



Impact of embryo transfer phenotypic records on large-scale beef cattle genetic evaluations

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ABSTRACT - We aimed to evaluate the impact of using embryo transfer (ET) information on weaning weight estimated breeding values (EBV) and its accuracy. Data from Hereford and Braford cattle, raised under extensive conditions in Southern Brazil, were used. A model that included ET information in addition to maternal (genetic and permanent environmental) effects as a function of foster dams was compared to a model without ET information. Accuracy of both bulls and calves increased due to inclusion of ET records in 0.04 and 0.12 points, respectively. In general, the inclusion of ET records provided a greater amount of phenotypic variance and most accurate EBV for sires and progeny. The results obtained in this study encourage the use of ET phenotypic records in large-scale genetic evaluation programs, especially for bulls that have most of their progeny coming from ET. Most of the Brazilian genetic evaluation programs do not use phenotypic records of ET animals. Therefore, breeding values are predicted based only on parentage average, which implies in underestimated accuracies. Considering that ET has been widely used in Brazil and that such information improves genetic predictions, we suggest modifying the traditional adopted models by considering ET information in the Brazilian genetic evaluations.

Key Words: accuracy, assisted reproduction, foster dam, genetic groups

Introduction

The success of a genetic evaluation program is closely related to correct understanding of all management system differences and adoption of suitable statistical methods that deals with such peculiarities. New reproduction technologies, as embryo transfer (ET), are widely used in beef and dairy cattle because they provide higher reproductive rates in comparison with traditional mating schemes. Consequently, higher genetic gain per generation may be achieved due to reduction of generation interval. Moreover, it results in larger amounts of progeny in a shorter period. Thus, higher breeding value accuracies are achieved and can also increase the genetic gain. One way

to improve breeding value accuracy may be to increase the amount of data used to estimate breeding values.

Despite the advantages from the use of reproductive technologies, some modeling challenges arise mainly because the genetic dam (which produced the zygote) is different from the dam that delivered and raised the calf (foster dam). The foster dam provides the maternal environment (genetic and permanent environment) during intrauterine and pre-weaning periods. Early growth traits in beef cattle are shown to be influenced by maternal effects; therefore, the genetic evaluations should account for both direct and maternal effects (BIF, 2010). When ET is not used, the maternal effect is estimated based on the genetic dams. In the presence of ET, some studies have suggested alternatives to include those records by an appropriate model (Schaeffer and Kennedy, 1989; Van Vleck, 1990). One alternative is to split additive and maternal effects as influenced by embryo donor (biological dam) and foster dams, respectively.

Usually, the adoption of ET in a breeding scheme is not an isolated strategy. The most common approach is the simultaneous use of top ranked sexed-semen sires. The

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expected benefits from using female- or male-sorted semen depend on strategies of breeding programs. Pedersen et al. (2012) evaluated the impact on genetic gain when using both technologies for a simulated population. The authors showed significantly positive impact on genetic gain and on breeding value accuracy. However, they did not evaluate the impact on breeding values of ET calves and sires and their accuracies for a real breeding population.

According to BIF (2010), many national cattle evaluations now have the option to include performance data from embryo transfer calves. Differently, most of the Brazilian genetic evaluation programs still do not use phenotypic records from ET. Thus, the objective of this study was to evaluate the impact of using ET information on weaning weight estimated breeding value (EBV) and its accuracy for Hereford and Braford cattle raised under extensive conditions in Southern Brazil.

Material and Methods

Approval of Animal care and use committee was not needed because it used existing datasets historically collected by the animal breeding program.

A total of 49,339 weaning weight records from 15,072 Hereford and 34,267 Braford cattle were used in this study. The weaning weight average and standard deviation observed were 187 and 37.59 kg, respectively.

