



## The value of recording live animal and carcass scan traits for the genetic selection of lean meat yield in lamb

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The value of a carcass is highly influenced by its saleable meat yield. Direct measures of lean meat yield (LMY) are currently not commercially available due to the high cost of measurement through the 'gold standard' of computed tomography (CT). Therefore, the objective of this study was to assess the use of post-weaning scan traits, carcass traits, and a dual-energy x-ray absorptiometry (DEXA)-derived lean, as indicator traits for selection to improve LMY in lamb. DEXA-derived lean was strongly genetically correlated to CT lean ( $r_g = 0.75$ ). This suggests that DEXA (which can be recorded under commercial processing conditions) has value as an indicator trait for CT lean. However, there are different implications for predicted genetic gains for ram breeding and progeny testing situations due to availability of records from different classes on animals. Since a ram breeder sells most animals as breeding stock and there is limited access to slaughter records, only 50% of potential genetic gains (compared to selection for CT lean) could be achieved through DEXA alone. The addition of post-weaning traits increased potential genetic gains to 67%. Therefore, the ram breeding industry will still need to rely on the correlated trait measured on the live animals and the rate of genetic gain will be slower. As seedstock producers will struggle to record DEXA and CT traits in sufficient numbers, resource populations such as the Information Nucleus Flock will continue to be required to validate the parameters presented in this study and improve the ability for ram breeders to make effective selection decisions for LMY improvement. Furthermore, since there are unfavourable associations between LMY and eating quality, genetic improvement of LMY will need to be managed, and eating quality included in the breeding objective for Australian lamb breeders.

### Summary

*Keywords: DEXA, CT, objective carcass measurements, genetic gain.*

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## Introduction

The value of a carcass is highly influenced by its saleable meat yield. Lean meat yield (LMY) represents the proportion of the carcass that is lean meat (muscle), with all visible subcutaneous and intermuscular fat removed. While the 'gold standard' to directly measure LMY is through computed tomography (CT), the cost of measurement through this technology is high, logistically difficult, and is not viable in the commercial processing environment. Therefore, the genetic selection for LMY is reliant on indirect selection, where gains are achieved through correlated responses from indicator traits.

Sustainable genetic gains in LMY have been achieved for terminal sheep breeds through selection indexes based on body weight, and eye muscle and fat depth from ultrasound scans on the live animal (Swan *et al.*, 2015). The search for new objective carcass measurements technologies (Brown *et al.*, 2017), such as dual-energy x-ray absorptiometry (DEXA) (Gardner *et al.*, 2015), provide potential indicator traits for LMY. The use of indicator traits can be associated with slower genetic gains and is reliant on their heritability and strength of correlations holding up across the population. Therefore, the objective of this study was to assess the value of post-weaning traits measured on-farm (weight, body condition and scan traits), measures on the carcass, and DEXA derived values of lean, for the genetic evaluation of LMY in lamb. The value of these indicator traits was assessed by predicting the potential genetic gain in LMY under a ram breeder or progeny test scenario where selection is based on a series of different indicator traits.

## Materials and methods

### Information Nucleus Flock data

An Information Nucleus Flock (INF) was established by the Australian Cooperative Research Centre (CRC) for Sheep Industry Innovation in 2007 (Fogarty *et al.*, 2007), which evolved into the Meat and Livestock Australia funded Resource Flock (RF) in 2012. The program was based around the annual mating of 100 sires to ~4500 dams (van der Werf *et al.*, 2010), with flocks located at eight research sites across Australia. A key objective of the INF program was to measure and estimate genetic parameters for a diverse range of traits, many of which either cannot be recorded on-farm or are prohibitively expensive, or are not widely or systematically recorded off-farm (such traits are often referred to as "hard-to-measure"). The LMY indicator traits assessed in this study were measured on the live animal, on the carcass, and by CT and DEXA (Table 1) in the INF and/or RF.

