[OFFICIAL]

Final report

Sheep meat eating quality prediction from dual energy X-ray absorptiometry

Project code: V.TEC.2500 Sheep meat eating quality prediction using dual energy X-ray absorptiometry.

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Abstract

Commercial processing plants in Australia have installed on-line DXA (dual energy x-ray absorptiometry) systems that can accurately and precisely predict lamb carcass composition. A DXA system has previously demonstrated a relationship between eating quality and the R value of carcass bone. This relationship is thought to reflect the effect of increasing maturity which decreases the eating quality of some cuts, similar to the association between ossification score and eating quality in cattle.

This project investigates the relationship between DXA images from four flocks. Sheep have been DXA scanned post slaughter at chain speed and their subsequent eating quality assessed. In this experiment DXA bone R has been shown to demonstrate a negative relationship with the MQ4 score within 3 flocks in range of cut and cook combinations across the carcass. The effect appears to be strongest in the saddle region with effects in the loin grill, rack cutlet roast and eye of rack grill. There were effects in other cuts in the hind section (outside grill, rump grill and topside grill). The fore section showed variation in the associations, with the roast shoulder demonstrating a negative and the eye of shoulder grill a positive relationship with DXA bone R.

Given the recent update of the MSA sheepmeat eating quality prediction model to include HCWT, loin IMF % and lean %, the DXA bone R term was included in this model and remained significant. The results for the associations with the eating quality traits that comprise the MQ4 score were similar, with a more pronounced magnitude of effect observed between DXA bone R and tenderness. To date the mechanism of the association between DXA bone R and eating quality is unclear. Although it is thought to be linked to maturity, the effect is not accounted for by loin shear force which also increases with maturity. The association of DXA bone R with eating quality was least consistent in flocks with a narrow age range with less variation in DXA bone R. Further experimental work should focus on expanding the number of samples, and ensuring a large range in animal age and explore the mechanism behind the relationship between DXA bone R and eating quality.

Executive summary

Background

Eating quality is an important attribute to consumers who express a willingness to pay for a high-quality product. The current Meat Standards Australia MSA sheepmeat eating quality prediction model incorporates carcass measures such as hot carcass weight, loin intramuscular fat (IMF) % and carcass lean %. This enables processing plants to sort carcasses prior to bone out for better utilisation and allow product segregation into quality grades. The carcass lean% input value can be predicted by abattoirs that have installed on-line Dual Energy Xray Absorptiometry (DXA) systems, with these DXA devices now accredited to predict computed tomography fat, lean and bone %. Previous studies have demonstrated a relationship between eating quality and the R values of carcass bone from these DXA images (Anderson et al., 2021). The relationship between DXA and eating quality in this experiment varied across the cuts assessed and appeared to be independent of loin intramuscular fat and carcass lean % (Anderson et al., 2021). Since this earlier study the methodology used to define DXA bone pixels has been improved, warranting further investigation into the relationship between DXA bone R and eating quality of cuts across the carcass.

The results of this experiment could identify a new trait that is directly linked to eating quality which could be incorporated into the Meat Standards Australia sheepmeat eating quality prediction model alongside the current traits (hot carcass weight, IMF % and carcass lean %). The implications of this are significant for processors and retailers, as enhanced prediction of eating quality of individual cuts under a variety of different cooking methods would enable better segregation of product into elite quality brands, and ultimately. This allows for value-based trading based on individual animal eating quality and for some supply chains allow brands to market based on quality and premium pricing. Although there is not currently price signalling based on eating quality flowing back to producers this is likely, with improved eating quality prediction using DXA bone potentially accelerating this process.

Objectives

- Explore the relationship between DXA bone R and eating quality traits across a range of cuts and flocks to and the inclusion of DXA bone R in the Meat standards Australia eating quality prediction model
- Evaluate whether there are differences in the predicted composition of sheep when they are scanned hot versus cold using in-line DXA scanning – completed, with further work required to investigate this research question
- Determine and outline the next steps required to develop a DXA related eating quality trait in collaboration with the Industry Calibration Working Group and Meat Standards Australia.

Methodology

A total of 4 data sets were compiled where sheep had been DXA scanned post slaughter in the abattoir and had subsequently been tested for eating.

- A DXA bone R values was calculated using the average R values of bone pixels which were identified using a recently refined method of identifying bone
- Linear mixed effects models were used to determine the association of DXA bone R with MQ 4 scores of a range of cut and roast cuts. The eating quality traits that comprise the MQ4

score (tenderness, juiciness, liking of flavour and overall liking) were also tested individually for their associations with DXA bone R.

- The analysis was performed with all data combined and also on an individual flock basis to better assess the magnitude of the relationship between DXA bone R and individual cuts.
- All animals had a range of phenotypic traits collected at slaughter (e.g hot carcass weight, loin intramuscular fat %, lean %, loin shear force (N), GR tissue depth). Models to also tested with these terms along-side DXA bone R to establish whether there is an independence of the association of DXA with eating quality.

Results/key findings

DXA bone R demonstrated a negative association with the MQ4 score of a range of cuts across the carcass. The relationship remained even when models were corrected for IMF%, carcase lean%, and carcass weight, indicating that DXA bone R describes MQ4 variation that is independent of these other traits. This is a crucial finding given that all of these traits are included in the existing MSA eating quality model. The results were most consistent in the grilled loin where there was a reduction in MQ4 within 3 of the 4 flocks analysed. There was only 1 flock in this study where eating quality was not influenced by DEXA bone R, however in this case the flock had no range in animal age, supporting the assertion that DEXA bone R may be a proxy for the effect of maturity on eating quality.

Benefits to industry

This research provides 3 keys benefits:

1) Enables supply chains to underpin elite brands with an enhanced eating quality claim.
2) Will allow accelerated adoption for any processors utilising a hot DXA system.
3) Enhances the MSA cuts-based model, with this complexity setting Australia apart from other nations with eating quality prediction systems in lamb.

Future research and recommendations

To robustly determine the coefficients for this trait, a carefully constructed experimental design is required. This should test a variety of cuts and cooking methods sampled from animals of a diverse age range are slaughtered as one group (removing the kill group effect). This should be done across a series of sites where DXA systems are available, with at least multiple reps undertaken at each site.

Furthermore, the biology of the trait should be investigated as this will help to ensure the proper integration of this trait into the MSA model and enhance the credibility of its implementation both nationally and internationally.

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1. Background

1.1 Project planning and design

This project investigated the relationship between DXA (dual energy x-ray absorptiometry) images from sheep scanned within processing plants and their subsequent eating quality as assessed by consumers. There are many production, genotypic and environmental factors that contribute to variations in eating quality. In cattle, the MSA eating quality model is a well-established method for using measured traits to provide cut based predictions of eating quality. In sheep a pathways system for predicting eating quality has historically been used in lamb, however more recently a cuts-based eating quality has been established which uses individual carcass measures to predict eating quality (Pannier et al., 2025).

Within the beef MSA model ossification is used in reference to the manual grading post slaughter of the calcification of the sacral and dorsal vertebrae (Polkinghorne et al., 2008). Ossification is a measure of animal maturity, with increasing maturity linked to reductions in eating quality through a negative relationship with tenderness (Shorthose & Harris, 1990). In beef it has demonstrated a better relationship with eating quality than age, prior to skeletal maturity (Bonny et al., 2016). In lamb there is evidence that eating quality decreases as animal age increases (Hopkins et al., 2006; Pethick, Davidson, et al., 2005).

Some Australian abattoirs have installed on-line Dual Energy Xray Absorptiometery (DXA) systems that can accurately and precisely predict lamb carcass composition, with these DXA devices now able to be accredited to predict computed tomography CT fat, lean and bone % (Connaughton et al., 2024). A key focus of the Advanced Livestock Measurement Technologies (ALMTech) project was the development and integration of lamb DXA within the lamb industry, culminating in the installation of 6 of these systems across Australia. The images captured using DXA are at two different energy levels, with the ratio of the pixels expressed as a ration (R value) which reflects the atomic mass of the tissue being scanned (Pietrobelli et al., 1996). In humans, DXA has been well established as a measure of changes in bone mineral density (Bachrach, 2000; Pouilles et al., 1991; Syed & Khan, 2002) and has been used to assess bone mineral density in different age classes of beef cattle (López-Campos et al., 2018). A commercial DXA system has been shown to demonstrate a relationship between eating quality and the R values of carcass bone and individual bones such as the lumbar vertebrae from a DXA scanned carcass (Anderson et al., 2021). The relationship between DXA and eating quality in this experiment varied across the cuts assessed and appeared to be somewhat independent of loin intramuscular fat and carcass lean % (Anderson et al., 2021). This relationship represents the potential to include a measure of maturity in the sheep meat MSA cuts-based eating quality model.

