

## EFFECT OF SEVERAL STRUCTURES OF CONTEMPORARY GROUPS ON ESTIMATES OF (CO)VARIANCE AND GENETIC PARAMETERS FOR WEANING WEIGHT IN NELLORE CATTLE

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### ABSTRACT

We used actual and adjusted weights to 120 d and 210 d of age of 72,731 male and female Nelore calves born in 40 PMGRN - *Nellore Brazil* herds from 1985 to 2005 aiming to compare the effect of different definitions of contemporary groups on estimates of (co)variance and genetic parameters. Four models, each one with a different structure of contemporary group (CG), were compared using the Akaike Information Criterion (AIC), the Bayesian Information Criterion (BIC), and the Consistent Akaike Information Criterion (CAIC). (Co)variance

estimates were obtained using a derivative-free restricted maximum likelihood procedure. Estimates of (co)variances and genetic parameters were similar for the four models considered. However, the BIC and CAIC indicated that the most appropriate model for this Nelore population was the one that considered CG to be random, and sex of calf to be fixed and separate from CG, in which CG was defined as the group of calves born in the same herd, year, season of birth (trimester), and undergone the same management.

KEYWORDS: beef cattle; contemporary groups; information criteria.

### EFEITO DE DIFERENTES MODELOS SOBRE AS ESTIMATIVAS DE (CO)VARIÂNCIAS E PARÂMETROS GENÉTICOS PARA PESOS ATÉ A DESMAMA EM GADO NELORE

### RESUMO

Com o objetivo de se comparar o ajustamento de modelos com diferentes definições de grupos contemporâneos sobre as estimativas de (co)variâncias e parâmetros genéticos para pesos padronizados e reais aos 120 e 210 dias de idade, analisaram-se dados de 72.731 bezerros Nelore, machos e fêmeas, nascidos de 1985 a 2005 em 40

rebanhos integrantes do PMGRN - *Nellore Brasil*. Foram comparados quatro modelos incluindo diferentes estruturas de grupos contemporâneos (CG), julgados pelos critérios de informação de Akaike, Bayesiano e modificado de Akaike. As estimativas foram obtidas pelo método da máxima verossimilhança restrita livre de

derivadas. As estimativas de (co)variâncias e parâmetros genéticos foram similares entre os modelos, porém os critérios de informação (BIC, CAIC) indicaram que o modelo mais adequado é o que considera o grupo contemporâneo como efeito aleatório, sendo este

constituído pela concatenação dos efeitos de rebanho, ano de nascimento, grupo de manejo e efeito sazonal de trimestre de nascimento, e com efeito do sexo do bezerro independente do CG.

**PALAVRAS-CHAVE:** critérios de informação; gado de corte; grupos contemporâneos.

## INTRODUCTION

The structure of contemporary groups (CG) is of primary importance for genetic evaluation of animals under selection; they are crucial to avoid potential biases in genetic evaluations due to differential treatment of animals in a population (VAN VLECK, 1987).

Contemporary groups have usually been considered as fixed effects in beef cattle genetic evaluations. This has been based on HENDERSON (1973) statement that in sire models, genetic predictions of sires would be associated to contemporary group effects, and to eliminate this bias, CG needed to be defined as fixed effects. Currently, the model of choice is an animal model where individuals are assumed to represent a random sample of the genetic material in a population; however, CG continues to be considered as fixed effects.

Some authors have found that random CG effects yield a better adjustment than models with fixed CG in various animal species. In small herds, BABOT et al. (2003) managed to estimate genetic values for litter size in herds with insufficient number of animals per CG using simulated data, whereas VASCONCELOS et al. (2005) estimated genetic values for milk production in dairy cattle in Portugal using contrast models. Treating CG as random effects was also found to be advantageous by GONZÁLEZ-RECIO & ALENDA (2005) when analyzing binary reproductive traits in Spanish dairy cattle, by WOLF et al. (2005) for growth and litter size in swine utilizing a multi-trait animal model, and by LEGARRA et al. (2005) for milk production in ewes using a Bayesian approach.

To obtain the best possible estimates of (co)variance and genetic parameters it is important to define mathematical models that fit the available data as accurately as possible. This will in turn yield the most accurate genetic predictions given the available information. Thus, the objective of this study was to compare models with different definitions of contemporary groups on estimates of (co)variances and genetic parameters for actual and adjusted weights at 120 and 210 d of age in Nellore cattle in Brazil.