Table 1. Summary of traits\*

Trait	Units	Records	Sires	Mean	SD	CV
Post-weaning weight	kg	41,698	1,427	30.53	8.26	27
Post-weaning eye muscle depth	mm	22,411	1,330	25.09	4.83	19
Post-weaning fat depth	mm	22,414	1,330	2.94	1.20	41
Post-weaning condition score	(1-5 score)	14,152	1,106	2.78	0.47	17
Hot carcass weight	kg	24,709	1,409	22.43	3.76	17
Carcass eye muscle depth (C site)	mm	22,879	1,407	29.82	4.72	16
Carcass fat depth (C site)	mm	22,643	1,406	4.11	2.37	58
CT lean	%	2,340	526	57.47	3.59	6
DEXA-derived lean		546	163	83.04	6.54	8

\*CT: computed tomography;

DEXA: dual-energy x-ray absorptiometry (unit-less);

SD: standard deviation;

CV: coefficient of variation (%)

Live animal traits were measured post-weaning, and were available for the lambs born between 2005 and 2016 from terminal, maternal and Merino sires. These were measured at an average age of  $213 \pm 46$  days. Carcase traits were measured on lambs slaughtered at commercial abattoirs at an average age of  $272 \pm 76$  days (Mortimer *et al.*, 2014). A subset of the 2011-born slaughtered lamb carcasses were chosen for CT scanning within 72 hours of slaughter, and the proportion of lean (CT Lean) was determined (Anderson *et al.*, 2015). The CT traits were expressed as a percentage of the weight of the scanned carcase. DEXA-derived lean (Gardner *et al.*, 2015) was available from 546 of the 2014-born progeny.

Genetic parameters were estimated as the average variance estimates from a series of bivariate sire models analysed in ASReml (Gilmour *et al.*, 2009). The models fitted were based on those previously developed and described in depth by Swan *et al.*, (2014). Due to the low number of records, sire by site interaction and genetic group effects were not fitted, and the models were reduced to a sire model to aid convergence.

### Statistical analysis

Fixed effects included birth type (1,2,3,4+), rearing type (1,2,3+), age of dam (linear), age of dam squared, dam breed, sire breed, age at trait measurement (linear) and contemporary group (defined by breed, flock, year of birth, sex, management group, date of measurement and kill group (Swan *et al.*, 2014)). Weight was fitted as a covariate for eye muscle depth and fat depth. Random effects included the sire genetic effect and, for post-weaning traits, the dam permanent environment effect.

The expected response to selection was evaluated using the MTINDEX spreadsheet for multiple trait selection index by van der Werf (2005). Two scenarios were explored. For the ram breeding program scenario, it was assumed that each ram had its own record, as did its sire and dam, 20 half-sibs and 20 progeny for live traits, where only 10% of their progeny and half-sibs were slaughtered. For the progeny testing situation, it was assumed that records for both live animal and carcase traits were only available for 30 progeny. Genetic gain for LMY under the different scenarios was expressed as a proportion of the gain that could be achieved if all animals had a recorded LMY phenotype. This reflects a situation where LMY is the only trait we are aiming to change by genetic selection (not the case in reality).

Genetic parameter estimates for all traits are presented in Table 2. The heritability estimate of CT lean was  $0.24 \pm 0.03$  ( $\pm$  SE). This was slightly lower than the  $0.34 \pm 0.05$  estimate reported by Mortimer *et al.* (2010) for the 2007- and 2008-born INF progeny, but certainly providing substantial scope for changing the trait by selection.

### Results and discussion

DEXA-derived lean was strongly correlated to CT lean, phenotypically ( $0.80 \pm 0.01$ ) and genetically ( $0.75 \pm 0.10$ ). While more data are required to validate these results, DEXA-derived lean provides a good indicator of both the phenotypic and genetic variation that exists for LMY. It is also viable to obtain DEXA-derived measures under commercial processing conditions, indicating it is a potential option as a correlated trait as part of a selection criterion to improve LMY.

The genetic correlations between CT lean and post-weaning traits ranged from -0.54 to 0.10. Similar correlations have been observed between live scan traits & LMY (Mortimer *et al.*, 2010). These correlations were weaker than observed between CT lean with the carcase and DEXA-derived lean. The results indicate that the traits measurable

on live animals are moderate to strongly genetically related to CT Lean, and are heritable themselves. Which, as was also observed with the DEXA-derived lean, makes them suitable for use as a correlated trait within the selection criterion.

The predicted genetic gain in LMY by selection for indicator traits is shown in Figure 1. The expected gain is expressed as a proportion of the genetic gain that could be achieved via direct selection for LMY where all animals are assumed to have a CT lean record.

