent environmental effects, as well as the genetic parameters for milk yield over multiple parities, using RRM.

MATERIAL AND METHODS - Records of 4,757 complete lactations of Murrah buffaloes from 12 herds were analyzed. Ages at calving were between 2 and 11 years. The model included the additive genetic and permanent environmental random effects and the fixed effects of contemporary groups (herd, year and calving season) and milking frequency (1 or 2). A cubic regression on Legendre orthogonal polynomials of ages was used to model the mean trend. The additive genetic and permanent environmental effects were modelled by Legendre orthogonal polynomials. Residual variances were considered homogenous or heterogeneous, modelled through variance functions or step functions. For variance functions, 3rd to 6th order ordinary polynomials were used. For step functions classes with 5, 7 and 10 variances residuals were considered. There were 11,760 animals in the relationship matrix. Variance components were estimated by restricted maximum likelihood method, using DFREML package (Meyer, 1998). Models were compared by Akaike's Information Criterion (AIC) and Schwarz's Bayesian Information Criterion (BIC), as reported by Wolfinger (1993). The different RRM are indicated as: ka.kp.fv or ka.kp.het, referring to the order of (co)variance functions for the additive genetic (ka) and permanent environmental (kp) effects and to the structures of residual variances which were modeled by variance functions (fv) or by step functions (het).

RESULTS AND CONCLUSIONS - Milk yield mean and standard deviation were $1,784.72 \pm 705.97$ kg. Results from AIC and BIC indicated that homogeneous residual variances were not adequate to fit the data. In general, models with step functions fitted better than those with residual variance functions (Table 1). The model containing a step function with 5 residual variances was the best to describe the changes in residual variances along the lactations. Increasing the orders of additive genetic and permanent environmental effects improved logL values. AIC and BIC values were smaller for 3.3.het10 and 3.3.het5 models. The phenotypic variance estimated with the 3.3.het5 model increased with age (Table 2). The genetic variances were lower at the youngest and oldest ages, reaching maximum values between 7 and 8 years. The permanent environmental variances showed the same tendency as phenotypic variances. Heritability estimates with the 3.3.het5 model varied from 0.10 to 0.28 (Figure 1). Similar results were reported by Sesana et al. (2006) and Ramos et al. (2006), using repeatability models. Phenotypic correlations estimated by 3.3.het5 model, were higher between adjacent ages and lower between milk yield at early and later ages. Genetic correlation estimates between adjacent ages were high and close to one. Estimates became smaller as the distance between ages increased. The three main eigenvalues of the additive genetic effect coefficient matrix for 3.3.het5 model accounted for 91.8%, of the total variance. The first eigenfunction was always positive and constant

for all ages; suggesting that, most of the variation is explained by the same group of genes. To model total milk yield over multiple parities is necessary to consider heterogeneity of residual variances. A third order random regression model for the additive genetic and permanent environmental effects was the most adequate for fitting the data.

Table 1. Orders of polynomials for additive genetic (k_a) and permanent environmental (k_p) effects, structures of residual variances (e), number of parameters (p), log likelihood function ($2 \log L$, +30,000), Akaike's Information Criterion (AIC, -61,000) and Schwarz's Bayesian Information Criterion (BIC, -61,000) for different random regression models.