Since the study by Anderson et al. (2021) was published, an additional 4 datasets have been identified where both consumer eating quality data and DXA images exist. Furthermore, these DXA images were collected from systems with the new calibration and image acquisition and analysis methods installed. This is crucial, as the previous analyses demonstrated a clear lack of calibration between data sets. It is hypothesised, based on previous experiments that a relationship will exist between DXA bone R values and eating quality in sheep. Given the recent advancements in image processing we also speculate that this relationship will be more consistent across data sets and have increased precision of prediction. A challenge of this experiment is the ability to compare the relationship of bone DXA and eating quality from sheep scanned on different days and locations. Although the DXA systems at different abattoirs have a calibration mechanism between sites and days, the comparison of sheep scanned on different days and location represent a wide variation in genetics and environment and developing a calibrated input to include in the MSA sheep eating quality model is required.

The overarching aim was to determine if the relationship between the bone DXA values and eating quality is reproducible, enabling it to be used as an input into the Meat Standards Australia (MSA) sheep eating quality model. If successful, this work would lead to a future project that in collaboration with MSA would acquire DXA images and eating quality measurements across a greater range of cuts, establish an auditable calibration system, alteration to the cuts-based MSA sheep-meat model, and ultimately Australian Meat Industries Language and Standards Committee approval for this commercial measurement and its use within MSA grading systems.

2. Objectives

The overall objective of the project is to conduct a scoping study to assess the potential to predict eating quality in sheep meat using DXA images, train initial prediction equations, and assess the feasibility of establishing a DXA bone trait and associated calibration system. The specific objectives of the project are:

1. Compile the 3 identified data and image sets that exist where both eating quality data and DXA images exist
2. Assess the feasibility of establishing a calibration system and training initial prediction equations
3. Evaluate, in consultation with MSA how prediction equations could be integrated into the MSA sheep cuts model, including scrutiny of 2016 DXA images comparing hot versus cold DXA to assess the potential for differences in DXA bone values across scanning times.
4. Determine and outline the next steps required to develop this trait, in collaboration with the Industry Calibration Working Group. This includes assessing the potential for introducing this trait into the AUS-MEAT trading language via the Australian Meat Industries Language and Standards Committee.
5. Conduct a workshop with the MSA team and selected industry representatives to provide an update on project findings and prioritise next steps.

3. Methodology

3.1 Experimental design and slaughter details

The current data has been obtained from animals originating from 3 separate experiments which were conducted using three flocks slaughtered in two abattoirs. A 4th data set was identified and has also been included as an additional part of this project.

Flock 1 (n = 120) were slaughtered at Gundagai Meat Processors and consisted of Merino ewes. These animals were born in 2014 at the Camden research site and slaughtered in 2020 at Gundagai over 2 consecutive days along with 20 unrelated lambs which were also included in the analysis of Flock 1 sheep.

Animals from Flock 2 (n = 98) and 3 (n = 72) were slaughtered at an abattoir in Katanning, Western Australia, and originated from the Meat and Livestock Australia Resource Flock Project. Data was available for a range of genetic and phenotypic traits.

Flock 4 consisted of animals that were enrolled in an eating quality experiment (n= 276) with a more limited range of cuts collected. These animals were sourced from a number of commercial farms in Western Australia and slaughtered at an abattoir in Katanning, Western Australia.

3.2 Carcass measurement and sampling

Carcass measures

Following slaughter, all carcasses were trimmed according to AUSMEAT standards (AUSMEAT 2005) and hot standard carcass weight (HCWT) (kg) was recorded. Carcasses were chilled overnight (3-4 °C) before further sampling, with carcass measures recorded, which included:, GR tissue depth (GR; measured 110 mm from the midline to the lateral surface of the 12th rib using vernier callipers), C-site fat depth (mm), eye muscle depth and width (mm).

A 40 g sample of the left loin cut (AUS-MEAT code 5150) was collected for the determination of intramuscular fat (IMF) %. This was done at the same time that cuts were collected for sensory testing. IMF samples were freeze-dried in a Coolsafe 95-15 Pro (Scanvac, Lillerød, Denmark) and chemical fat determined after analysed using near-infrared technology (Technicon InfrAlyser 450 (19 wavelengths)) (Perry et al., 2001).

As part of the experimental design the lambs were originally used for, an additional 65 g of loin was collected for the determination of shear force. All samples were vacuum packed, aged for 5 days at 1°C, then stored at -20°C prior to testing. Laboratory processing of samples was performed at the University of New England Meat Science Department (Armidale, New South Wales, Australia) according to a methods described by Thompson et al. (2005).

3.3 Dual energy x-ray absorptiometry scanning and image analysis

3.3.1 DXA scanning and image analysis

Animals underwent scanning immediately after weighing in the abattoir. The DXA image calibration and standardization has previously been described (Connaughton et al., 2020; Connaughton et al., 2024; Gardner et al., 2018) but is briefly summarised. A calibration scan consisting of a dark image of the detectors without X-ray production and a light image of fully unattenuated detectors with X-ray production were collected at the start of each production day for the purpose of standardizing each image produced throughout the production day. The unattenuated space in each image was standardized to a theoretical maximum value of 4095 for the purpose of the R-value equation as follows:

$$R = \frac{\ln\left(\frac{I_L}{4095}\right)}{\ln\left(\frac{I_H}{4095}\right)} \qquad (Eq. 1)$$

Here I_L and I_H are the attenuation values of the low and high energy detectors. To counteract any drift in values throughout the production day, the unattenuated space was sampled row by row, and all pixels in the row were scaled up or down by the same factor that the unattenuated space value varied from 4095.

The start-of-day calibration sequence involved the scanning of a synthetic phantom block, which extended across the entire height of the detector array, and consisted of 40 mixtures of acrylic, nylon, and high-density polyethylene, each combining to a thickness of 50 mm. This algorithm required only the two centermost acrylic blocks for calibration, as this material is most similar to the soft-tissue seen in the DXA scans (Kelly et al., 1998). The R-value for each of the two centermost acrylic blocks was calculated by Eq 1., and the mean of the two was calculated as R_A. Concurrently, the proxy for thickness was calculated for the acrylic blocks as the natural log of the low energy attenuation values, which were then also averaged as LE_A. The values of R_A and ST_{LE} were used to adjust the DXA images throughout the production day through linear transformations, which were determined by regressing these values from three different DXA devices and creating adjustment equations as described by Connaughton et al. (2024). These equations allow adjustments to the R value throughout the day and a convolution kernel was applied to each image as a smoothing algorithm (Connaughton et al., 2020).

A new method to identify bone containing pixels has been recently developed (IAEA, 2011) (Connaughton et al., 2024).

$$R_S * \ln\left(\frac{I_H}{4095}\right) - \ln\left(\frac{I_L}{4095}\right) \qquad (Eq. 2)$$

In this equation, R_S is the R-value of the adjacent soft tissue, and values greater than zero are indicative of containing bone. The limitation of this approach is that it requires either a consistent R-value for the soft tissue across the entire subject, or a known edge of the bone-soft tissue border. The existing DXA algorithm has no capacity for either, therefore a modification to this equation (Eq. 3) was derived:

$$\frac{\ln(R^2)}{t} \qquad (Eq. 3)$$

Where R is the R-value for the pixel of interest, and t is a proxy for thickness calculated as the natural log of the low energy image pixel value. The mean of this value across the whole carcass is then used as the threshold value, where pixels of a greater value to the mean are allocated as bone-containing, and pixels of a lesser value to the mean are allocated as soft-tissue only.