Despite DEXA-derived lean being a good indicator of CT lean, phenotypes can only be obtained on slaughtered animals. A ram breeder will sell most of their animals as breeding stock and thus only surplus animals will be slaughtered (assumed to be <=10%). Therefore, the ram breeder can only capture 50% of the potential genetic gains if they rely on DEXA records from the slaughter animals alone. The ram breeder would be able to achieve similar genetic gains if they were to base selection on the

Table 2. Genetic parameter estimates (standard error) for live animal and carcass traits, and estimated phenotypic and genetic correlation with CT lean

Trait	Phenotypic Variance		Heritability		Phenotypic Correlation		Genetic Correlation	
CT lean	8.90	(0.00)	0.24	(0.03)				
Post-weaning weight	20.61	(0.17)	0.26	(0.01)	-0.19	(0.05)	0.10	(0.12)
Post-weaning eye muscle depth	5.00	(0.05)	0.36	(0.01)	0.11	(0.05)	0.00	(0.11)
Post-weaning fat depth	0.50	(0.00)	0.22	(0.01)	-0.27	(0.04)	-0.54	(0.11)
Post-weaning condition score	0.09	(0.00)	0.20	(0.01)	-0.29	(0.08)	0.00	(0.15)
Hot carcass weight	5.10	(0.05)	0.27	(0.01)	-0.36	(0.02)	-0.11	(0.11)
Carcass eye muscle depth (C site)	9.42	(0.10)	0.24	(0.01)	0.17	(0.02)	0.35	(0.12)
Carcass fat depth (C site)	3.06	(0.03)	0.29	(0.01)	-0.35	(0.02)	-0.57	(0.09)
DEXA-derived lean	16.89	(1.05)	0.59	(0.07)	0.80	(0.01)	0.75	(0.10)

Abbreviations: CT: computed tomography; DEXA: dual-energy x-ray absorptiometry.

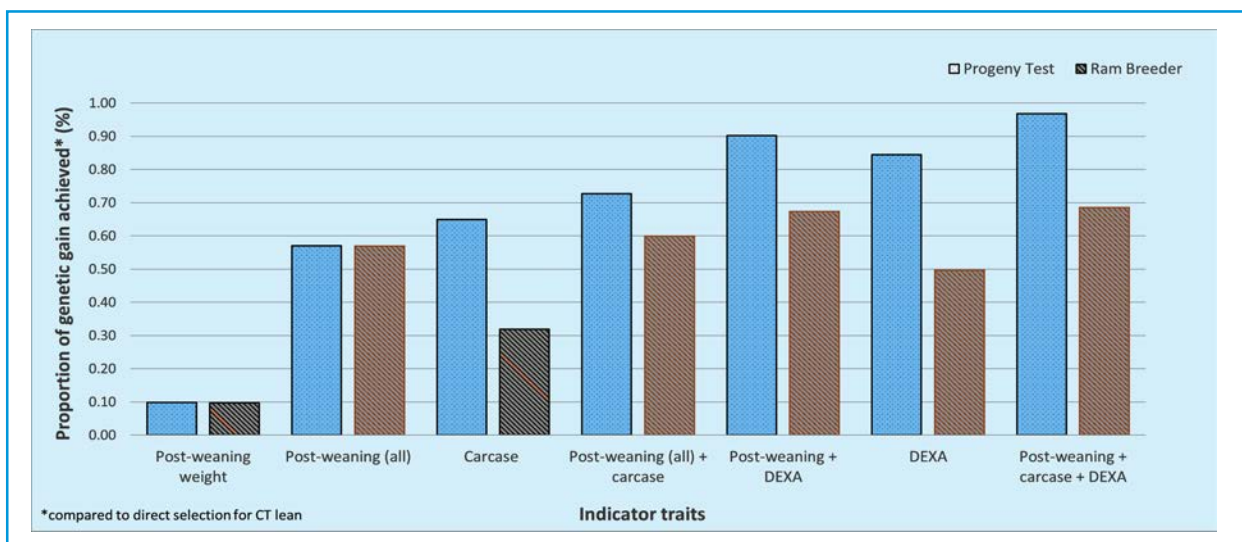


Figure 1. Proportion of genetic gain achieved in lean meat yield through use of indicator traits, compared to direct selection based on computed tomography (CT) lean, in progeny test and ram breeder situations

post-weaning traits (57% of the genetic gains). Despite the weaker genetic correlations between CT lean and post-weaning traits, post-weaning traits are useful predictors of LMY as they can provide an understanding of the genetic variation for LMY that exists within the flock without the need to slaughter animals. Including DEXA records with the post-weaning records as part of the selection criterion improve the relative genetic gain achieved to 67%.