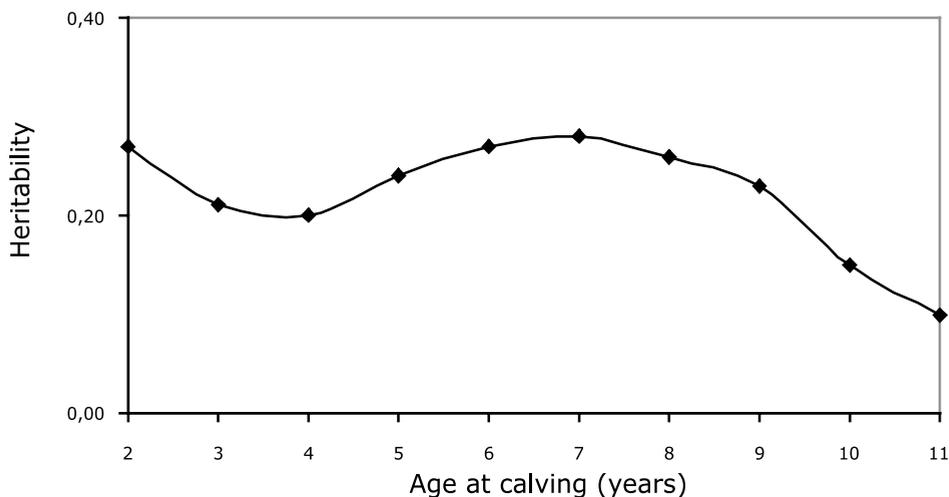
Model	k_a	k_{ap}	Order polynomials		$2 \log L$	AIC	BIC
			e	p			
1	3	3	fv3	15	-297.3	624.7	721.7
2	3	3	fv4	16	-286.1	604.2	707.7
3	3	3	fv5	17	-283.9	601.8	711.8
4	3	3	fv6	18	-281.8	599.6	716.0
5	3	3	hom	13	-312.1	650.1	734.2
6	3	3	het5	17	-281.4	596.9	706.8*
7	3	3	het7	19	-281.1	600.2	723.1
8	3	3	het10	22	-274.6	593.1*	735.4
9	3	4	het5	21	-279.6	601.2	737.0
10	3	5	het5	26	-274.8	601.7	769.8
11	3	6	het5	32	-274.3	612.7	819.6
12	4	5	het5	30	-269.7	599.5	793.5
13	4	6	het5	36	-270.9	613.9	846.7

*Indicates the best model.

Table 2. Estimates of total milk yield additive genetic ($\hat{\sigma}_a^2$), permanent environmental ($\hat{\sigma}_c^2$), residual ($\hat{\sigma}_e^2$) and phenotypic ($\hat{\sigma}_p^2$) variances and heritabilities (\hat{h}^2) obtained with model 3.3.het5, by ages at calving.

Ages at calving (years)	$\hat{\sigma}_a^2$	$\hat{\sigma}_c^2$	$\hat{\sigma}_e^2$	$\hat{\sigma}_p^2$	\hat{h}^2
2	39,777	97,255	8,747	145,779	0.27
3	37,156	77,183	57,161	171,500	0.22
4	45,895	67,996	115,200	229,091	0.20
5	58,947	67,248	115,200	241,395	0.24
6	70,872	73,250	115,200	259,322	0.27
7	77,840	85,068	115,200	278,108	0.28
8	77,623	102,521	115,200	295,344	0.26
9	69,602	126,184	109,324	305,110	0.23
10	54,767	157,385	142,604	354,756	0.15
11	35,711	198,209	142,604	376,524	0.10

Figure 1. Heritability estimates for total milk yield obtained with 3.3.het5 model.



REFERENCES - **Aamand**, G. P., J. Pedersen, U. S. Nielsen, J. Jensen, P. Madsen, J. R. Thomasen, Christensen, L. G., 1999. Animal model for ydelse. Report no. 86, Landsudvalget for kvæg. (In Danish). **Meyer**, K., 1998. DXMR – a program to estimate covariance functions for longitudinal data by REML. In: VI World congress of genetics applied to livestock production, Proceedings... *Amidale*, 27: 465-466. **Sesana**, R. C., Tonhati, H., Albuquerque, L. G., El Faro, L., Campos, R. V., Lima, A. L. F., 2006. Estudo genético da produção de leite para diferentes ordens de parto em bubalinos leiteiros In: III Simposio Búfalos de Las Américas, Medellín, CD-ROM. **Ramos**, A. A., Malhado, C. H. M., Carneiro, P. L. S., 2006. Caracterização fenotípica e genética da produção de leite, intervalo entre partos de búfalo da raça Murrah. *Pesquisa. Agropecuária Brasileira.*, 41:1261-1267. **Wolfinger**, R., 1993 *Commun. Statist.* 22:1079-1106.