

ACCOUNTING FOR SELECTIVE SLAUGHTER OVER TIME WHEN ESTIMATING BREEDING VALUES FOR CARCASS TRAITS – A SIMULATION STUDY

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SUMMARY

Progeny test data used to estimate breeding values (EBVs) of sires for carcass traits may come from measurements taken on animals that have been slaughtered over time based on individual animal market suitability. Confounding between genetic effects and age can result. However, in the current study appropriate adjustment for growth rate resulted in highly accurate sire EBVs for both the slaughtering criteria, namely liveweight, and for a second trait (e.g. a carcass trait) regardless of the genetic correlation between the two traits.

INTRODUCTION

In Australia, the need to meet market specifications commonly leads to selective slaughtering of cattle over time based on specified criteria such as weight and fatness, particularly for feedlot cattle. For a progeny test implemented to determine sire estimated breeding values (EBVs) for carcass traits, progeny may be sent to commercial feedlots and be selectively slaughtered as they meet market specifications. Thus non-random groups of progeny are killed at different times. It is likely that more progeny of the genetically better (poorer) sires for the market specifications will be slaughtered in the earlier (later) groups. The aim of this study was to quantify the effect of selective slaughter over time on the accuracy of sire EBVs produced from such progeny data, and to investigate methods of analyses that would yield more accurate EBVs in such cases.

MATERIALS AND METHODS

A population was simulated with 125 unrelated sires mated to 40 unrelated dams each, resulting in 40 half-sib steer progeny per sire. Progeny were born in a single year with birth dates simulated to follow a truncated normal distribution where the majority of progeny were born earlier in the calving season (90 days). This generated variation in age at each harvest, an important variable in considering the effect of selective slaughter on EBVs. It was assumed that all 5000 progeny remained in the same contemporary group until selected for slaughter. No additional fixed effects were simulated.

The random regression program RRGibbs (Meyer 2002) was modified, and used in combination with another program, to simulate additive genetic (a), permanent environmental (pe), and residual (e) random effects for liveweight (LWT) and eye muscle area (EMA) for each individual, taking into account the pedigree. Residual variance was simulated by drawing residual random effects from normal distributions based on different variances set for specific age ranges. Specific parameters for LWT were based on analysis of Angus cattle growth (Meyer 2005) with Legendre polynomials of order 3 used for a and pe random effects. Legendre polynomials of order 2 and 3 were fitted for EMA for these two effects, respectively, based on analysis of ultrasound measures of EMA growth in Angus cattle (Hassen *et al.* 2004).

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EMA was genetically correlated to LWT with varying values of 0.0, 0.6 and 0.9. A *pe* correlation of 0.8 was simulated between the two traits, but a residual correlation of 0 was simulated. These random effects were added to linear mean growth curves for LWT [based on analysis of Australian Shorthorn steer records (unpublished data)] and EMA (approximated from figure 1 in Hassen *et al.* 2004):

$$\begin{aligned} \text{LWT (kg)} &= 100.26 + 0.627 * \text{age (days)} \\ \text{EMA (cm}^2\text{)} &= 9.06 + 0.17 * \text{age (days)} \end{aligned}$$

The computed daily LWT (mean + *a* + *pe* + *e*) of each individual was used to harvest the data at 3 time points. The first and second harvests occurred when consecutive thirds of the 5000 progeny reached the minimum target LWT of 445 kg, and the final third was harvested when 7/12 of the remaining cattle reached this minimum target LWT. Using ASREML (Gilmour *et al.* 2002) the same univariate animal model was fitted to 4 traits. The traits for models 1 to 4 were LWT, pre-adjusted LWT, EMA and pre-adjusted EMA, respectively. The effects fitted for every trait were the overall trait mean and random *a* and *e* effects. Models 1 and 3 did not make a distinction between animals harvested on different days nor make any adjustment for age differences. Differences in age due to variation in birth day, in harvest day and in growth rate were accounted for in models 2 and 4 where records were pre-adjusted to a constant age based on growth rate according to the following equations:

$$\begin{aligned} \text{Pre-adjusted LWT}_i &= [\text{harvest LWT}_i - \text{birth LWT (=35 kg)}] / \text{age at harvest}_i \text{ (d)} * \text{standard age (580d)} \\ \text{Pre-adjusted EMA}_i &= [\text{harvest EMA}_i - \text{birth EMA (=9.06 cm}^2\text{)}] / \text{age at harvest}_i \text{ (d)} * \text{standard age (580d)} \end{aligned}$$