## MATERIAL AND METHODS

Actual and adjusted weights at 120 d (AW120, RW120) and 210 d (AW210, RW210) from 72,731 male and female Nellore calves born between 1985 and 2005 in 40 herds from PMGRN-Nellore Brazil were used in this study. Actual weights were the closest ones to 120 d and 210 d within the intervals of  $120 \pm 90$  d and  $210 \pm 90$  d, respectively. Calf ages were expressed as deviations (CAD) from 120 d and 210 d. Adjusted weights were computed by interpolation between a prior and a posterior weight to the standardized age (120 d or 210 d), allowing a maximum interval of 195 d between these two weights ( $\pm 90$  d plus an additional 15 d due to possible management changes). Birth weight was used as the prior weight for AW120 when there was no other weight (actual birth weight or breed mean: 33 kg for males, and 31 kg for females) to compute the interpolation. Computations were similar to PMGRN (LÔBO, 1996):

$$AW = W + [(W-W_p)/I] \times (A - A_w)$$

where, AW = adjusted weights at standard ages (AW120 or AW210); W = actual weight;  $W_p$  = prior weight; I = interval in days between W and  $W_p$ ; A = standard age (120 d or 210 d);  $A_w$  = age at measurement of W.

The effect of age of cow in years was grouped into six classes (DAC): 1 = 2 yr; 2 = 3 yr; 3 = 4 yr; 4 = 5 yr; 5 = 6 to 9 yr; and 6 = 10 yr and older cows.

Four structures of contemporary groups were defined by concatenation of individual effects, starting from a base subclass ( $CG_B$ ), as follows:

$CG_B$ : herd – year of birth – management group at each age.

$CG_1$ :  $CG_B$  – semester of birth.

$CG_2$ :  $CG_B$  – trimester of birth.

$CG_3$ :  $CG_1$  – sex of calf.

$CG_4$ :  $CG_2$  – sex of calf.

Based on these four CGs ( $CG_1$  to  $CG_4$ ), four analytical models were defined:

$$M_1: \text{Weight} = \alpha + CG_1 + SC + DAC + \varepsilon$$

$$M_2: \text{Weight} = \alpha + CG_2 + SC + DAC + \varepsilon$$

$$M_3: \text{Weight} = \alpha + CG_3 + DAC + \varepsilon$$

$$M_4: \text{Weight} = \alpha + CG_4 + DAC + \varepsilon$$

where, Weight = actual or adjusted weight at 120 d or 210 d of age;  $\alpha$  = constant; CG = contemporary group; SC = sex of calf; DAC = class of cow age at calving, and  $\varepsilon$  = random residual effect. In addition, models for actual weights included age of calf at weighing (CAD), modeled as a cubic polynomial regression, and expressed as a deviation from 120 d or 210 d.

A minimum of five observations per contemporary groups were required. Calves in CG with less than five observations were kept in the database but their weights were set to zero, thus their genetic evaluations were computed using solely information from their relatives. This allowed us to have the same inverse of the relationship matrix ( $A^{-1}$ ) with 119,586 animals in all analyses.

Models for the estimation of (co)variances and genetic parameters for AW120, RW120, AW210 e RW210 using single-trait analysis, considering CG fixed (1) or random (2), were as follows:

$$y = Xb + Z_1d + Z_2m + Z_3pe + e \quad (1)$$

$$y = Xb + Z_1d + Z_2m + Z_3pe + Z_4c + e \quad (2)$$

where,  $y$  = vector of observations;  $b$  = vector of fixed effects, including CG (Equation 1), and the effects of SC, DAC, and a cubic polynomial regression on CAD for the analysis of actual weights (Equations 1 and 2);  $d$ ,  $m$ ,  $pe$ ,  $c$  and  $e$  = vectors of additive direct genetic effects, additive maternal genetic effects, maternal permanent environmental effects, contemporary group, and residual, respectively; and  $X$ ,  $Z_1$ ,  $Z_2$ ,  $Z_3$  e  $Z_4$ , are known incidence matrices relating observations in vector  $y$  to vectors  $b$ ,  $d$ ,  $m$ ,  $pe$ , and  $c$ , respectively. The assumptions of these models were:

$$E[y] = Xb, \text{ and } E[d] = E[m] = E[pe] = E[c] = E[e] = 0, \text{ and}$$

$$\text{Var} \begin{bmatrix} d \\ m \\ pe \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_d^2 & A\sigma_{dm} & 0 & 0 \\ A\sigma_{dm} & A\sigma_m^2 & 0 & 0 \\ 0 & 0 & I\sigma_{pe}^2 & 0 \\ 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

