

EFFECT OF MODEL STRUCTURE ON DIRECT AND MATERNAL (CO)VARIANCE AND HERITABILITY ESTIMATES FOR 210 D WEIGHT IN NELLORE CATTLE

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ABSTRACT

Actual and adjusted weights to 210 days of age from 72,731 male and female Nellore calves born in 40 PMGRN - Nellore Brazil herds from 1985 to 2005 were used to compare the effect of different models on direct and maternal (co)variance and heritability estimates. Four structures of contemporary groups (CG) were defined: CG₁: CG_B – semester of birth; CG₂: CG_B – trimester of birth; CG₃: CG₁ – SC; CG₄: CG₂ – SC, where CG_B: herd – year of birth – management group at each age. Four analytical models were defined: M₁: Weight = α + CG₁ + SC + DAC + ε; M₂: Weight = α + CG₂ + SC + DAC + ε; M₃: Weight = α + CG₃ + DAC + ε; M₄: Weight = α + CG₄ + DAC + ε; where, α= constant; SC= sex of calf; DAC= class of cow age at calving, ε= random residual effect. (Co)variances were estimated using a derivative-free restricted maximum likelihood procedure, considering CG fixed (F) or random (R). Estimates of additive direct and maternal genetic variance (σ²_d, σ²_m) and direct and maternal heritability (h²_d, h²_m) were larger in models with semester than with trimester of birth in CG (Table 1) likely due to greater variation among weights when the season of birth considered in CG was longer. These estimates were similar in models with and without sex of calf in CG. Models with random CG yielded higher estimates of σ²_d,σ²_m, h²_d and h²_m and lower estimates of residual variance (σ²_e) than models with fixed CG.

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

MATERIAL AND METHODS

Actual and adjusted weights at 210 d (AW210, RW210) from 72,731 male and female Nellore calves born between 1985 and 2005 in 40 herds from PMGRN-Nellore Brasil were used in this study. Actual weights were the closest ones to 210 d within the intervals of 210 ± 90 d and calf ages were expressed as deviations (CAD) from 210 d. Adjusted weights were computed similar to PMGRN: $AW = W + [(W-Wp)/I] \times (A - Aw)$; where, AW = adjusted weights at 210d; W = actual weight; Wp = prior weight; I = interval in days between W and Wp; A = standard age (210 d); Aw = 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.

CG₁: CG_B – semester of birth.

CG₂: CG_B – trimester of birth.

CG₃: CG₁ – sex of calf.

CG₄: CG₂ - sex of calf.

Based on these four CG (CG₁ to CG₄), four analytical models were defined:

M₁: Weight = α + CG₁ + SC + DAC + ε

M₂: Weight = α + CG₂ + SC + DAC + ε

M₃: Weight = α + CG₃ + DAC + ε

M₄: Weight = α + CG₄ + DAC + ε

where, Weight = actual or adjusted weight at 210 d of age; α = constant; CG = contemporary group; SC = sex of calf; DAC = class of cow age at calving, and ε = 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 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 permitted to have the same inverse of the relationship matrix (A⁻¹). Models for the estimation of (co)variances and genetic parameters for AW210 and RW210 using single-trait analysis, considering CG fixed (1) or random (2), were as follows:
y = Xb + Z1d + Z2m + Z3pe + e (1)
y = Xb + Z1d + Z2m + Z3pe + Z4c + e (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, Z1, Z2, Z3 e Z4, are known incidence matrices relating observations in vector y to vectors b, d, m, pe, and c, respectively. Estimates of (co)variances and genetic parameters were obtained using a derivative-free restricted maximum likelihood procedure (DFREML). Computations were carried out using the MTDFREML (Multiple Trait Derivative Free Restricted Maximum Likelihood) 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

Table 1 present the estimates of (co)variances and genetic parameters for the two traits in this study (AW210 and RW210). Estimates for each trait differed little among models. Estimates of σ²_d, σ²_m, h²_d and h²_m were larger in models with semester of birth season effect in CG (M₁ and M₃) than those obtained in models with trimester of birth season effect in CG (M₂ e M₄). On the other hand, estimates of σ²_e 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 σ²_d, σ²_m, h²_d and h²_m were similar in models that included or not included the effect of sex of calf within CG (M₂ vs M₄ and M₁ vs M₃). Estimates of σ²_e ranged from 223.99 to 292.43 kg² for actual and adjusted weights, 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 σ²_d, σ²_m, h²_d and h²_m, and lower estimates of σ²_e than models that considered CG fixed. Larger estimates of σ²_d and smaller values of σ²_e 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; 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, which is not appropriate because comparisons among animals evaluated genetically occur within contemporary groups.