The accuracy of sire EBVs resulting from each analysis was calculated as the Pearson correlation between the EBVs and true breeding values (TBVs) simulated at a standard age of 580 days (approximate average age of slaughter). Results presented are means and standard deviations of 100 simulations.

RESULTS AND DISCUSSION

Harvesting on LWT was associated with increasing average age across harvest days as shown in Figure 1, with an increase of approximately 40 days occurring between consecutive harvest days. Average LWT however, showed a decline between harvest days, with similar LWT between harvests 1 and 2, but a sharper drop from the 2nd to 3rd harvests (see Figure 1). Conversely, average EMA showed an increasing trend over consecutive harvest days, even when LWT and EMA were highly correlated for both *a* and *pe* effects as illustrated in Figure 1. This can be explained by comparing the two linear mean growth curves simulated for EMA and LWT. The increase in EMA between consecutive harvests was proportionally greater than for LWT.

The expected uneven distribution of each sire’s progeny across harvests due to selection on LWT is illustrated in Table 1. There was a large range in progeny per sire for every harvest.

Table 1. Distribution of sire progeny across harvest days for 100 simulated populations

	Progeny per sire from 100 simulations	
	Minimum range	Maximum range
Harvest 1	0-5	24-36
Harvest 2	3-8	19-25
Harvest 3	0-4	24-33

Beef

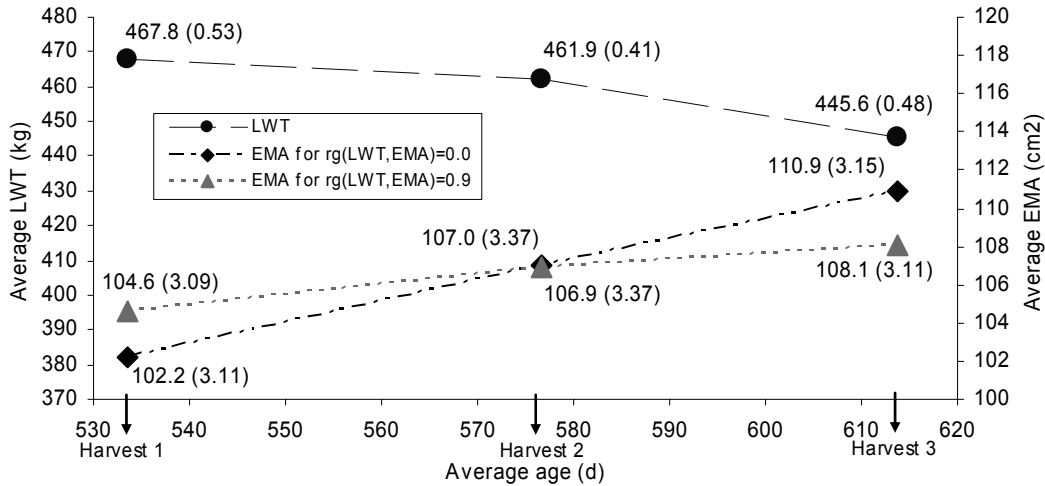


Figure 1. Average age, liveweight (LWT) and eye muscle area (EMA) (for two levels of genetic correlation) at consecutive harvests over 100 simulated populations (standard deviations).