To achieve stronger genetic gains ram breeders are reliant on either progeny testing rams in resource flocks or using genomics to create genetic links to resource flocks where hard-to-measure traits are routinely recorded. In a scenario where the progeny of the selection candidates (rams) have DEXA-derived lean records, 84% of the potential genetic gain could be achieved, compared to only 57% and 65% if the progeny are only recorded for post weaning or carcass traits. However, if post weaning, carcass and DEXA information was available on all progeny, then 97% of the potential genetic gain could be achieved.

Since DEXA measures can be implemented with minimal interruptions to processing, the combination of post-weaning and DEXA derived traits would appear to be of greatest value to breeders especially if animals of industry significance can be progeny tested in resource flocks.

DEXA has value and is a suitable replacement for CT especially since measurement can occur at normal chain speed. The cost of implementation needs to be weighed up against the returns generated by genetic progress for LMY. However, industry genetic progress for LMY will be considerably assisted by recording and using the correlated traits measured on the live animals in ram breeding flocks. As ram breeders will struggle to record DEXA and CT traits in sufficient numbers, resource populations such as the INF/RF are required to validate the parameters presented within this study and strengthen the ability to make sensible selection decisions to improve LMY. Furthermore, since there are unfavourable associations between LMY and eating quality, the genetic improvement of LMY will need to be managed, and eating quality should be included in the breeding objective.

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**Anderson, F., Williams, A., Pannier, L., Pethick, D.W., & Gardner, G.E.**  
2015. Sire carcass breeding values affect body composition in lamb - 1. Effects on lean weight and its distribution within the carcass as measured by computed tomography. *Meat Sci.* 108: 145-154.

## Conclusions

## Acknowledgements

## List of references

**Brown, D.J., Pethick, D.W., McGilchrist, P., Ruberg, C.K., Pitchford, W.S., Apps, R. & Gardner, G.E.** 2017. Objective carcass measurement to improve lean meat yield and eating quality in Australian beef, sheep and pork. In Proceedings of International Committee for Animal Recording 2017. Edinburgh, UK. In press.

**Fogarty, N.M., Banks, R.G., van der Werf, J.H.J., Ball, A.J. & Gibson, J.P.** 2007. The information nucleus – a new concept to enhance sheep industry genetic improvement. Proc. Assoc. Advmt. Ani. Breed. Genet. 17: 29–32.

**Gardner, G.E., Glendenning, R., Brumby, O., Starling, S., Williams, A.** 2015. The development and calibration of a dual X-ray absorptiometer for estimating carcass composition at abattoir chain-speed. In 'Farm Animal Imaging.' (Eds C Maltin, C Craigie, L Bunger. Edinburgh, UK.)

**Gilmour, A.R., Gogel, B.J., Cullis, B.R. & Thompson, R.** 2009. 'ASReml user guide release 3.0.' (VSN International: Hemel Hempstead HP1 1ES, UK).

**Mortimer, S.I., van der werf, J.H.J, Jacob, R.H., Pethick, D.W., Pearce, K.L., Warner, R.D., Geesink, G.H., Hocking Edwards, J.E., Gardner, G.E., Ponnampalam, E.N., Kitessa, S.M., Ball, A.J. & Hopkins, D.L.** 2010. Preliminary estimates for genetic parameters for carcass and meat quality traits in Australian sheep. Ani. Prod. Sci. 50:1135-1144.

**Swan, A.A., Brown, D.J. & van der Werf, J.H.J.** 2014. Genetic variation within and between sub-populations of the Australian Merino breed. Ani. Prod. Sci. 56(1): 87-94.

**van der Werf, J.H.J., Kinghorn, B.P. & Banks, R.G.** 2010. Design and role of an information nucleus in sheep breeding programs. Ani. Prod. Sci. 50: 998-1003.

**van der Werf, J.H.J.** 2005. MTINDEX, Multiple trait/desired gains 10-trait version. [https://jvanderw.une.edu.au/mtindex\\_desgains10T.xls](https://jvanderw.une.edu.au/mtindex_desgains10T.xls) (Accessed December 2017)