Abstract: M34

Sire x maternal grandsire interaction for pre-weaning growth traits in Brazilian Nellore cattle

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SUMMARY

Non-additive genetic effects are currently ignored in genetic evaluation of beef cattle in Brazil. However, non-additive genetic effects have been found to be important for beef cattle in several studies. The objective here was to assess the importance of the sire x maternal grandsire (SMGS) interaction on standardized weights at 120 d (W120) and at 240 d (W240) in a Brazilian Nellore cattle population. Weight records came from 10,302 calves born and raised on pasture in 60 herds, and collected from 1976 to 1998. The single-trait mixed model included: 1) the fixed effects of contemporary group (CG = herd-year-season-sex-management group) and calving age subclass (2, 3, 4, 5 to 9, 10 yr and older), 2) the random effects of animal additive genetic (direct and maternal), maternal permanent environmental, SMGS interaction and residual. Each CG had a minimum of 10 records, two different sires, and two different SMGS subclasses per sire. The REMLF90 program was used to estimate (co)variance components. Direct and maternal heritabilities were 0.31 and 0.12 for W120, and 0.18 and 0.10 for W240. Direct-maternal genetic correlations were -0.23 for W120 and -0.05 for W240. Maternal permanent environment ratios (relative to phenotypic variances) were 0.21 for W120 and 0.20 for W240. The SMGS interaction ratios (relative to phenotypic variances) were 0.09 for W120 and 0.08 for W240. These SMGS ratios were comparable to maternal heritabilities. Results indicated that, in this subpopulation of Nellore cattle, SMGS interaction effects may need to be included in genetic evaluation models for W120 and W240. However, this may not be the case in other Nellore subpopulations in Brazil. Thus, this research needs to be repeated within each subpopulation, and, if the objective were the development of a national genetic evaluation, then data from all Nellore subpopulations would need to be included in that study**.**

INTRODUCTION

Quantitative genetic models of inheritance include additive, dominance and epistatic effects. Genetic evaluations of beef cattle usually ignore genetic effects other than additive. Several studies have found that nonadditive effects, in particular dominance, are important for growth traits in beef cattle. For example, estimates of dominance variance for weight and height at birth and 205 days of age, on three composite genotype of beef cattle, explained between 11 and 28 % of their phenotypic variances. Thus, if nonadditive genetic effects are important in beef cattle, excluding them from genetic evaluation models would reduce the accuracy of genetic predictions.

Inclusion of sire x maternal grandsire interactions in genetic models for beef cattle takes into account, at least partially, nonadditive genetic effects. Thus, more accurate (co)variance estimations and prediction of genetic values would likely be achieved.

The objectives of this study were to assess the importance of sire x maternal grandsire interaction effects and to evaluate genetic trends for standardized weights at 120 d (W120) and at 240 d (W240) in Brazilian Nellore cattle.

MATERIAL AND METHODS

Standardized weights at 120 d (W120) and 240 d (W240) of age of Nellore calves of both sexes were analyzed. Weight records came from 10,302 calves born and raised on pasture, and collected from 1976 to 1998 in 60 herds from the "*Programa de Melhoramento Genético da Raça Nelore - USP*".

Data were edited to attain a consistent sample with appropriate structure to effectively estimate sire x maternal grandsire interaction (SMGS) variances. The following restrictions were imposed: each contemporary group had a minimum of 10 records, two different sires, and two different SMGS subclasses per sire. Table 1 shows some descriptive statistics of data by trait.

The complete mixed animal model for each trait included the fixed effects of contemporary group (herd-year-season-sex-management group) and calving age subclass (2, 3, 4, 5 to 9, 10 yr and older), and the random effects of animal additive genetic (direct and maternal), maternal permanent environmental, SMGS interaction and residual. Calving seasons were defined as calendar trimesters.

The model in matrix notation was: $\boldsymbol{y = X\beta + Z_1d + Z_2m + Z_3p + Z_4smg + e}$, where, $\boldsymbol{y}$ = is a vector of observations for each trait, $\boldsymbol{X}$ = is an incidence matrix of fixed effects, $\boldsymbol{\beta}$ = is a vector of fixed effects, $\boldsymbol{Z_1}$ = is an incidence matrix of additive direct genetic effect of each animal, $\boldsymbol{d}$ = is a vector of random additive direct genetic effects, $\boldsymbol{Z_2}$, $\boldsymbol{Z_3}$ = are incidence matrices of random additive maternal genetic and maternal permanent environmental effects, $\boldsymbol{m}$, $\boldsymbol{p}$ = are vectors of random additive maternal genetic and maternal permanent environmental effects, $\boldsymbol{Z_4}$ = is an incidence matrix of sire x maternal grandsire interaction effects, $\boldsymbol{smg}$ = is a vector of random sire x maternal grandsire interaction effects, $\boldsymbol{e}$ = is a vector of random residual effects.

The complete (co)variance components structure was used on single-trait analyses to estimate (co)variances by the REMLF90 program. The MTDFREML program was used to obtain complete (co)variance structure estimations and predictions of breeding value and of sire x maternal grandsire interaction on final single and two-trait analyses.

Table 1. Descriptive statistics of Brazilian Nellore data by trait

TRAIT[a]	Observ.	Mean (kg)	STD (kg)	CG[b]	Sires	Dams	MGS[b]	SMGS[b]
W120	9,614	**123.1**	**19.8**	687	290	6,632	246	1,899
W240	7,827	**192.0**	**32.5**	598	252	5,531	210	1,555

[a] Standardized weights at 120 d (W120) and 240 d (W240) of age. [b] Number of contemporary groups (CG), maternal grandsires (MGS) and sire x maternal grandsire subclasses (SMGS).