3.3.2 Calculation of CT fat %, lean % and bone %

Following the identification of bone containing pixels, the total weight of soft tissue in the carcass (STWt) was calculated through a function of the proportion of bone-containing pixels within the total carcass, hot carcass weight (HCWT), and the natural log of the phantom-adjusted mean low energy attenuation of the soft-tissue-containing pixels (ST_{LE}) acting as a proxy for tissue thickness. Following this, the proportion of fat in the soft-tissue-containing pixels (STfat%) was calculated through a function of the phantom-adjusted STLE, and the phantom adjusted mean of the R-values for the soft-tissue-containing pixels. The predictions of CT fat %, CT lean %, and CT bone % were then calculated (Connaughton et al., 2024), with the total of all three equaling 100%, as all three are functions of STWt.

3.3.3 Determination of bone DXA variables

All bones of the carcass were isolated using the newly developed bone algorithm described above and the mean and standard deviation of the R values calculated, which was termed DXA bone R Mean and DXA bone R SDev. In previous analysis individual bones (humerus, lumbar vertebrae and femur) were identified on the DXA images and the bone R and standard deviation of these isolated bone regions used in the analysis. With the improvement in bone isolation of the entire carcass, individual DXA bone R values are no longer used in the analysis.

3.4 Eating quality samples and assessment

Eating quality samples were collected from all animal's post slaughter, however the range of cuts collected from each site and ageing times differed. The number of animals sampled, the cuts collected, and their cooking methods are reported in Table 1

Table 1. Number and types of cuts, cooking methods and days of ageing for eating quality samples of animals from Flock 1, 2, 3 and 4.

		Flock 1		Flock 2		Flock 3		Flock 4	
Cut	**Cook method**	**Number of animals tested**	**No days aged**	**Number of animals tested**	**No days aged**	**Number of animals tested**	**No days aged**	**Number of animals tested**	**No days aged**
Eye of shoulder	Grill	-	-	98	10	72	10	-	-
Shoulder	Roast	118	10	-	-	-	-	-	-
Eye of rack	Grill	-	-	97	10	72	10	84	5
Rack cutlet	Roast	118	10	-	10	-	-	-	-
Loin	Grill	117	10	97	10	72	10	264	5
Knuckle	Grill	120	10	98	10	72	10	276	5
Outside	Grill	120	10	98	10	72	10	-	-
Rump	Grill	120	10	98	10	72	10	-	-
Topside	Grill	120	10	98	10	72	10	276	5
Topside	Roast	117	10	-	-	-	-	-	-

Sensory testing for grilled lamb cuts was conducted according to (Thompson et al., 2005), with cuts cooked on a Silex grill (S-tronic steaker, Silex, Hamburg, Germany) with the top plate set to 185 °C and bottom plate to 190 °C. Steaks were grilled to an approximate internal temperature of 65 °C as measured by a thermometer, rested for 90 seconds and halved before serving.

The roast cuts were cooked in an Electrolux 10 tray dry oven and set to a temperature of 160 °C. To cook to an internal temperature of 65 °C, the roasts were removed from the oven at an internal temperature of 60 °C and rested for 10 minutes. Roasts were then sliced into 4 mm samples and ten suitable slices from each cut were selected for consumer testing. External fat and connective tissue seams were removed and slices trimmed to 50 mm x 50 mm x 4 mm thick. The 10 consumer samples were placed in steel pans which were maintained at a temperature of 50 °C until serving. The exception to this was the rack cutlet in Flock 1 which was sliced into cutlets approximately 2.5 cm wide and served on the bone.

Untrained consumers were used to score each sample on a scale from 0 to 100, for tenderness, juiciness, liking of flavour, and overall liking. A score of 0 indicates a tough, dry, unliked sample. The study was conducted in accordance with the Declaration of Helsinki, and the protocol as approved by the Ethics Committee of Murdoch University on 11 October 2018 (2018/129).

3.5 Hot versus cold DXA scanning

As part of the objective relating to hot versus cold DXA scanning, historical data was obtained from an experiment conducted at a third processing plant in Bordertown (South Australia). These animals were separate to the animals included in Flocks 1, 2 and 3 and therefore unrelated to the eating quality analysis in this report. Sheep carcasses (n = 48) were scanned immediately post slaughter (hot) and then 24 hours later after they had been chilled (cold). These two scans were acquired at approximately the same time of day. It should be noted that this data was collected in 2016. At this time the modern scanning procedure and calibration system developed by Connaughton et al (2021) was not installed, and therefore the image values do not align with modern images. This was also prior to the development of the advanced bone identification techniques. None-the-less the raw R values from these images provide some capacity to compare bone DXA values acquired from hot versus cold carcases.

3.6 Statistical analysis

The statistical computing language R and the tidyverse suite of packages was used for data cleaning, filtering and analysis (Team, 2013; Wickham et al., 2019).

3.6.1 Correlations

Simple correlations were determined using Cor Matrix, R. Correlations between DXA measures (DXA bone R Mean and DXA bone R SDev) were made with other carcass measures including HCWT, c-site fat depth (mm), loin IMF % and DXA lean, fat and bone %. These correlations were made within a Flock (Flock 1, 2, 3 or 4).

3.6.2 Prediction of eating quality

Eating quality data was analysed using a linear mixed effects model in R using the lmerTest package (Kuznetsova et al., 2017), with the dependent variable MQ4 score. The MSA MQ4 score was derived as per Pannier et al. (2025):

MQ4 = (0.3 × tenderness) + (0.1 × juiciness) + (0.3 × flavour liking) + (0.3 × overall liking)

Additionally, the individual eating quality traits (tenderness, juiciness, liking of flavour and overall liking were included as the dependent variable in certain models as described below.

Models predicting MQ4 with flock included as a random term

All 10 consumer tasting results for each sample tested were include in the data set. Initially, an analysis was performed which is aligned with the data structure of the recently published lamb MSA paper (Pannier et al., 2025) with all 4 data sets combined. The "base model" consisted of the concatenated term cut_cook along with HCWT, loin IMF % and DXA lean %, which represent key covariates in the MSA eating quality model (Pannier et al., 2025). The first order interaction of these covariates with cut_cook was also tested, with non-significant terms removed in a stepwise manner where $P > 0.05$. Random terms included animal identification, consumer identification within eating quality session and flock. A second model (DXA bone R) was constructed, which included all terms from the base model as well as DXA bone R and their interaction with cut_cook. Non-significant terms were removed in a stepwise manner ($P > 0.05$).

To ensure the independence of the effect of DXA bone R from DXA lean %, we constructed a third model which replaced DXA lean % with GR tissue depth along with interactions with cut_cook. Finally, to test whether DXA bone R was acting as a proxy for SF, we constructed Model 4 which included all the terms from the DXA bone R model (Model 2) along with shear force and its interaction with cut_cook.

Models predicting MQ4 within flocks (cut_cook_flock)

In the initial analysis described above there was concern that there would be groups of animals without sufficient range in DXA bone R which may potentially mask the effect of this covariate on eating quality (MQ4). As such a further series of models were constructed which allows the flexibility of the model to reflect the different cut_cook combinations within the flocks. In these models cut_cook_flock was included as a term in the model along with its interaction with the combinations of covariates HCWT, IMF %, lean %, GR tissue depth and SF. In these models, random terms included animal identification and consumer identification within eating quality session.

Individual flock analysis

The forced interaction of cut_cook_flock may have over parametrised some of the sub sets of data by forcing interactions that are not present in some flocks and potentially caused magnification of the effects. Therefore, a third analysis was performed where models were fitted within each of the individual flocks (1, 2, 3 and 4). Similar to the previous analysis, cut_cook was included along with interactions with the MSA terms (HCWT, IMF %, lean %). A second model was constructed where cut_cook was included along with interactions with HCWT, IMF %, lean % and DXA bone R. Finally a third variation where DXA bone R was included along with IMF % and lean % but without HCWT in the model. Random terms included animal identification and consumer identification within eating quality session.

Initially, MQ4 was tested as the dependent variable and subsequently the other eating traits were included individually (tenderness, juiciness, liking of flavour and overall liking). For each of these eating quality traits, the coefficients ± SD are shown along with the magnitude of the effects across 4 times the standard deviation of the DXA bone R range for all flocks combined as a comparison of the magnitudes of effects across the flocks. Additionally, the magnitude of effect for each cut is demonstrated across the 4 SD range of DXA bone R relevant for each flock.

Hot versus cold DXA scanning

Given the historical nature of the data used for this part of the analysis the original images were not available in a format that allowed the current DXA processing techniques to be applied to them. Additionally, there was more primitive calibration between days and throughout the day. Therefore, a simple comparison between R values for hot v cold DXA scanning was performed using a t-test for mean carcass R, soft tissue R and bone R. This was repeated for the standard deviation.