This data derived from a newly established genetic evaluation program for Hereford and Braford located in Bagé, Rio Grande do Sul, Brazil (-31.330175; -54.100471) (Cardoso et al., 2016). PampaPlus Breeding Program and Embrapa Pecuária Sul jointly carried out this initiative that includes 48 herds located in the state of Rio Grande do Sul (RS), Brazil, and a total around 10,000 new weaning weight records per year. Pedigree file consisted of 99,265 animals from several breeds: Hereford, Braford (1/2, 1/4, 1/8, 3/4, and 5/8 of zebu composition), Nelore, Tabapuã, and Brahman (Table 1).

The use of phenotypic records from ET calves requires a specific fitting for maternal effects (additive and permanent environment). To evaluate the inclusion of ET records,

we used the animal model with genetic groups (AMGG) (Westell et al., 1988) and the animal model modified by Schaeffer and Kennedy (1989) (AMSK). In the AMGG used by the PampaPlus program until 2015, all ET records were removed from the data file. Genetic groups were formed by classes of sex and year of birth, which were grouped every six years, as a function of generation interval in this population. The AMSK is an extension of the AMGG to use foster dam information to predict maternal effects, whereas the genetic dam is used to predict additive direct effect; therefore, it allowed us to use all the ET records. This database did not have historical records of breed composition for foster dams, so they were all assumed to have the same genetic background origin.

All analyses were carried out using INTERGEN software, version 1.2 (Cardoso, 2010). This software uses sparse matrix libraries to store and solve equations using Gibbs sampling algorithm under a Bayesian approach. In this Bayesian context, the following distributions were assumed for data and unknown parameters:

$$y|\beta, u, m, mpe, cg, \sigma_u^2, \sigma_m^2, \sigma_{mpe}^2, \sigma_{cg}^2, \sigma_e^2 \sim N(X\beta + Z_1u + Z_2m + Z_3mpe + Z_4cg, I\sigma_e^2)$$

in which y is the vector of weaning weight records; β is the vector of systematic effects composed by an overall mean, linear, and quadratic regression coefficients associated with animal age at phenotyping, and the interaction between classes of dam age (from 2 to 12) with progeny sex; u and m are the vectors of additive direct and maternal genetic effects, respectively, with joint prior distribution given by $\begin{bmatrix} u \\ m \end{bmatrix} | A, G_0 \sim N(g, A \otimes G_0)$; A is the numerator relationship matrix modified to adjust unknown parent groups, so that breeding values are predicted as deviation from genetic group effects (g), and $G_0 = \begin{bmatrix} \sigma_u^2 & 0 \\ 0 & \sigma_m^2 \end{bmatrix}$ is the (co)variance matrix of genetic additive and maternal effects; $mpe \sim N(0, I\sigma_{mpe}^2)$ is the vector of maternal permanent environment effect; $cg \sim N(0, I\sigma_{cg}^2)$ is the vector of contemporary groups formed by animals within the same farm, year and season of birth, sex, sire breed composition, dam breed composition, pre-weaning management group, and weaning date within ninety days of weaning age interval. Contemporary groups with less than three animals or records which deviated from group mean in ± 3.5 standard deviation were removed from data file. X , Z_1 , Z_2 , Z_3 and Z_4 are known design matrices; σ_u^2 , σ_m^2 , σ_{mpe}^2 , σ_{cg}^2 and σ_e^2 are additive direct, additive maternal, maternal permanent environment, contemporary group, and residual variance components, respectively. The *a priori* density distributions for each variance component were a scaled inverse χ^2 – defined as $\sigma_i^2 \sim \chi_{(v, s^2)}^{-2}$ –, in which i relates each variance component. In addition, a vague prior has been assumed.

Table 1 - Description of information contained in data and pedigree file

Information	Quantity
Number of animals in pedigree	99,265
Number of sires	4,944
Number of dams	40,589
Number of embryo transfers	330
Number of contemporary groups	4,043

In this study, the EBV of each animal was defined as the mean of the full posterior conditional of u , so that their accuracy (\hat{r}_{uu}) was calculated as $\hat{r}_{uu} = \sqrt{1 - (PSD)^2/\sigma_u^2}$, in which PSD is the posterior standard deviation of breeding values from the MCMC sampling and σ_u^2 is the additive genetic variance estimated for each model.

