

MERITS OF USING DEXA TO MEASURE LEAN MEAT YIELD FOR THE GENETIC EVALUATION OF AUSTRALIAN LAMB

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SUMMARY

Dual-energy X-ray absorptiometry (DEXA) is rapidly gaining acceptance as a reference method for analysing body composition. Since initial developments in 2017, as part of the Advanced Livestock Measurement Technologies project, there has been an influx of DEXA measurements and some additional computed tomography (CT) measurements on genetically informative animals via the MLA funded Resource Flock and companion industry satellite flocks. Although more data is required, the results suggest that the DEXA lean meat yield is likely to be the same genetic trait as the CT measured lean meat yield. These results are promising and plans regarding the utilisation of DEXA data within Sheep Genetics national evaluation should begin. However, improving hook tracking technologies and data transfer pathways concurrently is also required.

INTRODUCTION

The financial value of a carcass is influenced by its saleable meat yield, which differs across supply chains, markets and cutting specifications. Historically, consumer preferences in domestic and international markets has driven the industry to produce meat cuts that are larger and leaner (Banks 2002). Terminal sheep breeders in Australia have been able to sustain genetic gains over a long period (Swan *et al.* 2017), partly due to breeding objectives targeting increased growth and lean meat yield. These traits can be accurately evaluated from a young age using selection indexes based on body weight, along with eye muscle and fat depth scanned on live animals (Swan *et al.* 2015). Due to a limited supply of carcass recording in seedstock flocks, the majority of genetic gain achieved in lamb lean meat yield has been reliant on a correlated response from index selection (Swan *et al.* 2015). This has driven interest and research funding to develop carcass based lean meat yield measuring technology within the supply chain.

Dual-energy X-ray absorptiometry (DEXA) has recently been accredited for commercial use in Australian lamb abattoirs for predicting carcass lean %. This accreditation is based upon its capacity to predict the carcass lean% reference standard measured using computed tomography (CT). This has excellent synergy with the existing Sheep Genetics databases in Australia which offer a lean meat yield breeding value that is also based upon the CT measurement of whole carcass lean% and is more cost effective and easier to implement within the processing environment.

Since initial developments in 2017, part of the Advanced Livestock Measurement Technologies (ALMTech) project (Gardner *et al.* 2021), DEXA technology and the algorithms behind the conversion of the DEXA image to measures of lean, bone and fat have been updated (Connaughton and Gardner 2023). Coinciding with these recent developments, there has been an influx of DEXA measurements and some additional CT measurements on genetically informative animals via the MLA funded Resource Flock (van der Werf *et al.* 2010) and companion industry satellite flocks.

* A joint venture of NSW Department of Primary industries and the University of New England

This study determines the genetic variation and the suitability of using DEXA lean meat yield as part of the National Genetic Evaluation, alongside or in conjunction with current CT lean meat yield records.

MATERIALS AND METHODS

Data. The analysis utilised carcass and lean meat yield records collected as part of the MLA funded Resource Flock and its previous iteration, the Information Nucleus Flock (van der Werf *et al.* 2010). As part of the broader Resource flock project, data was also collected on commercial (seedstock, non-research) animals as satellite flocks to the MLA Resource flock (Alexandri *et al.* 2022). This process involved animals from two sources: i) surplus animals – animals not selected for breeding based on phenotypic or genetic performance, and ii) structured progeny test – where dams were joined to sires to generate progeny for phenotyping. Consequently, to date, approximately 44 thousand lambs, of primarily a Merino ewe base but including both pure maternal and terminal breeds and their Merino cross progeny have been slaughtered and phenotyped. Carcasses were measured for key carcass characteristics, including but not limited to carcass eye muscle depth (CEMD), carcass fat depth at the c-site (CFAT) and chemical intramuscular fat (CIMF) (Table 1).

As a component of the larger project, a sub-section of lambs was measured for lean meat yield via CT and/or DEXA. The CT records on lambs were primarily observed on a subset of the Resource Flock animals recorded since 2007, for a total of 3,646 carcasses. The CT scanned lamb carcasses represented 22 different sire breeds and 936 sires, with a mean CT lean of 57.8% (SD = 3.5). DEXA measurements were primarily collected on the accompanying satellite flocks. Consequently, only 1,018 carcasses (320 sires represented) from the Resource Flock had both a CT lean and DEXA lean record. There were 4,104 lamb carcasses recorded via DEXA representing 750 sires and 22 sire breeds. The mean lean meat yield from DEXA was 55.7 (SD = 5.4).

Table 1: Summary of carcass and lean meat yield records analysed within this study (count of contemporary groups = CGs)

Trait	Records	CGs	Sires	Mean	SD
Carcass Eye Muscle Depth (mm)	37,278	1,341	2,646	31.0	5.1
Carcass Fat Depth (mm)	36,624	1,328	2,623	4.3	2.4
Chemical Intramuscular Fat (%)	33,874	1,298	2,634	4.5	1.2
CT lean meat yield (%)	3,646	212	936	57.8	3.5
DEXA lean meat yield (%)	4,104	86	750	55.7	5.4

Statistical Analysis. The DEXA and CT lean meat yield records were analysed using univariate models in ASReml (Gilmour *et al.* 2015). Genetic correlations between the lean meat yield technologies (DEXA and CT) with a subset of carcass traits, carcass eye muscle depth (CEMD), carcass c-site fat depth (CFAT) and intramuscular fat (IMF), were estimated from a series of bi-variate models in ASReml.

