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Abstract

Since the preliminary research in 2017 the DEXA technology and the algorithms behind the conversion of the DEXA image to measures of lean, bone and fat have been updated (Connaughton & Gardner 2023). Coinciding with these developments in technology there has been an influx of DEXA measurements on genetically informed animals via the MLA funded Resource Flock (van der Werf *et al.* 2010) and companion industry satellite flocks. The following study builds upon the preliminary research, with the objective to determine the genetic variation in DEXA measured lean and the suitability of using DEXA lean as part of Sheep Genetics which is the National Genetic Evaluation alongside or in conjunction with current CT derived lean meat yield records. Estimates on the DEXA lean data set produced a heritability of 0.32 ± 0.06 . However, this should not be considered the final parameter for implementation in genetic evaluations as the analysis is only a sire model (not all relationships accounted for) and genetic linkage between contemporary groups needs improvement. The phenotypic correlation between CT and DEXA lean measures was estimated at 0.84 ± 0.01 with a corresponding genetic correlation from the sire model of 0.77 ± 0.07 . Although more data is required, these results suggest that the DEXA-derived lean meat yield is likely to be the same genetic trait as the CT measured lean meat yield. These results are promising and plans in regards to the utilisation of DEXA data within Sheep Genetics national evaluation should begin.

Executive Summary

1. Since the preliminary research in 2017 the DEXA technology and the algorithms behind the conversion of the DEXA image to measures of lean, bone and fat have been updated (Connaughton & Gardner 2023).
2. Coinciding with these developments in technology, MLA and ALMTech have invested in recording CT and DEXA lean meat yield measurements on genetically informed animals via the MLA funded Resource Flock and companion industry satellite flocks. A total of 2,989 lamb carcasses were recorded via DEXA. The mean for DEXA measurements of lean, fat and bone were 54.0, 30.6, and 14.8, respectively.
3. DEXA lean was estimated to have a moderate heritability of 0.32 ± 0.06 using a univariate sire model. This is slightly lower but similar to expectations from heritability estimates for CT measured lean.
4. The phenotypic correlation between CT and DEXA lean measures was estimated at 0.84 ± 0.01 with a corresponding genetic correlation from the sire model of 0.77 ± 0.07 . The correlation is strongly favourable but is not one suggesting that there may be differences in how lean meat yield is measured across the technologies.
5. Although more data is required, these results suggest that the DEXA-derived lean meat yield is likely to be the same genetic trait as the CT measured lean meat yield. These results are promising and plans regards the utilisation of DEXA data within Sheep Genetics national evaluation should begin.

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1 Introduction

The financial value of a carcass is influenced by its saleable meat yield, which differs across supply chains, markets and cutting specifications. Consumer preferences in domestic and international markets has driven the industry in the past to produce meat cuts that are larger and leaner (Hall *et al.* 2000; Banks 2002; Laville *et al.* 2004). Terminal sheep breeders have been able to sustain genetic gains over a long period of time (Swan *et al.* 2009; Swan *et al.* 2017), partly due to simple 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 lack of carcass information, the majority of genetic gain for lean meat yield in lamb carcasses, has been reliant on indirect selection for growth, reduced fat depth and increased eye muscle depth. This has been recorded in live animals and in turn a correlated response has been achieved from index selection through the use of the LAMBPLAN indexes such as Carcass Plus and Lamb 2020. With the latest terminal indexes Eating Quality, Terminal Carcass Production and Lamb eating quality released in 2015 with an improved focus on improving lean meat yield and eating quality (Swan *et al.* 2015; Dehnavi & Swan 2022). The use of indicator traits is reliant on the strength of correlations holding up across the populations and is associated with slower genetic gains and potential tissue redistributed within the carcass.

In an earlier ALMTECH I technical report (Walkom *et al.* 2017), a study of DEXA measurements on 559 Merino and Merino cross lambs, produced moderately strong heritability estimates for DEXA-predicted values of fat, lean and bone. The phenotypic and genetic correlations between the DEXA value and the corresponding CT trait (% of carcass weight) were very strong, with estimates all greater than 0.82. Although more data was required, those preliminary results suggested that the DEXA-derived traits may be considered the same genetic trait as the CT measured traits.