for model 1, and

$$\text{Var} \begin{bmatrix} d \\ m \\ pe \\ c \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_d^2 & A\sigma_{dm} & 0 & 0 & 0 \\ A\sigma_{dm} & A\sigma_m^2 & 0 & 0 & 0 \\ 0 & 0 & I\sigma_{pe}^2 & 0 & 0 \\ 0 & 0 & 0 & I\sigma_c^2 & 0 \\ 0 & 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

for model 2, where,  $A$  = matrix of additive relationships among individuals;  $I$  = identity matrices of appropriate order,  $\sigma_d^2$ ,  $\sigma_m^2$ ,  $\sigma_{pe}^2$ ,  $\sigma_c^2$  and  $\sigma_e^2$  = additive direct genetic variance, additive maternal genetic variance, permanent environmental variance, contemporary group variance, and residual variance, respectively; and  $\sigma_{dm}$  = covariance between direct and maternal genetic effects.

Models were compared using the logarithm of the likelihood function ( $\log L$ ), using the Akaike Information Criterion (AIC; AKAIKE, 1972), the Bayesian Information Criterion (BIC; SCHWARZ, 1978), and Consistent Akaike Information Criterion (CAIC, BOZDOGAN, 1987). The CAIC gives higher penalties to hyperparametrized models compared to AIC. Thus, BIC and CAIC favor parsimonious models. These criteria are defined as follows:

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

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

$$CAIC = -2\log L + k(\log(n)+1)$$

where,  $k$  = number of estimated parameters;  $n$  = number of observations;  $\log L$  = logarithm of the likelihood function.

Models with lower values of these information criteria are considered to better fit the data.

Estimates of (co)variances and genetic parameters were obtained using a derivative-free restricted maximum likelihood procedure (DFREML; SMITH & GRASER, 1986). Computations were carried out using the MTDFREML (Multiple Trait Derivative Free Restricted Maximum Likelihood; BOLDMAN et al., 1995) software package using a single-trait animal model. Because comparisons among animals were done within contemporary groups, the variance due to CG, in those models that considered CG to be random, was not included in the phenotypic variance.

## RESULTS AND DISCUSSION

### Model Fitting

Values for the information criteria AIC, BIC and CAIC obtained using models 1 through 4 with CG either fixed or random are presented in Table 1 for 120 d and in Table 2 for 210 d of age. By any of these criteria, better fitting models have smaller values.

Table 1. Number of observations (n), number of estimated parameters (k), log-likelihood function (-2logL); information criteria AIC, BIC and CAIC to evaluate model fit for actual and adjusted weights at 120 days of age (AW120 and RW120)

Model	CG	n	-2logL	k	AIC	BIC	CAIC
----- Adjusted Weight at 120 days of age (AW120) -----							
M <sub>1</sub>	F	70,543	442,782	696	444,174	450,553	450,553
	R	70,543	446,807	8	446,823	446,896	446,896
M <sub>2</sub>	F	70,543	439,996	1085	442,166	452,109	452,110
	R	70,543	446,301	8	446,317	446,390	446,390
M <sub>3</sub>	F	70,543	440,877	1099	443,075	453,146	453,146
	R	70,543	447,416	6	447,428	447,483	447,483
M <sub>4</sub>	F	70,543	437,225	1676	440,577	455,936	455,936
	R	70,543	447,211	6	447,223	447,278	447,278
----- Actual Weight at 120 days of age (RW120) -----							
M <sub>1</sub>	F	70,677	458,902	699	460,300	466,707	466,707
	R	70,677	463,026	11	463,048	463,149	463,149
M <sub>2</sub>	F	70,677	456,037	1088	458,213	468,186	468,186
	R	70,677	462,487	11	462,509	462,609	462,609
M <sub>3</sub>	F	70,677	456,949	1102	459,153	469,254	469,254
	R	70,677	463,623	9	463,641	463,723	463,723
M <sub>4</sub>	F	70,677	453,163	1679	456,521	471,910	471,910
	R	70,677	463,357	9	463,375	463,457	463,457

AIC = Akaike Information Criterion; BIC = Bayesian Information Criterion; CAIC = Consistent Akaike Information Criterion; CG = Contemporary group fixed (F) or random (R).