4. Results

4.1 Raw data

There is data available from four Flocks where there are DXA measures from the abattoir along-side eating quality assessment from a range of cuts. The raw mean ± SD (minimum, maximum) for HCWT (kg), c-site fat depth (mm), EMA, and DXA scanning measures are reported in Table 2.

The range of DXA bone R values across all 4 flocks was 1.22 to 1.36 (see Figure 1).

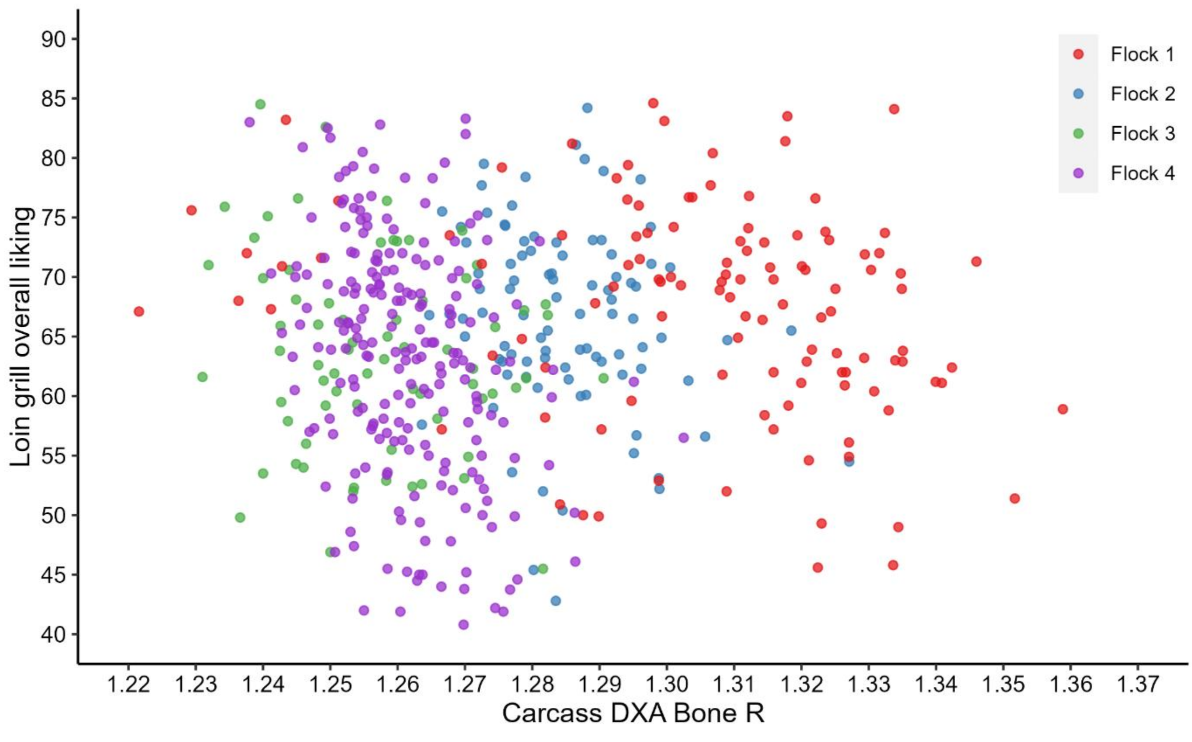

Figure 1. Plot of loin grill overall liking (average of 10 consumer scores) against the carcass DXA Bone R for Flocks 1, 2, 3 and 4.

Table 2. Raw Mean ± SD (min, max) for hot carcass weight (kg), c-site fat depth (mm), loin intramuscular fat (%), loin shear force (N), eye muscle area (cm²), carcass fat %, lean % and bone %, DXA Bone R and DXA Bone R standard deviation (Std) for sheep from Flocks 1, 2, 3 and 4.

	Flock 1			Flock 2			Flock 3			Flock 4		
	n	mean ± std	(min, max)	n	mean ± std	(min, max)	n	mean ± std	(min, max)	n	mean ± std	(min, max)
Hot carcass weight (kg)	120	20.11 ± 4.3	(13.50, 34.40)	98	22.29 ± 2.9	(12.80, 29.40)	72	28.39 ± 4.9	(17.80, 38.30)	220	22.63 ± 2.3	(18.00, 30.10)
C-site fat depth (mm)	120	2.35 ± 2.0	(0.00, 10.00)	98	1.99 ± 1.6	(0.00, 10.00)	72	3.69 ± 1.9	(0.00, 9.00)	228	3.63 ± 1.5	(1.00, 11.0)
GR Tissue depth (mm)	120	7.78 ± 6.3	(1.00, 25.00)	98	9.53 ± 4.6	(1.00, 21.00)	72	17.64 ± 6.1	(1.00, 28.00)	228	12.10 ± 4.1	(3.00, 22.00)
Loin intramuscular fat %	119	5.86 ± 2.4	(1.73, 13.16)	98	3.81 ± 1.3	(1.53, 11.20)	72	4.62 ± 1.0	(2.99, 6.76)	227	4.71 ± 1.4	(1.98, 9.31)
Loin shear force (N)	118	35.20 ± 6.8	(22.00, 60.60)	98	36.41 ± 9.6	(18.15, 67.72)	71	30.10 ± 4.9	(18.07, 43.38)	184	35.83 ± 11.2	(20.54, 85.02)
Loin eye muscle area (cm2)	120	10.82 ± 3.2	(1.44, 23.52)	98	11.96 ± 2.1	(7.45, 16.63)	72	15.99 ± 2.9	(9.75, 22.96)	228	12.63 ± 2.4	(2.20, 19.91)
Carcass DXA fat %	118	17.11 ± 6.6	(5.32, 38.98)	93	21.00 ± 4.4	(11.76, 32.02)	70	26.70 ± 3.2	(19.40, 33.08)	227	25.52 ± 2.8	(12.19, 32.06)
Carcass DXA lean %	117	59.36 ± 3.4	(50.94, 66.56)	93	58.41 ± 2.8	(49.67, 66.48)	70	56.09 ± 2.5	(50.77, 62.33)	227	56.34 ± 2.5	(51.55, 69.17)
Carcass DXA bone %	118	21.75 ± 3.6	(14.52, 30.09)	93	20.25 ± 1.8	(17.21, 27.28)	70	17.21 ± 1.0	(15.44, 20.70)	227	18.14 ± 1.0	(16.24, 22.74)
DXA bone R	118	1.31 ± 0.0	(1.22, 1.36)	93	1.29 ± 0.0	(1.26, 1.33)	70	1.26 ± 0.0	(1.23, 1.29)	227	1.26 ± 0.0	(1.24, 1.30)
DXA bone R SD	116	0.11 ± 0.0	(0.08, 0.17)	93	0.38 ± 0.0	(0.29, 0.48)	70	0.09 ± 0.0	(0.07, 0.10)	227	0.09 ± 0.0	(0.08, 0.11)

4.2 Correlations

Across all four flocks there was a moderate to high negative correlation between HCWT and DXA bone % ($P < 0.01$, range -0.76 to -0.87) (Table 3). The correlation between DXA bone R and HCWT was high in Flocks 1, 2 and 3 ($P < 0.001$, range -0.86 to – 0.89) (Table 3), however in flock 4 this correlation was much lower (- 0.45). There was a weak negative correlation between loin IMF % and loin SF which was significant in Flocks 1, 2 and 3 ($P < 0.01$, range -0. 27 to -0.43). Within all flocks there was a moderate negative relationship between loin IMF % and DXA lean %, ranging from -0.44 to -0.52 ($P < 0.01$, Table 3) There was a low negative correlation between IMF % and DXA bone R which was significant in Flock 2 ($P < 0.05$, -0.25) and site 3 ($P < 0.01$, -0.36)(Table 3). Loin shear force demonstrated a weak positive relationship with DXA bone R, however the strength of this relationship varied between flocks and was only significant in Flock 1 (0.30) and flock 4 (0.45) ($P < 0.01$).

Table 3. Partial correlations between slaughter measures for hot carcass weight, c-site fat depth (mm), loin intramuscular fat %, loin shear force (N), DXA measures of fat lean and bone %, bone DXA R and carcass bone R SDev.