Since the preliminary research in 2017 the DEXA technology and the algorithms behind the conversion of the DEXA image to measures of lean, bone and fat have been updated (Connaughton & Gardner 2023). Coinciding with these developments in technology there has been an influx of DEXA measurements and some additional CT measurements on genetically informed animals via the MLA funded Resource Flock (van der Werf *et al.* 2010) and companion industry satellite flocks. The following study builds upon the preliminary research, to determine the genetic variation in DEXA measured lean and the suitability of using DEXA lean as part of the National Genetic Evaluation alongside or in conjunction with current lean meat yield records.

2 Methodology

2.1 DEXA Data

Dual-energy X-ray absorptiometry (DEXA) is rapidly gaining acceptance as a reference method for analysing body composition (Pietrobelli *et al.* 1998). Both CT and DEXA are based

on the measurement of the attenuation of X-rays (photons) passing through a carcass (post-mortem). Tissues or elements in the body or carcass are characterized by specific mass attenuation coefficients, depending on the photon energy level being applied for the measurement (Scholz *et al.* 2015). DEXA (sometimes with the nomenclature 'DXA' (ISCD, 2013)) utilises two X-ray beams with different energy levels (high and low X-ray photon energy level) that are aimed at the carcass.

DEXA records were collected as part of the MLA funded Resource Flock and its previous iteration the Information Nucleus Flock (van der Werf *et al.* 2010). DEXA was also recorded from commercial (seedstock, non-research) animals as satellite flocks to the MLA Resource flock. This process involved animals from two different sources: i) surplus animals – animals selected based on phenotypic or genetic performance, and ii) structured progeny test – when dams were joined to sires to generate progeny for testing.

A total of 2,989 lamb carcasses were recorded via DEXA and represent 604 sires and 22 sire breeds. The carcasses were killed at an average age of 204 days and a hot carcass weight of 25.1 kg (Table 1). The mean for DEXA measurements of lean, fat and bone were 54.0, 30.6, and 14.8, respectively. The mean DEXA lean within kills ranged from 49.0 to 56.4 across the 17 satellite projects (Table 1).

Table 1: Data summary of DEXA measurements from the Resource Flock and associated satellite flocks (SF).

	Sire Breed	Animals	Sires	Age (days)		HCWT (kg)		DEXA Lean	
				Mean	SD	Mean	SD	Mean	SD
All Animals	Mix	2,989	604	240	77	25.1	4.5	54.0	4.3
RF Animals	Mix	1,290	413	298	56	24.4	4.8	54.2	5.7
SF 1	Poll Dorset	131	19	123	7	24.3	3.7	55.2	2.7
SF 2	Poll Dorset / White Suffolk	42	10	290	19	24.2	2.3	54.8	1.8
SF 3	Poll Dorset	24	4	218	4	24.0	2.8	53.8	1.7
SF 4	Poll Dorset	47	9	321	10	25.9	2.0	54.5	1.9
SF 5	Poll Dorset	219	20	140	7	27.9	3.8	51.4	2.4
SF 6	White Suffolk	15	3	221	6	24.5	1.4	52.2	1.7
SF 7	White Suffolk	35	11	262	16	32.3	2.5	49.0	1.7
SF 8	White Suffolk	101	14	303	20	26.3	3.2	56.0	2.0
SF 9	White Suffolk	82	5	263	37	22.6	4.7	56.4	3.2
SF 10	White Suffolk	55	6	185	2	31.1	4.0	52.8	1.9
SF 11	Composite Maternal	50	21	233	0	24.7	2.8	51.1	1.9
SF 12	Texel	232	16	157	27	25.1	4.8	55.0	3.0
SF 13	Suffolk	116	10	198	0	26.5	3.6	52.7	1.9
SF 14	White Suffolk	164	15	160	0	23.7	2.7	54.3	2.2
SF 15	Composite Terminal	200	9	169	5	24.1	2.5	53.8	2.2
SF 16	Booroola	12	2	221	7	22.0	2.5	53.3	2.1
SF 17	Border Leicester / White Suffolk / Merino / Composite Maternal	174	32	251	8	26.0	5.0	53.5	2.7