Table 2. Number of observations (n), number of estimated parameters (k), log-likelihood function (-2logL); information criteria AIC, BIC and CAIC to evaluate model fit for actual and adjusted weights at 210 days of age (AW210 and RW210)

Model	CG	n	-2logL	k	AIC	BIC	CAIC
----- Adjusted Weight at 210 days of age (AW210) -----							
M <sub>1</sub>	F	65,607	457,355	682	458,719	464,919	464,919
	R	65,607	462,078	8	462,094	462,167	462,167
M <sub>2</sub>	F	65,607	452,714	1050	454,814	464,360	464,360
	R	65,607	459,959	8	459,975	460,048	460,048
M <sub>3</sub>	F	65,607	454,879	1063	457,005	466,669	466,669
	R	65,607	462,329	6	462,341	462,396	462,396
M <sub>4</sub>	F	65,607	449,238	1615	452,468	467,150	467,150
	R	65,607	460,562	6	460,574	460,628	460,628
----- Actual Weight at 210 days of age (RW210) -----							
M <sub>1</sub>	F	69,878	498,866	710	500,286	506,787	506,787
	R	69,878	503,780	11	503,802	503,902	503,902
M <sub>2</sub>	F	69,878	494,407	1092	496,591	506,589	506,589
	R	69,878	501,960	11	501,982	502,082	502,082
M <sub>3</sub>	F	69,878	496,282	1107	498,496	508,632	508,632
	R	69,878	504,031	9	504,049	504,131	504,131
M <sub>4</sub>	F	69,878	490,810	1676	494,162	509,507	509,507
	R	69,878	502,563	9	502,581	502,664	502,664

AIC = Akaike Information Criterion; BIC = Bayesian Information Criterion; CAIC = Consistent Akaike Information Criterion; CG = Contemporary group fixed (F) or random (R).

In all cases, the criterion AIC had the smallest values for models with CG fixed. On the other hand, BIC and CAIC, by imposing higher penalties than AIC for models with higher number of

estimated parameters, favored models with random CG. These results were in agreement with results from the literature. UGARTE et al. (1991), working with simulated data, and VISSHER & GODDARD

(1992), working with dairy data from small herds, estimated lower prediction error variances (PEV) and mean squared errors (MSE) for models with random CG. Contrarily, VALVERDE et al. (2008), using Braunvieh cattle weaning weight data, found somewhat higher accuracies of genetic predictions for direct genetic effects when CG were considered fixed, and no difference between models with CG fixed or random for maternal genetic effects.

For weights at 120 d (AW120 and RW120), the criteria BIC and CAIC indicated that models with trimester seasonal effect had the best fit when CG was random (Table 1). A similar result was obtained for weights at 210 d (AW210 and RW210; Table 2). However, when CG was fixed, the best fitting models were those with semester seasonal effects for 120 d (AW120 and RW120), whereas for weights at 210 d, model M<sub>2</sub> (trimester) was better than M<sub>1</sub> (semester), but model M<sub>3</sub> (semester) was better than M<sub>4</sub> (trimester) for AW210 and RW210. On the other hand, REYES et al. (1998) found out that it was better to consider trimester over semester when they compared the efficiency of two fixed effects models containing season (trimester or semester) as part of the structure of contemporary groups for weaning weight in Nellore cattle.

According to the BIC and CAIC criteria, models that had sex of calf effect separated from CG, provided a better fit to the data. These models allowed the construction of contemporary groups with larger number of individuals and permitted better genetic connections among CG and higher accuracies of prediction of genetic evaluations. These results are in agreement with those found by REYES et al. (2006) for growth between birth and weaning in a multibreed Nellore x Hereford cattle population.

Among models with random CG, model M<sub>2</sub> was the most parsimonious and provided the best fit. Thus, for 120 d and 210 d of age and actual or adjusted data, results here suggest that models that had random CG with trimester seasonal effect, and sex of calf effect separated from CG effect were the most appropriate for growth from birth to weaning in Nellore cattle.

#### (Co)variance components and genetic parameters

Tables 3 and 4 present the estimates of (co)variances and genetic parameters for the four traits in this study (AW120, RW120, AW210 e RW210). Estimates for each trait differed little among models.

Table 3. Estimates of (co)variances and genetic parameters for actual and adjusted weights at 120 days of age in Nellore cattle in Brazil using several models