	Hot carcass weight (kg)	C-site fat depth (mm)	Loin intramuscular fat %	Loin shear force (N)	C- site eye muscle area (cm2)	DXA fat %	DXA lean %	DXA bone %	DXA bone R	DXA bone R SDev
Flock 1										
Hot carcass weight (kg)	1.00	0.71***	0.10	-0.28**	0.75***	0.58***	-0.10	-0.76***	-0.86***	-0.31***
C-site fat depth (mm)	-	1.00	0.25**	-0.29**	0.51***	0.71***	-0.47***	-0.7***	-0.73***	-0.23*
Loin intramuscular fat %	-	-	1.00	-0.43***	-0.05	0.43***	-0.36***	-0.38***	-0.17	-0.05
Loin shear force (N)	-	-	-	1.00	-0.26**	-0.34***	0.14	0.4***	0.3**	0.03
C- site eye muscle area (cm2)	-	-	-	-	1.00	0.36***	0.07	-0.57***	-0.71***	-0.27**
DXA fat %	-	-	-	-	-	1.00	-0.77***	-0.89***	-0.75***	-0.19*
DXA lean %	-	-	-	-	-	-	1.00	0.42***	0.25**	-0.03
DXA bone %	-	-	-	-	-	-	-	1.00	0.91***	0.3**
Carcass bone R	-	-	-	-	-	-	-	-	1.00	0.38***
Carcass bone R SDev	-	-	-	-	-	-	-	-		1.00
Flock 2										
Hot carcass weight (kg)	1.00	0.53***	0.28**	-0.04	0.52***	0.69***	-0.29**	-0.84***	-0.86***	-0.53***
C-site fat depth (mm)	-	1.00	0.35***	-0.13	0.09	0.71***	-0.63***	-0.59***	-0.44***	-0.58***
Loin intramuscular fat %	-	-	1.00	-0.35***	-0.09	0.52***	-0.45***	-0.47***	-0.25*	-0.59***
Loin shear force (N)	-	-	-	1.00	0.25*	-0.23*	0.28**	0.15	0.07	0.2*
C- site eye muscle area (cm2)	-	-	-	-	1.00	0.18	0.15	-0.42***	-0.52***	-0.17
DXA fat %	-	-	-	-	-	1.00	-0.86***	-0.85***	-0.59***	-0.88***
DXA lean %	-	-	-	-	-	-	1.00	0.49***	0.15	0.73***
DXA bone %	-	-	-	-	-	-	-	1.00	0.88***	0.82***
Carcass bone R	-	-	-	-	-	-	-	-	1.00	0.45***
Carcass bone R SDev	-	-	-	-	-	-	-	-		1.00
Flock 3										
Hot carcass weight (kg)	1.00	0.39***	0.31**	-0.13	0.75***	0.71***	-0.56***	-0.87***	-0.89***	-0.84***
C-site fat depth (mm)	-	1.00	0.35**	-0.10	0.24*	0.7***	-0.71***	-0.48***	-0.56***	-0.44***
Loin intramuscular fat %	-	-	1.00	-0.17	0.28*	0.49***	-0.5***	-0.31**	-0.36**	-0.22
Loin shear force (N)	-	-	-	1.00	-0.07	-0.25*	0.27*	0.14	0.24	0.23
C- site eye muscle area (cm2)	-	-	-	-	1.00	0.53***	-0.38**	-0.75***	-0.69***	-0.55***
DXA fat %	-	-	-	-	-	1.00	-0.97***	-0.78***	-0.88***	-0.63***
DXA lean %	-	-	-	-	-	-	1.00	0.61***	0.77***	0.51***
DXA bone %	-	-	-	-	-	-	-	1.00	0.89***	0.74***
Carcass bone R	-	-	-	-	-	-	-	-	1.00	0.87***
Carcass bone R SDev	-	-	-	-	-	-	-	-		1.00

	Hot carcass weight (kg)	C-site fat depth (mm)	Loin intramuscular fat %	Loin shear force (N)	C- site eye muscle area (cm2)	DXA fat %	DXA lean %	DXA bone %	DXA bone R	DXA bone R SDev
						Flock 4				
Hot carcass weight (kg)	1.00	0.26***	0.17*	-0.28***	0.17*	0.38***	-0.15*	-0.76***	-0.45***	-0.35***
C-site fat depth (mm)	-	1.00	0.24***	-0.24**	0.00	0.54***	-0.49***	-0.33***	-0.48***	-0.28***
Loin intramuscular fat %	-	-	1.00	-0.27***	-0.02	0.48***	-0.44***	-0.27***	-0.39***	-0.19**
Loin shear force (N)	-	-	-	1.00	0.08	-0.51***	0.45***	0.32***	0.45***	0.33***
C- site eye muscle area (cm2)	-	-	-	-	1.00	-0.12	0.21**	-0.19**	0.04	0.06
DXA fat %	-	-	-	-	-	1.00	-0.94***	-0.49***	-0.8***	-0.47***
DXA lean %	-	-	-	-	-	-	1.00	0.17*	0.67***	0.4***
DXA bone %	-	-	-	-	-	-	-	1.00	0.6***	0.36***
Carcass bone R	-	-	-	-	-	-	-	-	1.00	0.77***
Carcass bone R SDev	-	-	-	-	-	-	-	-	-	1.00

*P < 0.05 ** P< 0.01 *** P < 0.001

4.3 Combined flock analysis to predict MQ4 scores

4.3.1 Combined data set analysis, assessing DEXA bone R impact on MQ4 across all flocks.

When all 4 flocks were combined and Flock was included as a random term, the terms used in the MSA eating quality prediction model (HCWT, IMF % and DXA lean %) were all significant predictors of MQ4 ($P < 0.01$, Table 4, Model 1), with the impact of these terms varying by cut and cook method.

The DXA bone R term was significant ($P < 0.01$) when included along with HCWT, IMF % and DXA lean % (Table 4, Model 2), with the magnitude of effect varied according to cut and cook method. The key covariates from Model 1 also remained significant, however the F Value for HCWT was considerably reduced, with this term no longer significant as a main effect.

Model 3 (Table 4) was designed to test the associations of DXA bone R with an alternative to DXA lean % (GR tissue depth) along with HCWT, IMF %. In Model 3 GR tissue depth was not significant as a main term, however was significant as an interaction with cut_cook with a similar F Value to when DXA lean % was included.

Model 4 included the same terms as Model 2 (HCWT, IMF %, DXA lean % and DXA bone R) along with SF. The SF term demonstrated a strong association with MQ4 as shown by its F Value (Table 4, Model 4, 96.6) with the effect of SF also varying by cut_cook methods. All other terms in the model remained significant, including DXA bone R.

In Models 1, 2 and 3, IMF % remained a strong predictor of MQ4. In Model 4, the F value was somewhat reduced when SF was included in the models and was approximately a third of the magnitude compared to Model 1.

Table 4. F values, numerator (NDF) and denominator (DDF) degrees of freedom for the prediction of MQ4 scores using hot carcass weight (kg), loin intramuscular fat %, DXA bone R, GR tissue depth (mm) and shear force (N) across roast and grill cuts for the combined flocks. Random terms included were animal identification, consumer number(session) and flock.