2.2 CT Data

Carcases were transported for CT scanning to either Murdoch University (Picker PQ 5000 spiral CT scanner) or the University of New England (Picker, Bavaria, Germany) within 72 h of slaughter to determine the proportions of fat, lean and bone. Prior to scanning, the carcasses were split into three primal components: fore-section, saddle and hind section, to enable more rapid post scanning processing of the CT images for the distribution analysis. The fore section was separated from the saddle by a cut between the fourth and fifth ribs. The hind section was separated from the saddle by a cut through the mid-length of the sixth lumbar vertebrae. The method used for determination of muscle, fat and bone was similar to that described by Gardner *et al.* (2010), with the discrimination between fat, lean and bone adapted from work by Alston *et al.* (2005). A more detailed description of the CT scanning protocol and image analysis is presented in (Anderson *et al.* 2015).

CT measured lean meat yield records were available for a total of 3,381 carcasses. The lamb carcasses represented 22 different sirebreeds and 821 sires. The mean weight (and range) of the CT scanned lamb carcasses was 23.7 kg (stdev = 4.39 kg), with the mean CT lean of the carcasses 57.62% (stdev = 3.47 %). Only 752 carcasses (320 sires represented) from the Resource Flock had both a CT lean and DEXA lean record.

2.3 Statistical analysis

The DEXA lean records were analysed using a series of uni-variate models in ASReml (Gilmour *et al.* 2015). The analysis was carried out with a sire model that incorporated each sire's pedigree. Maternal effects were not tested as there were insufficient records. The fixed effects model included birth type, age, age of dam, age of dam squared and sire breed. Contemporary group was fitted as a sparse fixed effect. Contemporary group was defined by breed, flock, management group, sex, date of measurement and kill group (Huisman *et al.* 2008). Carcase weight was not fitted as a co-variate. The sire model did not include genetic group effects to avoid issues with analyses converging due to the small number of records. It should be noted 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.

The genetic correlation between DEXA lean and CT lean was calculated from a bi-variate model in ASReml. The fixed effects model fitted to CT lean and DEXA lean was as described for the univariate analysis of DEXA lean. Contemporary group was fitted as a sparse fixed effect. Carcase weight was not fitted as a co-variate in this analysis.

3 Results and Discussion

3.1 Genetic Evaluation of DEXA Lean

The previous preliminary genetic evaluation of DEXA Lean by (Walkom *et al.* 2017) reported a heritability of 0.55 ± 0.12 on a 559 animal subset of this study. Estimates on the larger DEXA lean data set produced a slightly lower heritability of 0.32 ± 0.06 (Table 2). The heritability is

most likely closer to the true heritability. However, this should not be considered the final parameter for implementation in genetic evaluations as the analysis is only a sire model (not all relationships accounted for), thus genetic group effects were not accounted for and genetic linkage between contemporary groups needs improvement.

This supports previous studies of CT measured lean, where moderate to high heritability's were reported in Charolais (0.47), Suffolk (0.45), Texel (0.46; (Jones *et al.* 2004), Norwegian White (0.57; (Kvame & Vangen 2007)) and Scottish Blackface (0.48; (Karamichou *et al.* 2006)). Heritability for CT lean (kg), in the Resource Flock population, has previously been reported as 0.53 (0.63 if carcass weight fitted as covariate) (Walkom *et al.* 2021).

Alexandri *et al.* (2022) previously concluded, data collected from the satellite flocks can be used to complement managed progeny test sites to create an industry reference population. The effectiveness of commercial data depends on the trait measured (completeness of data and good representation of the flock's diversity) and the influence of fixed effects recorded on the flock. These conclusions are supported in this study with heterogeneous variation observed across the flocks. The heritability of DEXA lean varied from 0.29 ± 0.10 to 0.43 ± 0.11 (Table 2) when the satellite flocks were analysed one by one with the RF data. The variation in heritability across flocks is within the standard error of estimation suggesting that the data from the satellite flocks reflects what is observed in the Resource Flock.

