

# ESTIMATION OF BREEDING VALUES FOR ANIMALS SELECTIVELY SLAUGHTERED

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## DECLARATION

I certify that the substance of this thesis has not already been submitted for any degree and is not currently being submitted for any other degree or qualification.

I certify that any help received in preparing this thesis, and all sources used, have been acknowledged in this thesis.

A solid black rectangular box used to redact the signature of the author.

Signature

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## **ABSTRACT**

Progeny testing in beef cattle can be used to provide phenotypes for estimating carcass trait breeding values. However, progeny are commonly selectively slaughtered over time based on live-animal indicators of market requirements for carcass traits, particularly if feedlot finished. This harvesting results in carcass trait records for non-random groups of animals because harvesting on liveweight (LWT) causes the progeny of genetically faster growing sires to be in earlier harvest groups. This can lead to confounding of genetic and harvest group effects in genetic evaluation models. Additionally, harvesting can lead to the effect of age not being partitioned. Therefore, the aim of this thesis was to find appropriate statistical methodology that can be applied to harvested data to give unbiased and accurate estimated breeding values (EBVs) for carcass traits.

Firstly, data were simulated based on the half-sib design, consisting of 125 sires with 40 or 15 progeny, each dam having only one offspring. 100 replicates were subjected to harvesting over time based on LWT into three harvest groups with different levels of harvest group effects added post-harvest. Univariate and bivariate animal models were fitted to the harvesting criteria LWT and an age-influenced carcass trait, eye muscle area (EMA) with varying levels of assumed genetic correlation with LWT. EBV accuracy was calculated as the correlation between true and estimated breeding values, and EBV bias as the difference between estimated and true breeding values for the top and bottom third of sires based on EBV.

Results showed that in the absence of harvest group effects, univariate analyses of harvested LWT and EMA that were pre-adjusted for age resulted in accurate and unbiased sire EBVs. For the same analyses, the addition of harvest group effects to the data reduced the EBV accuracy, increased the variability of accuracy between replicates and resulted in significant EBV bias for both age-adjusted LWT and age-adjusted EMA when EMA was positively genetically correlated to LWT. However, using normal distribution theory to adjust harvested LWT records to their expected records at the first harvest was found to account for harvest group effects and result in accurate LWT EBVs of sires.

When LWT records were available for all animals at the first harvest, a bivariate analysis resulted in accurate and unbiased sire EBVs for the correlated carcass trait EMA affected by specific harvest day effects. Furthermore, when only harvested LWT records were available, bivariate analyses of both LWT and EMA pre-adjusted for age resulted in accurate sire EBVs for EMA. This was the case when EMA was affected by specific harvest day effects, for genetic correlation ranging from 0.0 to 0.9, for 15 progeny per sire, and whether LWT was affected by specific harvest day effects or not. Sire EBV bias was small but increased with increasing genetic correlation between LWT and EMA.

Univariate analyses were fitted to a field dataset of beef cattle LWTs considered to represent harvested data. Accuracy of sire EBVs was measured as the correlation between EBVs from alternative models fitted to harvested data and EBVs estimated using non-harvested data. Appropriately pre-adjusting LWT for age resulted in accurate sire EBVs. Adjusting the LWTs of harvest 2 to the estimated normal distribution at harvest 1 was shown to result in a high EBV correlation with non-harvested data that was robust against the addition of a large artificial specific harvest day effect.

The study gives evidence that appropriate trait adjustments for age along with certain models are able to estimate accurate and unbiased sire EBVs for harvested data. This holds for data affected by specific harvest day effects, including for age-influenced carcass traits varying in level of genetic correlation with the harvesting criteria.

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