Dependent variable MQ4	**Model 1**		**Model 2**		**Model 3**		**Model 4**	
Terms in model	**MSA terms (HCWT; IMF%; DXA lean %)**		**MSA terms & DXA bone R**		**HCWT, IMF % & GR tissue depth & DXA bone R**		**MSA terms & Shear force & DXA bone R**	
	NDF, DDF	**F-value**	**NDF, DDF**	**F-value**	**NDF, DDF**	**F-value**	**NDF, DDF**	**F-value**
cut_cook	9, 21679	7.96***	9, 21846	13.50***	9, 21528	13.13***	9, 19508	9.74***
Hot carcass weight	1, 326	17.88***	1, 560	1.80	1, 586	1.22	1, 488	0.63
Loin intramuscular fat %	1, 450	27.94***	1, 500	26.27***	1, 500	30.79***	1, 486	8.32***
DXA lean %	1, 461	3.01*	1, 468	0.15	NA	NA	1, 426	1.73
DXA bone R	NA	NA	1, 440	26.48***	1, 436	28.28***	1, 344	15.77***
GR tissue depth	NA	NA	NA	NA	1, 547	0.00	NA	NA
Shear force	NA	NA	NA	NA	NA	NA	1, 709	105.85***
Hot carcass weight *cut_cook	9, 23256	18.87***	9, 22664	9.03***	9, 22629	6.75***	9, 21377	6.14***
Loin intramuscular fat %*cut_cook	9, 23835	8.11***	9, 23971	4.80***	9, 23616	5.28***	9, 21776	4.54***
DXA lean %*cut_cook	9, 23161	2.62***	9, 23850	1.80*	NA	NA	9, 22175	1.76*
Bone DXA R*cut_cook	NA	NA	9, 22318	11.11***	9, 21653	11.48***	9, 20137	7.93***
GR tissue depth*cut_cook	NA	NA	NA	NA	9, 23917	1.95**	NA	NA
Shear force*cut_cook	NA	NA	NA	NA	NA	NA	9, 21012	7.47***

*P < 0.1; **P < 0.05; ***P < 0.01
NA term not in the starting model

4.3.2 Combined data set analysis, assessing DEXA bone R impact on MQ4 allowing variation of cut and cook between flocks.

For the models described above, with all data combined and flock included as a random term there were concerns that groups of animals within the data, for example Flock 3, which consistent of lambs that were young and had a small age range (10 days), may mask the effect of DXA bone R within the remaining data. As such the following analysis was performed in the combined 4 flocks, however the covariates included were allowed to interact with the term cut_cook_flock.

Prediction of MQ4 using Meat standards Australia eating quality prediction model terms (HCWT, IMF % and lean %) and DXA bone R

Model 5 (Table 5) includes the terms used in the MSA eating quality prediction model (HCWT, IMF % and DXA lean %) to predict MQ4 across the various cut_cook combinations in all flocks. All terms were significant as a main effect, however the magnitude of effect was varied between the cut_cook combinations. When DXA bone R was included along with HCWT, IMF % and DXA lean %, it was significant, with the strength of the relationship varied between cuts, cooks and flocks (Table 5, Model 6). The other terms in this model remained significant although the strength of their associations was diminished, most notably for HCWT which was no longer significant as a main effect ($P > 0.1$).

GR tissue depth and prediction of MQ4

When GR tissue depth was included in place of DXA lean % (Table 5, Model 7, $P < 0.05$) the GR measure remained significant alongside HCWT and IMF %. When DXA bone R was included along with GR tissue depth, DXA bone R demonstrated a significant association with MQ4 in addition to GR tissue depth (Table 5, Model 8, $P < 0.05$). The magnitudes of these effects varied depending on the cut, cook and flock combination. In this scenario HCWT was no longer significant ($P > 0.1$) and the main driver of MQ4 was IMF %.

Shear force prediction of MQ4

In a final model (Table 5, Model 9), both DXA bone R and SF were included in the base model. In this model, DEXA bone R remained significant ($P < 0.01$) with a similar magnitude as when included in the base model alone. As expected, SF demonstrated a strong association with MQ4 ($P < 0.01$), with the effect varying by cut, cook and flock.

Table 5. F values, numerator (NDF) and denominator (DDF) degrees of freedom for the models predicting MQ4 scores across cut_cook combinations in different flocks using hot carcass weight (kg), loin intramuscular fat %, DXA Bone R, GR tissue depth (mm) and shear force (N) across roast and grill cuts for combined flocks. Random terms included include animal identification and consumer number(session).

Dependent variable MQ4	**Model 5**		**Model 6**		**Model 7**		**Model 8**		**Model 9**	
Terms in model	**MSA terms (HCWT; IMF%; DXA lean %)**		**MSA terms & DXA bone R**		**HCWT; IMF; GR tissue depth**		**HCWT; IMF%; GR tissue depth & bone DXA R**		**MSA terms & Bone DXA R & shear force**	
	NDF, DDF	**F-value**	**NDF, DDF**	**F-value**	**NDF, DDF**	**F-value**	**NDF, DDF**	**F-value**	**NDF, DDF**	**F-value**
Cut_cook_flock	25, 4402	3.09***	25, 4347	1.36	25, 3807	7.18***	25, 4212	1.75**	25, 3370	1.47*
HCWT	1, 446	5.97**	1, 408	0.31	1, 422	6.88***	1, 401	0.11	1, 355	0.24
IMF%	1, 400	11.56***	1, 396	9.40***	1, 414	18.25***	1, 397	15.33***	1, 342	2.45
DXA lean %	1, 398	1.56	1, 421	1.65	NA	NA	NA	NA	1, 360	0.32
DXA bone R	NA	NA	1, 422	1.26	NA	NA	25, 4212	1.85***	1, 364	0.45
GR tissue depth	NA	NA	NA	NA	1, 414	0.68	25, 4019	2.06***	NA	NA
Shear force	NA	NA	NA	NA	NA	NA	NA	NA	1, 348	44.51***
HCWT*cut_cook_flock	25, 3999	4.44***	25, 4300	1.61**	25, 4339	2.17***	25, 4057	1.40*	25, 3677	1.39*
IMF %*cut_cook_flock	25, 4087	1.92***	25, 4044	1.82***	25, 4197	2.10***	25, 4032	1.79***	25, 3692	1.65**
DXA lean %*cut_cook_flock	25, 4338	3.14***	25, 4342	2.11***	NA	NA	NA	NA	24, 3638	2.14***
DXA bone R*cut_cook_flock	NA	NA	25, 4172	1.46*	NA	NA	25, 4212	1.85***	24, 3519	1.39*
GR tissue depth*cut_cook_flock	NA	NA	NA	NA	25, 4634	2.56***	25, 4019	2.06***	NA	NA
Shear force*cut_cook_flock	NA	NA	NA	NA	NA	NA	NA	NA	24, 3646	3.26***

*P < 0.1; **P < 0.05; ***P < 0.01

NA term not in the starting model

4.4 Individual flock analysis assessing DXA bone R impact on eating quality traits.

In the initial 2 analysis using the combined data from all 4 flocks, there were concerns that some of the magnitudes of effects may not be adequately reflected due to over parametisation of the model. Therefore, a third analysis was performed on each flock individually to determine the magnitude of effect of DXA bone R on eating quality traits alongside HCWT. Due to the relatively high correlation of HCWT and DXA bone R, 3 models are reported: the first included terms used in the current MSA sheep meat eating quality prediction model (HCWT, IMF %, DXA lean %) along with DXA bone R; the second contained only HCWT, IMF %, DXA lean %; the third contained only IMF %, DXA lean % and DXA bone R. In these models the non-significant terms were retained to compare the effect of the covariates across the different models and flocks enabling direct comparison of the magnitude of effect for the cut_cook combinations.

The magnitude of effects for the cut_cook combinations are expressed across a 4 standard deviation range of the relevant covariate (HCWT or DXA bone R), for the combined flocks to allow comparisons between flocks, despite this representing an extrapolation of the data in some cases. However, the magnitude of the effects on eating quality is also expressed within the 4 standard deviation range of the flock being analysed and displayed in brackets within the tables.

4.4.1 The effect of HCWT and DXA bone R on MQ4

The model results for the prediction of MQ4 are show in Table 6. Flock 1 and 2 demonstrated the greatest associations of DXA bone R with MQ4 (Table 6, Model 10), with this term remaining significant when included in models with HCWT, IMF % and DXA lean %. The strength of the association of DXA bone R with MQ4 was increased in Model 12 which does not include HCWT. Similarly for Flock 4, Model 12 demonstrated a stronger effect of DXA bone R on MQ4 than when HCWT was included in model 10.

Table 6. F Values, numerator and denominator degrees of freedom (NDF, DDF) for models predicting MQ4 scores in flocks (1, 2, 3, 4) using hot carcass weight (kg), loin IMF %, DXA lean % and DXA bone R. Random terms included animal identification and consumer within session.