RESULTS AND DISCUSSION

Effects and (co)variance estimations. The initial model included permanent environmental effects. However, inclusion of maternal permanent environmental effects in the model caused a reduction of direct and maternal variances, and of genetic direct-maternal covariances on both traits. Heritabilities for W120 direct changed from 0.24 to 0.21 and for W120 maternal fell from 0.20 to 0.12. Corresponding changes for W240 direct were (0.20 to 0.18) and (0.15 to 0.11), respectively. Analysis of number of calf records per cow showed that only 31.9 % of dams had two or more records in this data sample. Such data structure is likely to result in an unreliable estimate of maternal permanent environmental variance, which may in turn negatively affect estimates of other (co)variances in the model. Consequently, it was decided to exclude the maternal permanent environmental effect in final analyses.

The SMGS interaction effect explained between 2.8 and 3.1 % of total phenotypic variances on single and two-trait analyses. The inclusion of SMGS in single-trait analyses produced smaller estimates of direct and maternal additive genetic variances and larger estimates of direct-maternal additive covariances. Changes in heritabilities were (0.24 to 0.20) for W120 direct and (0.17 to 0.13) for W120 maternal. Corresponding values for W240 direct and maternal were (0.24 to 0.19) and (0.20 to 0.16), respectively. Changes in genetic direct-maternal correlations were (0.05 to 0.29) for W120, and (-0.12 to 0.01) for W240. Results from two-trait analyses showed similar trends as those for single traits, but they were of lesser magnitude.

EPD predictions and annual trends. A sub-sample of data, including 1987-1997 year of birth period, was used to predict breeding values (EPD - Expected Progeny Difference) for direct and maternal effects of 20,097 animals included in the relationship matrix ***A***, and to predict SMGS interaction effects. Trends for EPD and SMGS means by year of birth are showed in **Figure 1**, for calves with records (8,084), sires (212), dams (5,521) and SMGS interaction (940).

Maximum changes of EPD means for calf direct genetic effects (DEPD120C, DEPD240C) were 1.78 kg for W120 (0.14 % of phenotypic mean per year) and 3.23 kg for W240 (0.17 % of phenotypic mean per year). Individual sire means (DEPD120SI, DEPD240SI) showed a very similar pattern of those of calves for both traits. Individual EPD means for dam direct genetic effects (DEPD120DI, DEPD240DI) were negative or near zero during the 11-year period. Trends for weighted sire EPD means (DEPD120S, DEPD240S) also showed positive change for both traits, especially after 1991 (**Figure 1**).

Mean values for genetic maternal effects were negative or near zero for calves (MEPD120C, MEPD240C), sires (MEPD120SI, MEPD240SI) and dams (MEPD120DI, MEPD240DI) for both traits for the 11-year period (**Figure 1**). Brazilian Nellore cattle producers should try to reverse this trend because the important contribution of maternal ability to economic returns in cow-calf operations.

These ***low genetic trends*** may be largely due to the intensive use of some sires during this 11-year period. Thus, in the sub-sample of data analyzed there were 63 sires, born between 1974 and 1990, in common as sires (29.7 % of sires) of 44.5 % of calves, and as maternal grandsire (32.8 % of maternal grandsires) of 52.5 % of dams. It was also verified that 18.4 % of sires and 43.2 % of maternal grandsires, present in 4 to 7 years, produced 47 % of calves and 79.4 % of dams, respectively. Thus, if this situation persists, it would be expected an increasing rate of co-ancestry and inbreeding in a middle and long-term in this population. Consequently, the present and future results in this population could be strongly affected by the inbreeding depression.

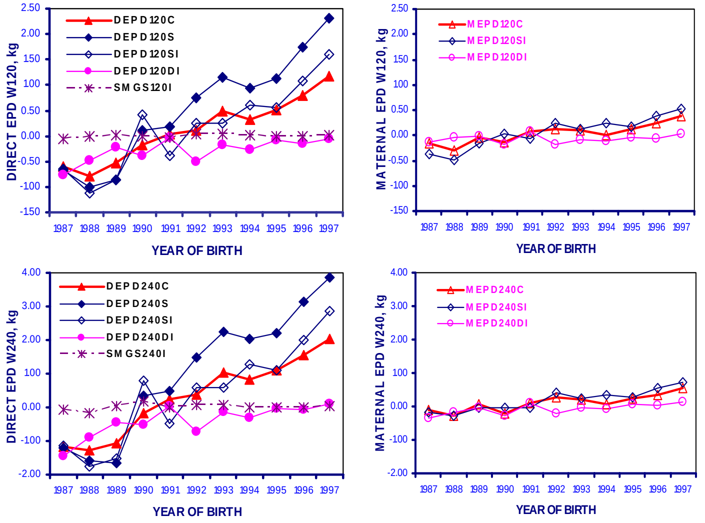

Figure 1. Trends of mean additive direct (DEPD) and maternal (MEPD) expected progeny differences for standardized weights at 120 d (W120) and 240 d (W240) of age by year of birth for calves (C), sires (S = weighted, SI = individual) and dams (DI = individual), and of sire x maternal grandsire interaction effects (SMGS).

CONCLUSIONS

- **Sire x maternal grandsire interaction effects were important for pre-weaning growth traits, and may need to be included in genetic evaluation models for Brazilian Nellore cattle.**

- **Trends for direct and maternal EPD means showed small genetic changes during this 11-year period, particularly for maternal effects. Intensive use of few sires during many years may be a major reason for these low genetic trends. Brazilian Nellore cattle producers would need to increase their use of sires with superior direct and maternal predicted genetic values if substantial genetic progress for growth traits is to be achieved.**

AKNOWLEGMENT

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