The accuracy of sire EBVs are in Table 2. The highly accurate EBVs for LWT and EMA resulting from fitting models 2 and 4 show that appropriately adjusting the traits for growth rate removed the problem of genetic effects being confounded with age.

Table 2. Mean accuracy of sire EBVs (correlation between EBVs and TBVs) for four univariate animal models fitted to harvested data with varying genetic correlation simulated between liveweight (LWT) and eye muscle area (EMA) (standard deviations of 100 simulations)

	Additive genetic correlation between LWT and EMA		
	0.0	0.6	0.9
Model 1 - LWT	0.87 (0.02)	0.87 (0.02)	0.87 (0.02)
Model 2 - Pre-adjusted LWT	0.92 (0.01)	0.92 (0.01)	0.92 (0.01)
Model 3 - EMA	0.68 (0.05)	0.44 (0.08)	0.25 (0.09)
Model 4 - Pre-adjusted EMA	0.91 (0.02)	0.91 (0.02)	0.91 (0.02)

Consideration of the TBVs and EBVs separately can explain the results. Considering TBVs, when harvesting is on LWT we expect progeny of sires with higher LWT TBVs to be harvested first, and therefore sires represented more in earlier harvests to have greater LWT TBVs than those in later harvests. The magnitude of sire LWT and EMA TBVs at each harvest can be gauged from the corresponding magnitude of average progeny TBVs, given in Table 3. When $r_g(EMA, LWT) = 0$, the EMA TBVs of sires are expected to show no association with harvest days, but as $r_g(EMA, LWT)$ increases, we expect a strengthening trend for sires more represented in earlier harvests to have greater EMA TBVs, increasingly approaching the trend seen for LWT TBVs.

Table 3. Progeny liveweight (LWT) TBVs and eye muscle area (EMA) TBVs, for varying levels of genetic correlation, for consecutive harvests (standard deviations of 100 simulations)

	Average LWT TBV	Average EMA TBV		
		Genetic correlation (EMA, LWT)		
		0.0	0.6	0.9
Harvest 1	17.48 (1.28)	-0.01 (0.20)	1.68 (0.21)	2.53 (0.21)
Harvest 2	-0.12 (1.20)	0.01 (0.21)	0.00 (0.20)	-0.01 (0.20)
Harvest 3	-18.58 (1.18)	0.02 (0.21)	-1.78 (0.19)	-2.69 (0.18)

Considering EBVs, under models 1 and 3, where neither age nor harvest day was fitted, we expect the trait EBV of an individual sire to simply match the phenotypic ranges of harvests in proportion to the number of progeny it has in each one. LWT shows a negative phenotypic trend across consecutive harvests, but EMA shows a positive trend regardless of r_g (EMA, LWT), as explained earlier (Figure 1). Therefore, the LWT EBVs of sires follow the same trend as their TBVs across harvests leading to a high EBV accuracy under model 1. The EMA EBVs of sires followed the opposite trend to their TBVs across harvests when r_g (EMA,LWT) = 0.6 or 0.9, resulting in low EBV accuracy under model 3. When r_g (EMA,LWT) = 0, EMA TBVs of sires were not related to harvest days, but the EBVs of random sires resulting from fitting model 3 followed the positive phenotypic trend in EMA across consecutive harvests leading to a low EBV accuracy.

CONCLUSIONS

This study highlights the potential problem confounding of genetic effects with age can cause to the estimation of carcass trait EBVs in a progeny test when animals are selected for slaughter over time. Under the assumption of linear mean growth curves, linearly pre-adjusting for growth rate enabled simple univariate analyses to give accurate sire EBVs for both the trait harvesting was based on, namely LWT, and the carcass trait regardless of its genetic correlation with LWT.

This study provides insight into carcass EBV estimation when the data to be used are from selectively slaughtered animals. Other issues for further consideration are the effect of specific harvest days, non-linear mean growth curves, differences in harvesting strategy and environments, and sensitivity analyses of other parameters including the effective number of progeny per sire.

ACKNOWLEDGEMENT

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