Results

The Geweke convergence criterion indicated the convergence for additive and maternal variance and heritabilities. Similar posterior probability values (credibility interval overlapping) for variance components in AMGG and AMSK suggested no statistical differences. Additive direct variance in AMSK was higher than in AMGG (Table 2). However, the maternal heritability estimates remained similar between the models.

To evaluate possible statistical differences between posterior standard deviation (PSD) of EBV densities of ET progenies, the Graybill test (Leite and Oliveira, 2002) between predictions of AMGG and AMSK was performed. No statistical difference was observed between PSD values, suggesting similar estimates between the models. As expected, greater PSD estimates were observed for sires with fewer progenies; thereby, the lowest PSD (3.94 kg) belongs to a sire with 275 progenies.

Table 2 - Variance components and genetic parameters estimated under different maternal modeling assumptions, considering embryo transfer progeny weaning weight records

Model	Parameter	PM	PSD	Z	CI_95%
AMGG	σ_a^2	125.53	12.87	1.50	[101.21, 152.74]
	σ_m^2	42.88	6.65	-0.04	[30.09, 56.16]
	σ_{mpe}^2	83.24	7.84	-0.87	[67.48, 98.43]
	σ_{cg}^2	641.63	20.90	-2.03	[600.70, 683.61]
	σ_e^2	549.57	9.89	-2.89	[529.81, 568.73]
	h_a^2	0.087	0.008	1.53	[0.06, 0.10]
	h_m^2	0.030	0.004	-0.03	[0.02, 0.04]
AMSK	σ_a^2	141.91	13.03	0.91	[117.89, 169.40]
	σ_m^2	40.07	6.00	-0.58	[28.84, 51.86]
	σ_{mpe}^2	82.36	7.64	0.36	[67.20, 97.14]
	σ_{cg}^2	644.45	21.31	-2.15	[603.06, 686.65]
	σ_e^2	541.22	10.06	-1.09	[521.30, 560.32]
	h_a^2	0.098	0.01	0.93	[0.08, 0.11]
	h_m^2	0.028	0.004	-0.55	[0.02, 0.035]

PM - *a posteriori* mean; PSD - *a posteriori* standard deviation; Z - Z-Geweke, CI_95%: credibility interval; AMGG - animal model with embryo transfer records fitted as genetic groups; AMSK - animal model with embryo transfer records fitted as in Schaeffer and Kennedy (1989); σ_a^2 - additive direct variance; σ_m^2 - additive maternal variance; σ_{mpe}^2 - maternal permanent environment variance; σ_{cg}^2 - contemporary group variance; h_a^2 - direct heritability; h_m^2 - maternal heritability.

The evaluation of changes in EBV due to the inclusion of ET records was performed by seeking for differences between predicted breeding values and their accuracies. We identified that 48 bulls were used to produce 330 ET calves and 44 of them showed greater EBV when ET records were considered. Additionally, the accuracy of breeding value for all sires with ET records increased (Figure 1). The gain in accuracy was calculated as the difference between the model appropriately fitting foster dam effect and traditional model (genetic group model). Four sires showed an increase of more than 0.1 point in accuracy when ET records were included in the AMSK model. This improvement in accuracy was correlated with an increasing proportion of ET progeny over natural mating or regular artificial insemination. Surprisingly, two of those sires had an absolute accuracy change from 0.19 to 0.41 (difference of 0.22 points) and from 0.46 to 0.67 (difference of 0.21 points). Greater accuracy estimates imply more reliable EBV. The average breeding value and accuracy obtained for bulls under the AMGG model was 3.02 and 0.75, respectively, which is lower than those estimates obtained under AMSK model (5.02 and 0.79, respectively). In addition, we found average EBV of 3.30 and accuracy of 0.44 for calves under AMGG and breeding value of 6.97 and accuracy of 0.56 under AMSK. Moreover, the inclusion of ET records considerably changed EBV for sires and progeny, given that the Spearman correlation was 0.77 and 0.40, respectively.