Estimates for σ²_d ranged from 116.61 to 155.44 kg² and estimates of σ²_m ranged from 41.91 to 52.05 kg². Estimates of σ²_{dm} were negative, ranging from -38.94 to -21.41 kg² for W210. These estimates indicated antagonism between additive direct and maternal genetic effects, in agreement with previous beef cattle research (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 σ²_{pe} ranged from 66.59 to 74.27 kg² for W210. These estimates were higher than those reported by Garnero et al. (2001) for weights at 220 d of age (48.01 kg²). Direct heritability estimates ranged from 0.25 to 0.32. Estimates of maternal heritabilities ranged from 0.09 to 0.11. Garnero et al. (2001) estimated values of heritability for weights at 220 d of age for direct genetic effects (0.19) and for maternal genetic effects (0.06) lower to those obtained here. Differences among estimates of (co)variances and genetic parameters were small across models here, 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.

Table 1. Estimates of (co)variances and genetic parameters for actual and adjusted weights at 210 days of age in Nellore cattle in Brazil using several models.

M	CG	σ ² _d	σ ² _m	σ _{dm}	σ ² _{pe}	σ ² _e	h ² _d	h ² _m	r _{dm}	e ²
---- Adjusted Weight (AW210 - 1 st row) and Actual Weight (RW210) - 2 nd row) at 210 days of age ----										
M ₁	F	145.24	49.44	-33.64	67.26	234.41	0.31	0.11	-0.40	0.51
	R	153.89	52.05	-38.61	72.98	292.43	0.29	0.10	-0.43	0.55
M ₂	F	146.35	49.39	-33.97	67.84	233.65	0.32	0.11	-0.40	0.50
	R	155.44	52.05	-38.94	73.51	291.46	0.29	0.10	-0.43	0.55
M ₃	F	119.35	42.25	-20.84	66.59	231.23	0.27	0.10	-0.29	0.53
	R	127.12	44.98	-26.09	72.15	290.03	0.25	0.09	-0.35	0.57
M ₄	F	121.88	42.44	-21.41	67.19	229.66	0.28	0.10	-0.30	0.52
	R	130.60	45.41	-26.89	72.70	287.93	0.27	0.09	-0.35	0.56
M ₅	F	142.78	49.27	-33.91	67.87	230.08	0.31	0.11	-0.40	0.50
	R	151.25	51.87	-38.47	73.71	287.45	0.29	0.10	-0.43	0.55
M ₆	F	144.49	49.26	-34.25	68.46	229.01	0.32	0.11	-0.41	0.50
	R	153.57	51.96	-38.86	74.27	286.03	0.29	0.10	-0.44	0.54
M ₇	F	116.61	41.91	-21.14	67.55	226.68	0.27	0.10	-0.30	0.53
	R	123.75	44.51	-25.60	73.24	285.04	0.25	0.09	-0.34	0.57
M ₈	F	121.22	42.55	-22.00	67.95	223.99	0.28	0.10	-0.31	0.52
	R	129.81	45.42	-26.86	73.63	281.57	0.26	0.09	-0.35	0.56

For each term: Adjusted weights (1st row) and actual weights (2nd row). M = Model; CG = Contemporary group fixed (F) or random (R); σ²_d = additive direct genetic variance; σ²_m = additive maternal genetic variance; σ_{dm} = direct-maternal genetic covariance; σ²_{pe} = maternal permanent environmental variance; σ²_e = residual variance; h²_d = direct heritability; h²_m = maternal heritability; r_{dm} = direct-maternal genetic correlation; e² = ratio of residual variance to phenotypic variance.

CONCLUSIONS

Differences among estimates of (co)variances and genetic parameters were small across models. However, estimates of (co)variances and genetic parameters, predictions of breeding values, and ranking of animals obtained with the model that included trimester of birth in contemporary groups are expected to be more accurate and reliable.

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