The analyses were carried out with an animal model that incorporated all pedigree available on phenotyped animals within the LAMBPLAN database (Brown *et al.* 2007). Maternal effects were not fitted within this analysis, as is the standard approach for carcass traits in the LAMBPLAN analysis. Fixed effects in the model included birth type, age, age of dam (linear and quadratic covariates) and sire breed. The bi-variate analysis between trait pairs were completed with hot carcass weight fitted as a covariate to all carcass traits. Contemporary group was fitted as a sparse fixed effect and defined by flock, management group, sex, date of measurement and kill group (Huisman *et al.* 2008). The model did not include genetic group effects to avoid issues with analyses converging due to the small number of records. Due to the low number of records and the diversity

of breeds and genetic makeup represented in the sires, the inability to correctly account for genetic group effects is likely to lead to some inflation of the heritability estimates.

RESULTS AND DISCUSSION

Heritability estimates for the DEXA and CT lean meat yield measures were high and similar, 0.51 and 0.50, respectively (Table 2). Including hot carcass weight as a covariate resulted in a slight increase in heritability for both traits. Estimates within this study are consistent with previous heritability estimates of CT measured lean meat yield, where moderate to high heritabilities were reported in Charolais (0.47), Suffolk (0.45), Texel (0.46; Jones *et al.* 2004), Norwegian White (0.57; Kvame and Vangen 2007) and Scottish Blackface (0.48; Karamichou *et al.* 2006). Heritability for CT lean meat yield, in a smaller subset of this population, has previously been reported as 0.53 (0.63 if carcass weight fitted as a covariate) (Walkom *et al.* 2021). Unfortunately, whilst the heritability and variances observed are similar (Table 2) between the two technologies, the small number of animals recorded with both is a limitation, and further examination is required to be able to declare that lean meat yield technologies are interchangeable in the genetic evaluation.

Table 1. Estimates of phenotypic (σ_p^2), additive (σ_a^2) and residual (σ_e^2) variance and heritability (h^2) for DEXA and CT recorded lean meat yield (LMY). Standard error in parentheses

Trait	Model	h^2	σ_p^2	σ_a^2	σ_e^2
DEXA LMY		0.51 (0.06)	5.36 (0.13)	2.71 (0.34)	2.65 (0.29)
DEXA LMY	HCWT co-variate	0.58 (0.06)	3.99 (0.10)	2.32 (0.27)	1.67 (0.22)
CT LMY		0.50 (0.06)	5.82 (0.15)	2.88 (0.39)	2.94 (0.34)
CT LMY	HCWT co-variate	0.54 (0.06)	4.90 (0.13)	2.63 (0.33)	2.27 (0.29)

The phenotypic correlation between DEXA and CT lean meat yield was 0.81 ± 0.01 , but as highlighted, this is based on only 1,018 carcasses. The corresponding genetic correlation between lean meat yield recorded with the two technologies was 0.87 ± 0.03 (Table 3). The correlation is very high but significantly different from each other, suggesting that there may be differences in how lean meat yield is measured across the two technologies despite the fact that DEXA has been trained to predict the CT measurement. However, this discrepancy may also be due to differences in samples measured by each method and the low number of sires with significant numbers of progeny recorded for both traits.

Genetic correlations between the two lean meat yield measures and a subset of key carcass traits are relatively consistent between the two technologies for estimating LMY (Table 3). The similarity of genetic correlations with the other carcass traits suggests that whilst the two technologies have primarily been recorded on separate sub-populations, they seem to capture the genetic (co)variation in lean meat yield consistently.

To make use of commercially available DEXA data it will be crucial to ensure that these records are correctly linked to the corresponding animal. This can be challenging in an abattoir environment where routine processing practices (ie. retain for trimming) can affect carcass sequences and identification. Therefore, until hook tracking is reliably implemented in plants with DEXA, collection of these data should be observed by technical staff to ensure animals' identities are correctly linked to the carcass and DEXA data. To assist with quality control, all consignments should have pre-slaughter weights and condition scores immediately prior to the kill.

Table 3. Genetic correlations between DEXA LMY and CT LMY and other carcass and meat quality traits. Standard error in parentheses. HCWT: hot carcass weight, IMF: chemical intramuscular fat, CEMD: eye muscle depth, CFAT: fat at the c-site

Trait	DEXA LMY	CT LMY
CT LMY	0.87 (0.03)	-
CEMD	0.36 (0.06)	0.46 (0.05)
CFAT	-0.60 (0.05)	-0.63 (0.04)
IMF	-0.34 (0.05)	-0.37 (0.04)

CONCLUSION

Although more data is required, very high genetic correlations suggest that the DEXA lean meat yield is likely to be the same trait as the CT measured lean meat yield. These results are promising and plans regarding the utilisation of DEXA data within Sheep Genetics national evaluation should begin. Rigorous data collection protocols are also required to ensure efficient collection of accurate data.

ACKNOWLEDGEMENTS

This work was part of the Advanced Measurement Technologies for globally competitive Australian meat project, funded by the Australian Government Department of Agriculture and Water Resources and many industry partners. The authors thank the teams behind the Sheep CRC Information Nucleus Flock, MLA resource flock and industry flocks which contributed to this study.

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