Dependent variable: MQ4	**Model 10: MSA prediction model terms (HCWT, IMF %, lean %) & DXA bone R**		**Model 11: MSA prediction model terms (HCWT, IMF %, lean %)**		**Model 12: IMF %, lean % & DXA bone R (no HCWT)**	
	NDF, DDF	**F-value**	**NDF, DDF**	**F-value**	**NDF, DDF**	**F-value**
Terms in models			**Flock 1**			
cut_cook	7, 7920	1.10	7, 7131	1.65	7, 7621	6.04***
Hot carcass weight	1, 109	0.06	1, 111	20.15***	NA	NA
Loin intramuscular fat %	1, 113	12.38***	1, 114	12.35***	1, 114	12.30***
DXA lean %	1, 111	1.53	1, 114	0.34	1, 113	1.87
DXA bone R	1, 110	4.25**	NA	NA	1, 112	24.89***
Hot carcass weight *cut_cook	7, 8094	1.39	7, 7955	8.07***	NA	NA
Loin intramuscular fat %*cut_cook	7, 7767	1.39	7, 7784	1.43	7, 7775	1.39
DXA lean %*cut_cook	7, 7960	1.00	7, 7760	0.74	7, 7818	1.18
Bone DXA R*cut_cook	7, 8000	1.29	NA	NA	7, 7850	7.87***
			Flock 2			
cut_cook	6, 5916	1.54	6, 5966	5.96***	6, 5999	3.18***
Hot carcass weight	1, 89	4.92**	1, 86	0.12	NA	NA
Loin intramuscular fat %	1, 89	5.88**	1, 89	7.04***	1, 90	5.76**
DXA lean %	1, 88	0.07	1, 89	0.81	1, 89	0.91
DXA bone R	1, 89	7.70***	NA	NA	1, 87	2.82*
Hot carcass weight *cut_cook	6, 5916	1.36	6, 6010	2.75**	NA	NA
Loin intramuscular fat %*cut_cook	6, 5887	2.85***	6, 5899	3.03***	6, 5894	2.84***
DXA lean %*cut_cook	6, 5930	5.06***	6, 5952	5.91***	6, 5948	6.33***
Bone DXA R*cut_cook	6, 5924	1.95*	NA	NA	6, 6009	3.35***
			Flock 3			
cut_cook	6, 4411	1.68	6, 4490	0.75	6, 4520	1.61
Hot carcass weight	1, 68	0.26	1, 63	0.97	NA	NA
Loin intramuscular fat %	1, 62	0.01	1, 62	0.08	1, 62	0.03
DXA lean %	1, 66	2.12	1, 63	0.89	1, 64	1.91
DXA bone R	1, 68	1.22	NA	NA	1, 63	1.96
Hot carcass weight *cut_cook	6, 4413	1.29	6, 4514	0.87	NA	NA
Loin intramuscular fat %*cut_cook	6, 4487	0.75	6, 4502	0.90	6, 4501	0.94
DXA lean %*cut_cook	6, 4425	0.34	6, 4489	0.76	6, 4476	0.24
Bone DXA R*cut_cook	6, 4404	1.56	NA	NA	6, 4509	1.13
			Flock 4			
cut_cook	3, 5851	0.59	3, 6084	1.55	3, 5976	2.73**
Hot carcass weight	1, 344	1.60	1, 374	4.12**	NA	NA
Loin intramuscular fat %	1, 377	12.45***	1, 380	13.09***	1, 354	12.85***
DXA lean %	1, 354	6.42**	1, 262	22.37***	1, 368	9.74***
DXA bone R	1, 413	0.75	NA	NA	1, 536	1.68
Hot carcass weight *cut_cook	3, 5706	3.43**	3, 5694	4.54***	NA	NA
Loin intramuscular fat %*cut_cook	3, 5770	4.38***	3, 5778	4.43***	3, 5894	4.60***
DXA lean %*cut_cook	3, 5869	0.43	3, 6062	1.59	3, 6189	0.23
Bone DXA R*cut_cook	3, 5830	0.47	NA	NA	3, 5982	2.39*

*P < 0.1; **P < 0.05; ***P<0.01
NA term not in the starting model

The magnitude of effect of HCWT and DXA bone R on MQ4 across the flocks and their range of cuts using models 10, 11 and 12 are shown in Table 7 when all terms were retained in the model. For Flock 1 there were 5 grill cuts and 3 roast cuts assessed. DXA bone R demonstrated a negative association with MQ4, with a decrease in MQ4 score observed in the shoulder roast, rack cutlet and loin grill of 13.1, 14.3 and 15.2 across 4 times the population SD. Without the inclusion of DXA bone R, (Table 7, Model 11) HCWT demonstrated a significant positive association with the shoulder roast, rack cutlet roast, loin grill, along with the grill outside and rump from the hind section and top side roast. When DXA bone R is included in models without HCWT, all cuts except the knuckle grill demonstrated a negative relationship (Table 7, Model 12 results), with the magnitude of the effects increased compared to when HCWT was included in the models. In many cases the magnitude of effect of DXA bone R in Model 12 is of a similar magnitude but in the opposite direction to the HCWT effects shown by Model 11. This demonstrates prediction of MQ4 in these cuts may be predicted without DXA bone R, with the exception to this being the loin grill, where the effect on this cut is not fully accounted for by HCWT.

For Flock 2, there were 7 grill cuts assessed, and using model 10, DXA bone R demonstrated strong negative associations with multiple cuts across the carcass ($P < 0.1$). Across the 4 SD range of DXA bone R of all Flocks this resulted in a decrease in MQ4 in the eye of rack (23.1), loin (22.6), outside (50.8), rump (26.3) and topside (29.3). When these magnitudes were expressed across the more constrained range of DXA bone R for Flock 2, the magnitude of the effect on MQ4 was just under half. When HCWT or DXA bone R were included individually along with IMF % and DXA lean % (Model 11 and 12 outputs shown in Table 7) there were less cuts that demonstrated a significant association with MQ4 and shows the inclusion of HCWT and DXA bone R simultaneously provides a better prediction of MQ4.

In Flock 4, only 4 grill cuts were assessed (eye of rack, loin, knuckle and topside). For the loin, (Table 7, output from model 10), an increase in DXA bone R across the combined flock 4 SD range resulted in a reduction of 15.8 MQ4 scores. The impact of HCWT on this same cut was only evident when DXA bone was not included (Model 11) and did not describe the same magnitude of effect as DXA bone R. When DXA bone R was included without HCWT there was a negative relationship with both the loin and topside. For the topside, the reduction of MQ4 was of a similar magnitude to that of HCWT using Model 11 indicating that inclusion of DXA bone R did not greatly improve the predictive power of this cut, but was the case for the loin grill.

In contrast to the other Flocks, Flock 3 did not demonstrate a consistent relationship between DXA bone R or any of the other terms in Models 10, 11, 12 (Table 6). When coefficients were generated for cuts from this flock there were few significant effects in any cut_cook methods. For the eye of the shoulder grill there was a positive association of DXA bone R with MQ4 which is the opposite to the effect observed in all other instances. Additionally there was no significant relationship of MQ4 with HCWT, IMF, DXA lean % or SF indicating there was little ability to predict eating quality in this group of animals using any phenotypic data that would commonly be associated with eating quality.

4.4.2 The effect of IMF % and DXA lean % on MQ4

As a comparison to HCWT and DXA bone R, the magnitude of effect of terms such as loin IMF % and DXA lean % have been determined for each of the flocks and the cut_cook combinations within them.

Intramuscular fat %

For the remaining Flocks (1, 2 and 4), loin IMF % demonstrated the strongest and most consistent relationship with MQ4. The F-values for this term were generally the highest in each of the models (Table 6) and these remained stable across Models 10, 11 and 12. For Flock 1, IMF % demonstrated a positive relationship with MQ4 with all cuts, with the exception of the topside roast. The magnitude of effect of increasing IMF % across 4 times the population SD using Model 10 resulted in an increased MQ4 score for the shoulder roast (6.3), rack roast cutlet (8.0) and loin grill (7.7) which are the cuts where DXA bone R demonstrated a significant relationship. For these cuts the magnitude of effect of IMF was less than the effect of DXA bone R on these same cuts. However, there were additional grill cuts demonstrating a relationship with IMF %, with increases in MQ4 for the rump, knuckle, topside, outside ranging from 4.1 to 5.5 scores.

In Flock 2, when the magnitude of effect if IMF % was expressed across the population 4 SD range in it was not a great as the impact of DXA bone R. There was only a significant positive association with IMF % and the eye rack (13.5), rump (11.6) and topside (11.4) (individual coefficients not shown).

For Flock 4, IMF % demonstrated the strongest association with MQ4 with an increase in MQ4 noted for the eye of rack (16.3), loin (13.5) and knuckle (4.9) grill cuts.