M	CG	$\sigma_d^2$	$\sigma_m^2$	$\sigma_{dm}$	$\sigma_{pe}^2$	$\sigma_c^2$	$\sigma_e^2$	$h_d^2$	$h_m^2$	$r_{dm}$	$c_{pe}^2$	$e^2$
---- Adjusted Weight (AW120 - 1 <sup>st</sup> .row) and Actual Weight (RW120 - 2 <sup>nd</sup> .row) at 120 days of age ----												
M <sub>1</sub>	F	63.03	27.26	-14.90	30.38		121.90	0.28	0.12	-0.36	0.13	0.54
		67.01	29.47	-15.39	33.06		163.01	0.24	0.11	-0.35	0.12	0.59
	R	63.90	27.38	-15.16	30.65	111.12	121.32	0.28	0.12	-0.36	0.09	0.53
		68.17	29.67	-15.71	33.35	127.09	162.25	0.25	0.11	-0.35	0.08	0.58
M <sub>2</sub>	F	58.27	25.51	-12.20	30.56		120.58	0.26	0.11	-0.32	0.14	0.54
		62.18	27.75	-12.60	33.18		160.79	0.23	0.10	-0.30	0.12	0.59
	R	59.77	25.92	-12.60	30.74	108.70	119.68	0.27	0.12	-0.32	0.09	0.54
		64.17	28.21	-13.11	33.46	122.91	159.57	0.24	0.10	-0.31	0.08	0.59
M <sub>3</sub>	F	60.99	26.83	-14.35	30.69		121.33	0.27	0.12	-0.35	0.14	0.54
		64.87	28.94	-14.83	33.56		162.19	0.24	0.11	-0.34	0.12	0.59
	R	62.00	27.06	-14.56	30.91	128.00	120.67	0.27	0.12	-0.36	0.09	0.53
		66.12	29.26	-15.07	33.82	143.15	161.34	0.24	0.11	-0.34	0.08	0.59
M <sub>4</sub>	F	56.20	24.86	-11.65	31.08		119.87	0.26	0.11	-0.31	0.14	0.54
		59.93	26.98	-11.99	33.86		159.79	0.22	0.10	-0.30	0.13	0.59
	R	58.31	25.56	-12.09	31.16	123.82	118.61	0.26	0.12	-0.31	0.09	0.54
		62.58	27.85	-12.55	33.97	138.74	158.17	0.23	0.10	-0.30	0.08	0.59

For each term: Adjusted weights (1<sup>st</sup> row) and actual weights (2<sup>nd</sup> row). M = Model; CG = Contemporary group fixed (F) or random (R);  $\sigma_d^2$  = additive direct genetic variance;  $\sigma_m^2$  = additive maternal genetic variance;  $\sigma_{dm}$  = direct-maternal genetic covariance;  $\sigma_{pe}^2$  = maternal permanent environmental variance;  $\sigma_c^2$  = contemporary group variance;  $\sigma_e^2$  = residual variance;  $h_d^2$  = direct heritability;  $h_m^2$  = maternal heritability;  $r_{dm}$  = direct-maternal genetic correlation;  $c_{pe}^2$  = ratio of maternal permanent environmental variance to phenotypic variance;  $e^2$  = ratio of residual variance to phenotypic variance.

Table 4. Estimates of (co)variances and genetic parameters for actual and adjusted weights at 210 days of age in Nelore cattle in Brazil using several models

M	CG	$\sigma_d^2$	$\sigma_m^2$	$\sigma_{dm}$	$\sigma_{pe}^2$	$\sigma_c^2$	$\sigma_e^2$	$h_d^2$	$h_m^2$	$r_{dm}$	$c_{pe}^2$	$e^2$
---- Adjusted Weight (AW210 - 1 <sup>st</sup> .row) and Actual Weight (RW210) - 2 <sup>nd</sup> .row) at 210 days of age ----												
M <sub>1</sub>	F	145.24	49.44	-33.64	67.26		234.41	0.31	0.11	-0.40	0.15	0.51
		153.89	52.05	-38.61	72.98		292.43	0.29	0.10	-0.43	0.14	0.55
	R	146.35	49.39	-33.97	67.84	369.29	233.65	0.32	0.11	-0.40	0.08	0.50
		155.44	52.05	-38.94	73.51	372.46	291.46	0.29	0.10	-0.43	0.08	0.55
M <sub>2</sub>	F	119.35	42.25	-20.84	66.59		231.23	0.27	0.10	-0.29	0.15	0.53
		127.12	44.98	-26.09	72.15		290.03	0.25	0.09	-0.35	0.14	0.57
	R	121.88	42.44	-21.41	67.19	344.51	229.66	0.28	0.10	-0.30	0.09	0.52
		130.60	45.41	-26.89	72.70	350.62	287.93	0.27	0.09	-0.35	0.08	0.56
M <sub>3</sub>	F	142.78	49.27	-33.91	67.87		230.08	0.31	0.11	-0.40	0.15	0.50
		151.25	51.87	-38.47	73.71		287.45	0.29	0.10	-0.43	0.14	0.55
	R	144.49	49.26	-34.25	68.46	383.40	229.01	0.32	0.11	-0.41	0.08	0.50
		153.57	51.96	-38.86	74.27	382.35	286.03	0.29	0.10	-0.44	0.08	0.54
M <sub>4</sub>	F	116.61	41.91	-21.14	67.55		226.68	0.27	0.10	-0.30	0.16	0.53
		123.75	44.51	-25.60	73.24		285.04	0.25	0.09	-0.34	0.15	0.57
	R	121.22	42.55	-22.00	67.95	372.24	223.99	0.28	0.10	-0.31	0.08	0.52
		129.81	45.42	-26.86	73.63	371.83	281.57	0.26	0.09	-0.35	0.08	0.56