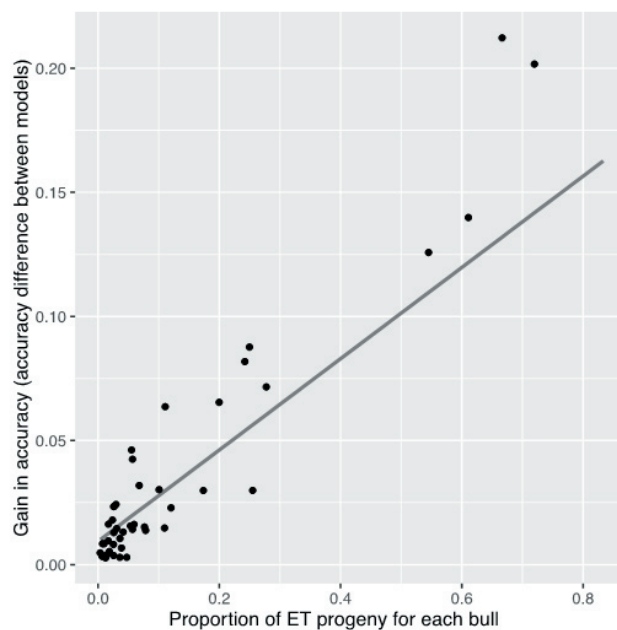


Figure 1 - Influence of embryo transfer (ET) progeny proportion on accuracy gain for each of 48 bulls used as ET semen donors.

Discussion

The results emphasize the importance of using ET phenotypic records in a large-scale genetic evaluation program, especially for bulls that have most of their progeny from ET. The inclusion of ET records showed an expected improvement in breeding value accuracy of sires (Figure 1) and their calves. This can be easily viewed for those four bulls that had more than half of their progeny consisted of ET calves (gain of more than 0.10 points). However, most reliable breeding values may be obtained in circumstances in which more precise information on foster dams (e.g., breed composition) is available. Schaeffer and Kennedy (1989) argued that all management peculiarities should be included on modelling, since all inaccurate information could act as confounding factors. Brazil is a country of continental dimension, which creates very diverse environments and conditions for livestock husbandry. For example, depending on the region in Brazil, it is common to use females of different breeds or crossings as foster dams.

Besides the benefits on EBV and accuracies, the use of ET also affects the rate of annual genetic gain, which is the most important measure of a breeding scheme success. Genetic gain is proportional to accuracy and inversely proportional to generation interval (Falconer and Mackay, 1996). Since the goal of embryo transfer is the production of more calves overtime (i.e., decreasing the interval between generation), genetic gain might be improved. The use of embryo transfer and *in vitro* fertilization is a reality in Brazilian livestock systems. However, most Brazilian breeding programs still do not use phenotypic records of such calves, and their breeding values have been historically predicted based only on parent average. In the same way, accuracies are not high because they are also based only on parent average (VanRaden and Wiggans, 1991).

The adoption of assisted-reproduction techniques may lead to an increase in the rate of annual inbreeding as a consequence of substantial reduction in generation interval. Strategies should be developed to avoid such negative impact. Moreover, future studies should focus on the evaluation of the most efficient breeding schemes which use embryo transfer records, sexed semen, and genomic approach altogether. Pedersen et al. (2012) previously evaluated some dairy cattle scenarios, but it would be important to perform additional analysis under Brazilian conditions.

Considering that ET has been widely used in Brazil and that such information improves genetic predictions,

we suggest modifying the traditionally adopted models by considering ET information in the Brazilian genetic evaluations.

Conclusions

The inclusion of embryo transfer phenotypic records provides the most reliable breeding values. Well-designed schemes must be developed to correctly record foster dam information, including birth date and breed composition, to be appropriately accounted for in genetic evaluation programs.

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