Table 2: Genetic evaluation of DEXA lean and the impact of individual satellite flocks (SF) on variance estimates. *Additive variance is estimated as four times the estimated sire variance.

	Phenotypic Variance	Additive Variance*	Residual Variance	Heritability
All Animals	5.53 (0.15)	1.82 (0.40)	5.08 (0.15)	0.32 (0.06)
RF Animals	5.76 (0.24)	2.17 (0.71)	5.22 (0.25)	0.37 (0.11)
RF & SF 1	5.85 (0.23)	2.36 (0.68)	5.26 (0.23)	0.40 (0.11)
RF & SF 2	5.69 (0.23)	2.26 (0.70)	5.13 (0.24)	0.39 (0.11)
RF & SF 3	5.72 (0.23)	2.18 (0.70)	5.18 (0.24)	0.38 (0.11)
RF & SF 4	5.69 (0.23)	2.16 (0.69)	5.15 (0.24)	0.37 (0.11)
RF & SF 5	5.76 (0.22)	1.68 (0.60)	5.34 (0.23)	0.29 (0.10)
RF & SF 6	5.74 (0.24)	2.21 (0.71)	5.19 (0.25)	0.38 (0.11)
RF & SF 7	5.70 (0.23)	2.22 (0.70)	5.15 (0.24)	0.39 (0.11)
RF & SF 8	5.64 (0.22)	2.14 (0.68)	5.10 (0.23)	0.37 (0.11)
RF & SF 9	5.89 (0.24)	2.59 (0.72)	5.24 (0.24)	0.43 (0.11)
RF & SF 10	5.69 (0.23)	2.11 (0.69)	5.16 (0.24)	0.37 (0.11)
RF & SF 11	5.69 (0.23)	2.11 (0.69)	5.16 (0.24)	0.37 (0.11)
RF & SF 12	5.83 (0.22)	2.25 (0.64)	5.27 (0.22)	0.38 (0.10)
RF & SF 13	5.60 (0.22)	2.00 (0.66)	5.10 (0.23)	0.35 (0.11)
RF & SF 14	5.68 (0.22)	1.86 (0.63)	5.21 (0.23)	0.32 (0.10)
RF & SF 15	5.70 (0.22)	1.76 (0.63)	5.26 (0.23)	0.30 (0.10)
RF & SF 16	5.76 (0.24)	2.25 (0.72)	5.20 (0.25)	0.39 (0.11)
RF & SF 17	5.94 (0.23)	2.25 (0.69)	5.38 (0.24)	0.37 (0.11)

3.2 Genetic Correlation with CT Lean

The heritability of CT lean and DEXA lean in the bi-variate analysis was 0.42 ± 0.06 and 0.37 ± 0.07 , respectively. The phenotypic variance was similar for the two traits with the slightly higher variance observed for CT lean (6.13 ± 0.15) compared to DEXA lean (5.17 ± 0.13). The phenotypic correlation between CT and DEXA lean measures was estimated at 0.84 ± 0.01 with a corresponding genetic correlation from the sire model of 0.77 ± 0.07 . The correlation is strongly favourable but is not one suggesting that there may be differences in how lean meat yield is measured across the technologies. The lower than expected genetic correlation is in part due to the limitations of the data and the low number of sires with progeny recorded for both traits.

3.3 Technical notes on DEXA data collection

It should be noted that during this analysis several cohorts of DEXA data was found to contain data quality issues, resulting in the wrong DEXA lean records being assigned to animals. As DEXA records become available to industry greater effort will need to be made to ensure DEXA records and carcasses are correctly linked to the animal in the database. Until hook tracking is reliably implemented in plants with DEXA, collection of these data should be observed by technical staff to ensure animal identities are correctly linked to carcass and DEXA data. To assist with quality control all consignments should have pre-slaughter weights and condition scores immediately prior to the kill.

4 Conclusions

Although more data is required, these results suggest that the DEXA-derived 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.

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