For each term: Adjusted weights (1<sup>st</sup> row) and actual weights (2<sup>nd</sup> row). M = Model; CG = Contemporary group fixed (F) or random (R);  $\sigma_d^2$  = additive direct genetic variance;  $\sigma_m^2$  = additive maternal genetic variance;  $\sigma_{dm}$  = direct-maternal genetic covariance;  $\sigma_{pe}^2$  = maternal permanent environmental variance;  $\sigma_c^2$  = contemporary group variance;  $\sigma_e^2$  = residual variance;  $h_d^2$  = direct heritability;  $h_m^2$  = maternal heritability;  $r_{dm}$  = direct-maternal genetic correlation;  $c_{pe}^2$  = ratio of maternal permanent environmental variance to phenotypic variance;  $e^2$  = ratio of residual variance to phenotypic variance.

Estimates of  $\sigma_d^2$ ,  $\sigma_m^2$ ,  $h_d^2$  and  $h_m^2$  were larger in models with semester of birth season effect in CG (M<sub>1</sub> and M<sub>3</sub>) than those obtained in models with trimester of birth season effect in CG (M<sub>2</sub> e M<sub>4</sub>). On the other hand, estimates of  $\sigma_{pe}^2$  and  $\sigma_e^2$  were similar in all models. These results may have been due to greater variation among weights when the period of time (season effect) considered in CG was longer.

Estimates of  $\sigma_d^2$ ,  $\sigma_m^2$ ,  $h_d^2$  e  $h_m^2$  for weight at 120 d and 210 d of age were similar in models that included or not the effect of sex of calf within CG (M<sub>2</sub> vs M<sub>4</sub> and M<sub>1</sub> vs M<sub>3</sub>). Estimates of  $\sigma_e^2$  ranged from 118.61 to 163.01 kg<sup>2</sup> for actual and adjusted weights at 120 d (W120), and from 223.99 to 292.43 kg<sup>2</sup> for actual and adjusted weights at 210 d (W210), with smaller values in CG of larger size, i.e., those in models that considered semester seasonal effects and sex of calf separately from CG.

Models that considered CG random yielded higher estimates of  $\sigma_d^2$ ,  $\sigma_m^2$ ,  $h_d^2$  and  $h_m^2$ , and lower estimates of  $\sigma_e^2$  than models that considered CG fixed. Larger estimates of  $\sigma_d^2$  and smaller values of  $\sigma_e^2$  in models with random CG were also obtained for weaning weights in Braunvieh cattle in México (VALVERDE et al., 2008). Literature values

reported higher values of heritability estimates for models with fixed CG than for models with random CG (PHOCAS & LALOE, 2003; CHANVIJIT et al., 2005; VALVERDE et al., 2008). However, these lower heritability estimates for models with random CG were computed with phenotypic variances that included the variance due to contemporary group ( $\sigma_c^2$ ), which is not appropriate because comparisons among animals evaluated genetically occur within contemporary groups.

Estimates for  $\sigma_d^2$  ranged from 56.20 to 68.17 kg<sup>2</sup> and estimates for  $\sigma_m^2$  from 24.86 to 29.67 kg<sup>2</sup> for weight at 120 d of age (W120). For weights at 210 d of age (W210),  $\sigma_d^2$  estimates ranged from 116.61 to 155.44 kg<sup>2</sup> and estimates of  $\sigma_m^2$  ranged from 41.91 to 52.05 kg<sup>2</sup>. Estimates of  $\sigma_{dm}$  were negative, ranging from -38.61 to -20.84 kg<sup>2</sup> for W120 and from -38.94 to -21.41 kg<sup>2</sup> for W210. These estimates indicated antagonism between additive direct and maternal genetic effects, in agreement with previous beef cattle research (FERREIRA et al., 1999; LEE & POLLAK, 2002; ROSALES et al., 2004). This implies that if producers perform selection for growth in calves without considering maternal additive genetic effects, this may produce a decrease

in milk production of future mothers and a reduction in weaning weights of their progenies (VALVERDE et al., 2008).

Estimates of  $\sigma_{pe}^2$  ranged from 30.38 to 33.97 kg<sup>2</sup> for W120 and from 66.59 to 74.27 kg<sup>2</sup> for W210. These estimates were higher than those reported by GARNERO et al. (2001) for weights at 120 d of age (19.1 kg<sup>2</sup>) and at 220 d of age (48.01 kg<sup>2</sup>).

