

Fat prediction using an online Dual Energy X-ray Absorptiometer is accurate in genetically divergent lambs

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Abstract – Dual Energy X-ray Absorptiometry (DEXA) is an imaging modality that is used to determine tissue composition and bone density. A DEXA system operating at chain speed within an abattoir has been used to predict carcass fatness in a population of lambs (n=468) with high precision ($R^2=0.88$; RMSE=1.46), when compared against computed tomography determined fat percentage. Further analysis of the fat % residuals (computed tomography prediction minus DEXA prediction) for each lamb investigated potential biases over the range of the sire's Australian Sheep Breeding Values; including post-weaning eye muscle and fat depth. Results showed that there was minimal bias over the range these sire breeding values. These findings indicate that DEXA is an accurate and precise method of determining carcass composition in a genetically diverse population of lambs – giving confidence that this will provide valuable feedback to both processors and producers.

Key Words – Bias, breeding values, composition

I. INTRODUCTION

The Australian Sheep Breeding Values (ASBVs) for post-weaning eye muscle depth (PEMD) and post-weaning fat depth (PFAT) are used to select for increased whole carcass muscularity and reduced fatness [1]. However, studies have demonstrated that the PEMD also redistributes lean to the saddle region, at the expense of the fore section [2]. This implies that if carcass composition is predicted from a single point measure taken in the saddle region, such as the current industry standard of measuring GR tissue depth, it may be biased in genetically diverse populations. Alternatively, systems that measure whole carcass composition, such as DEXA, are likely to eliminate this bias. Therefore, we hypothesise that a whole carcass DEXA scanner will accurately predict carcass fatness within lambs that are the progeny of sires with divergent sire PEMD and PFAT values.

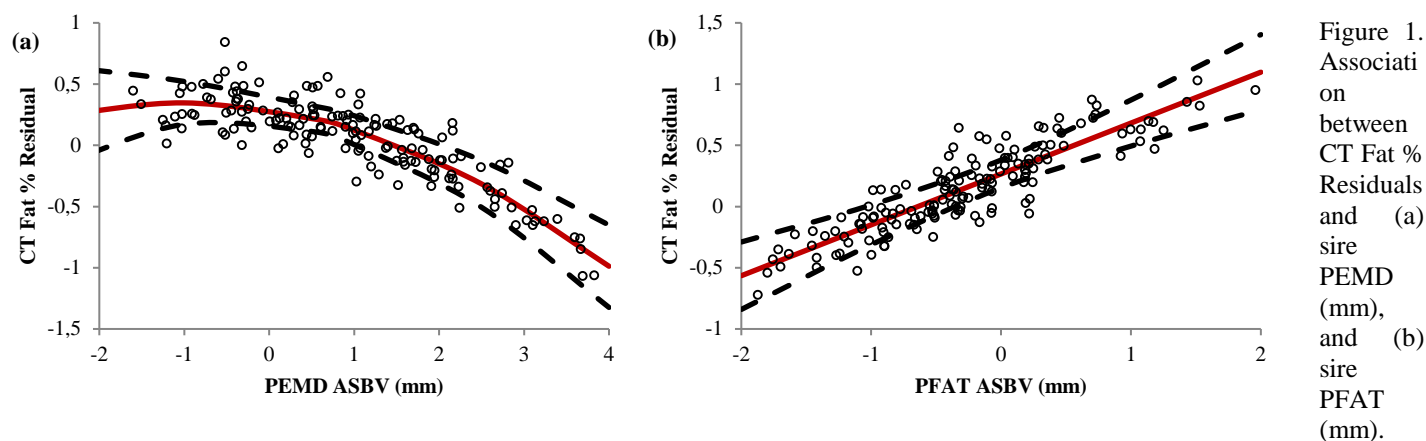
II. MATERIALS AND METHODS

Lamb carcasses (n=468) of varying sire breeds, sire types and sexes were scanned using an online prototype DEXA, installed in an abattoir at Bordertown, South Australia, in order to predict carcass fat %. Carcass fat % was subsequently measured by CT - considered to be the gold standard in tissue composition prediction [3]. Lambs were the progeny of sires with a diverse range in PEMD and PFAT ASBVs, and with carcass fat percentages ranging from 15% to 40% as determined by CT. The residual values for fat prediction (CT Fat % Residual), calculated as CT predicted fat % minus DEXA predicted fat %, were analysed using a linear mixed effects model with sire as a random term. Fixed effects included sire-type, sire-breed, sex, and kill group, and covariates included PEMD and PFAT, along with all relevant interactions.

III. RESULTS AND DISCUSSION

There was a negative association between PEMD and CT Fat % Residual (Figure 1), with residuals varying from zero by maximums of +0.34 and -0.98 over the range of sire PEMD values (-2.5mm to 4.0mm).

There was a positive association between PFAT and CT Fat % Residuals (Figure 2), with residuals varying from zero by maximums of -0.56 to +1.1 over the range of sire PFAT values (-2.0mm to 2.0mm).



Lines are predicted means (\pm standard errors; broken lines) and icons (o) represent the mean residual for individual sires.

Contrary to our hypothesis, there was a small bias across the range in PFAT and PEMD breeding values, as shown by their association with the CT Fat % Residual values. A portion of this small bias is likely to be due to the imperfect precision of the DEXA prediction of carcass fatness, causing the regression paradox error described by Chen *et al* (2009). Hence it under-predicts the fattest carcasses (i.e. positive residuals) and over-predicts the leanest (i.e. negative residuals). As an increased PEMD is selecting for lambs with higher muscling, and thus lower fatness, we see the expected increase in negativity of CT Fat % Residuals as PEMD increases. Similarly, an increase in PFAT selects for fatter lambs, which will result in more positive CT Fat % Residuals. This was further demonstrated by correcting the model for CT Fat %, which accounted for the impacts of both PFAT and PEMD on CT fat % residuals. Although statistically significant, these biases in the CT Fat % predictions are minimal when considering the range in actual CT fat % values, which extend from 15% to 40% across the sample population.

IV. CONCLUSION

Statistical bias was identified across the range of sire PEMD and PFAT ASBVs; however these were small relative to the data range within the sample population. These results will provide confidence to the sheep meat industry that DEXA not only predicts carcass fatness with great precision, but also with great accuracy across a genetically diverse population.

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