Direct heritability estimates ranged from 0.22 to 0.28 for W120 and from 0.25 to 0.32 for W210. Estimates of maternal heritabilities ranged from 0.10 to 0.12 for W120 and from 0.09 to 0.11 for W210. MARCONDES et al. (2002) and SIQUEIRA et al. (2003) found similar estimates of direct heritability for W120 (0.24 and 0.29, respectively), and of maternal heritability (0.08) in Nelore cattle. GARNERO et al. (2001) also estimated values of heritability for direct genetic effects (0.19) and for maternal genetic effects (0.06) similar to those obtained here.

Differences among estimates of (co)variances and genetic parameters were small across models in this study, perhaps due to the utilization of the same matrix of additive relationships. However, one could expect that estimates from models that yield better fit would be more accurate and reliable.

## CONCLUSIONS

The most appropriate model for the estimation of (co)variances and genetic parameters for actual and adjusted weights at 120 d and 210 d of age in Brazilian Nelore cattle was the one that had random CG and sex of calf separated from CG, where CG was defined as a group of calves born in the same herd, year, season measured as trimester of birth, and had the same management. Estimates of (co)variances and genetic parameters, predictions of breeding values, and ranking of animals obtained with the best model are expected to be more accurate and reliable.

## REFERENCES

AKAIKE, H. Information theory and an extension of maximum likelihood principle. In: INTERNATIONAL SYMPOSIUM ON INFORMATION THEORY, 2., **Proceedings...** p.267-281, 1972. Disponível em [http://www.sortind.org/lme/Statistical%20Papers/Akaike\\_1973%20with%20commentary.pdf](http://www.sortind.org/lme/Statistical%20Papers/Akaike_1973%20with%20commentary.pdf), acesso em 03 de março de 2013.

BABOT, D.; NOGUERA, J.L.; ALFONSO, L.; ESTANY, J. Fixed or random contemporary groups in genetic

evaluation for litter size in pigs using a single trait repeatability animal model. **Journal of Animal Breeding and Genetics**, v. 120, n. 1, p.12-22, 2003.

BOLDMAN, K.; KRIESE, L.; VAN VLECK, L.D. **A manual for use of MTDFREML** : A set of programs to obtain estimates of variances and covariances. USDA. ARS., 1993.

BOZDOGAN, H. Model selection and Akaike's information criterion (AIC): the general theory and its analytical extensions. **Psychometrika**, v. 52, p.345-370, 1987.

CHANVIJIT, K.; DUANGJINDA, M.; PATTARAJINDA, V.; REODECHA, C. Model comparison for genetic evaluation of Milk yield in crossbred Holsteins in the tropics. **Journal of Applied Genetics**, v. 46, n. 4, p.387-393, 2005.

FERREIRA, G.B.; MACNEIL, M.D.; VAN VLECK, L.D. Variance components and breeding values for growth traits from different statistical models. **Journal of Animal Science**, v. 77, p. 2641-2650, 1999.

GARNERO, A.V.; LOBO, R.B.; BEZERRA, L.A.F.; OLIVEIRA, H.N. Comparação entre alguns critérios de seleção para crescimento na raça Nelore. **Revista Brasileira de Zootecnia**, v.30, n. 3, p.714-718, 2001.

GONZÁLEZ-RECIO, O.; ALENDA, R. Genetic parameters for female fertility traits and a fertility index in Spanish dairy cattle. **Journal of Dairy Science**, v. 88, p. 3282-3289, 2005.

HENDERSON, C.R. Sire evaluation and genetics trends. In: ANIMAL BREEDING AND GENETIC SYMPOSIUM IN HONOR OF DR. JAY L. LUSH, Illinois, USA. **Proceedings...** Illinois, v. 1, p.10-41, 1973. Disponível em: <http://jas.fass.org/cgi/reprint/1973/Symposium/10> Acesso em: 15 mar. 2011.

LEE, C.; POLLAK, E.J. Genetic antagonism between body weight and milk production in beef cattle. **Journal of Animal Science**, v. 80, p.316-32, 2002.

LEGARRA, A.; LÓPEZ-ROMERO, P.; UGARTE, E. Bayesian model selection of contemporary groups for BLUP genetic evaluation in Latxa dairy sheep. **Livestock Production Science**, v. 93, p.205-212, 2005.

LÔBO, R.B. **Programa de Melhoramento Genético da Raça Nelore**, 2 Ed. Ribeirão Preto, SP: ANCP, 1996.

MARCONDES, C.R.; GAVIO, D.; BITTENCOURT, T.C.C.; LÔBO, R.B.; BEZERRA, L.A.F.; TONHATI, H. Estudo de modelo alternativo para estimação de componentes de (co)variância e predição de valores genéticos de características de crescimento de bovinos da raça Nelore. **Arquivo Brasileiro de Medicina Veterinária e Zootecnia**, v. 54, n. 1, p. 93-99, 2002.

PHOCAS, F.; LALOË, D. Evaluation models and genetic parameters for calving difficulty in beef cattle. **Journal of Animal Science**, v. 81, p.933-938, 2003.

- REYES, A.; LOBO, R.B.; BEZERRA, L.A.F.; MARTINS, E.N. Critérios de época na conformação de grupos contemporâneos para características de crescimento em Nelore. In: REUNIÃO ANUAL DE SOCIEDADE BRASILEIRA DE ZOOTECNIA, 35., Botucatu. **Anais...** Botucatu : SBZ, v. 3, n. 1, p. 437-439, 1998. Disponível em [http://www.sbz.org.br/reuniaoanual/anais/arg\\_reuniao\\_anual/sbz1998.rar](http://www.sbz.org.br/reuniaoanual/anais/arg_reuniao_anual/sbz1998.rar). Acesso em 03 março 2013.
- REYES, A.; ELZO, M.A.; ROSO, V.M.; FRIES, L.A.; CARVALHEIRO, R. Efeitos não genéticos na composição dos grupos contemporâneos para o ganho de peso do nascimento a desmama de uma população multirracial Nelore x Hereford. In: REUNIÃO ANUAL DA SOCIEDADE BRASILEIRA DE ZOOTECNIA, 43., João Pessoa. **Anais...** João Pessoa, 2006. Disponível em: <<http://www.animal.ufl.edu/elzo/Publications/Proceedings/2006/Sociedad%20Brazileira%20de%20Zootecnia/Reyes%20et%20al.%20al.%20SBZ43%20July-24-27-2006%20Trabalho%20HOMEPAGE.pdf>>. Acesso em 20 out. 2009.
- ROSALES, A.J.; ELZO, M.A.; MONTANO, B.M. Parámetros y tendencias genéticas para características de crecimiento predestete em la población mexicana de Simmental. **Revista Mexicana de Ciencias Pecuarias**, v. 42, p. 171-180, 2004.
- SCHWARZ, G. Estimating the dimension of a model. **The Annals of Statistics**, v. 6, n. 2, p.461-464, 1978. Disponível em: < <http://www.jstor.org/stable/2958889>> Acesso em: 15 mar. 2011.
- SIQUEIRA, R.L.P.G.; OLIVEIRA, J.A.; LOBO, R.B.; BEZERRA, L.A.F.; TONHATI, H. Análise da variabilidade genética aditiva de características de crescimento na raça Nelore. **Revista Brasileira de Zootecnia**, v. 32, n. 4, p. 880-886, 2003.
- SMITH, S.P.; GRASER, H.U. Estimating Variance Components in a Class of Mixed Models by Restricted Maximum Likelihood. **Journal of Dairy Science**, v. 69, p. 1156-1165, 1986.
- UGARTE, E.; ALENDA, R.; CARABAÑO, M.J. Fixed or random contemporary groups in genetic evaluations. **Journal of Dairy Science**, v. 75, p. 269-278, 1991.
- VALVERDE, R.R.; DOMÍNGUEZ, R.N.; FLORES, A.R.; MUÑÍS, J.G.G.; VALENCIA, F.M. Comparación de definiciones de grupos contemporâneos en la evaluación genética de bovinos Suizo Europeo. **Revista Mexicana de Ciencias Pecuarias**, v. 46, n. 4, p. 359-370, 2008.
- VAN VLECK, L.D. Contemporary Groups for Genetic Evaluations. **Journal of Dairy Science**, v. 70, p. 2456-2464, 1987.
- VASCONCELOS, J.; MARTINS, A.; FERREIRA, A.; CARVALHEIRA, J. Consequências da eliminação de rebanhos pequenos da avaliação genética de bovinos leiteiros em Portugal. **Revista Portuguesa de Zootecnia**, v. 12, p. 105-117, 2005.
- VISSHER, P.M.; GODDARD, M.E. Fixed and random contemporary groups. **Journal of Dairy Science**, v. 76, p. 1444-1454, 1992.
- WOLF, J.; ZAKOVA, E.; GROENEVELD, E. Genetic parameters for a joint genetic evaluation of production and reproduction traits in pigs. **Czech Journal of Animal Science**, v. 50, n. 3, p. 96-103, 2005.

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