Lean %

With regard to DXA lean %, the greatest effects were sown in flock 4 where there was a strong negative effect on MQ4 for the loin (11.2), knuckle (6.7) and topside (8.4) grill. For the other Flocks there was a lack of consistency of the association of DXA lean % and MQ4 and few cuts that demonstrated a significant effect. In general, there was a negative association of DXA lean % with MQ4, however this was only significant for the eye of shoulder grill in Flock 3.

Table 7.Coefficients ± s.e. and magnitude of effect of hot carcass wight (kg) and DXA bone R for models predicting MQ4 scores showing magnitude of the effect across a 4 standard deviation range of all animals combined and across a 4 SD within individual flocks shown in brackets.

Dependent variable: MQ4		Model 10: MSA prediction model terms (HCWT, IMF%, lean%) & DXA bone R				Model 11: MSA prediction model terms (HCWT, IMF%, lean%)		Model 12: IMF%, lean % & DXA bone R	
Covariate tested		Hot carcass weight (kg)		DXA bone R		Hot carcass weight (kg)		DXA bone R	
Cut	Cook	coefficient ± s.e.	Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)	coefficient ± s.e.	Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)	coefficient ± s.e.	Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)	coefficient ± s.e.	Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)
Flock 1									
Shoulder	**RST**	0.39 ± 0.4	6.6 (6.8)	**-128.95 ± 57.2**	**-13.1 (-14.1)**	**1.10 ± 0.2**	**18.5 (18.9)**	**-185.86 ± 25.9**	**-18.9 (-20.4)**
Rack cutlet	**RST**	0.17 ± 0.4	2.9 (3.0)	**-141.01 ± 58.2**	**-14.3 (-15.5)**	**0.95 ± 0.2**	**15.9 (16.3)**	**-166.14 ± 26.3**	**-16.9 (-18.2)**
Loin	**GRL**	-0.43 ± 0.4	-7.3 (-7.4)	**-149.33 ± 59.0**	**-15.2 (-16.4)**	**0.38 ± 0.2**	**6.3 (6.5)**	**-85.97 ± 27.3**	**-8.7 (-9.4)**
Knuckle	**GRL**	-0.37 ± 0.4	-6.3 (-6.4)	-67.11 ± 58.5	-6.8 (-7.4)	-0.01 ± 0.2	-0.1 (-0.1)	-12.88 ± 26.7	-1.3 (-1.4)
Outside	**GRL**	0.11 ± 0.4	1.9 (1.9)	-38.16 ± 58.5	-3.9 (-4.2)	**0.32 ± 0.2**	**5.3 (5.5)**	**-53.67 ± 26.7**	**-5.5 (-5.9)**
Rump	**GRL**	0.47 ± 0.4	8.0 (8.1)	-26.08 ± 58.5	-2.7 (-2.9)	**0.61 ± 0.2**	**10.3 (10.6)**	**-94.61 ± 26.7**	**-9.6 (-10.4)**
Topside	**GRL**	**-0.12 ± 0.4**	**-2.0 (-2.0)**	-67.25 ± 58.5	-6.8 (-7.4)	0.25 ± 0.2	4.2 (4.2)	**-49.90 ± 26.7**	**-5.1 (-5.5)**
Topside	**RST**	0.24 ± 0.4	4.1 (4.2)	-20.69 ± 57.2	-2.1 (-2.3)	**0.36 ± 0.2**	**6.0 (6.1)**	**-56.18 ± 25.9**	**-5.7 (-6.2)**
Flock 2									
Eye of shoulder	**GRL**	-0.02 ± 0.5	-0.3 (-0.2)	-27.05 ± 129.8	-2.8 (-1.2)	0.08 ± 0.3	1.4 (0.9)	-23.11 ± 66.5	-2.4 (-1.0)
Eye of rack	**GRL**	**-1.26 ± 0.5**	**-21.1 (-14.5)**	**-227.09 ± 129.7**	**-23.1 (-10.2)**	**-0.48 ± 0.3**	**-8.0 (-5.5)**	44.12 ± 66.6	4.5 (2.0)
Loin	**GRL**	-0.77 ± 0.5	-13.0 (-8.9)	**-222.48 ± 129.9**	**-22.6 (-10.0)**	-0.01 ± 0.3	-0.2 (-0.1)	-54.21 ± 66.6	-5.5 (-2.4)
Knuckle	**GRL**	-0.14 ± 0.5	-2.3 (-1.6)	-113.53 ± 129.7	-11.6 (-5.1)	0.27 ± 0.3	4.5 (3.1)	-85.82 ± 66.4	-8.7 (-3.9)
Outside	**GRL**	**-1.04 ± 0.5**	**-17.5 (-11.9)**	**-499.17 ± 130.0**	**-50.8 (-22.5)**	**0.68 ± 0.3**	**11.4 (7.8)**	**-274.41 ± 66.4**	**-27.9 (-12.3)**
Rump	**GRL**	-0.82 ± 0.5	-13.8 (-9.4)	**-258.82 ± 129.7**	**-26.3 (-11.6)**	0.07 ± 0.3	1.2 (0.9)	-82.11 ± 66.5	-8.4 (-3.7)
Topside	**GRL**	**-1.18 ± 0.5**	**-19.8 (-13.5)**	**-287.68 ± 129.6**	**-29.3 (-12.9)**	-0.18 ± 0.3	-3.0 (-2.1)	-34.36 ± 66.5	-3.5 (-1.5)
Flock 3									
Eye of shoulder	**GRL**	**0.66 ± 0.4**	**11.2 (13.1)**	**476.61 ± 186.3**	**48.5 (26.1)**	-0.23 ± 0.2	-3.8 (-4.5)	**206.05 ± 89.3**	**21.0 (11.3)**
Eye of rack	**GRL**	0.52 ± 0.4	8.7 (10.3)	193.75 ± 185.3	19.7 (10.6)	0.16 ± 0.2	2.7 (3.1)	-19.03 ± 89.1	-1.9 (-1.0)
Loin	**GRL**	-0.29 ± 0.4	-4.8 (-5.6)	-102.43 ± 184.8	-10.4 (-5.6)	-0.10 ± 0.2	-1.7 (-1.9)	12.98 ± 88.8	1.3 (0.7)
Knuckle	**GRL**	0.13 ± 0.4	2.2 (2.6)	211.08 ± 186.4	21.5 (11.6)	-0.27 ± 0.2	-4.5 (-5.3)	**159.30 ± 88.9**	**16.2 (8.7)**
Outside	**GRL**	-0.27 ± 0.4	-4.6 (-5.4)	-29.09 ± 185.3	-3.0 (-1.6)	-0.23 ± 0.2	-3.8 (-4.5)	82.12 ± 89.0	8.4 (4.5)
Rump	**GRL**	-0.12 ± 0.4	-2.0 (-2.3)	14.09 ± 186.2	1.4 (0.8)	-0.15 ± 0.2	-2.5 (-2.9)	61.46 ± 89.2	6.3 (3.4)
Topside	**GRL**	0.25 ± 0.4	4.3 (5.0)	133.25 ± 186.2	13.6 (7.3)	0.01 ± 0.2	0.1 (0.1)	28.93 ± 89.2	2.9 (1.6)
Flock 4									
Eye of rack	**GRL**	0.72 ± 0.6	12.0 (6.5)	92.54 ± 218.4	9.4 (3.9)	0.66 ± 0.6	11.1 (6.0)	101.22 ± 188.5	10.3 (4.3)
Loin	**GRL**	0.43 ± 0.3	7.2 (3.9)	**-154.93 ± 83.2**	**-15.8 (-6.5)**	**0.68 ± 0.2**	**11.4 (6.2)**	**-232.61 ± 65.1**	**-23.7 (-9.8)**
Knuckle	**GRL**	-0.28 ± 0.3	-4.8 (-2.6)	-108.09 ± 82.9	-11.0 (-4.5)	-0.10 ± 0.2	-1.7 (-0.9)	-74.35 ± 63.5	-7.6 (-3.1)
Topside	**GRL**	0.44 ± 0.3	7.3 (4.0)	-109.82 ± 82.6	-11.2 (-4.6)	**0.62 ± 0.2**	**10.4 (5.6)**	**-133.69 ± 63.2**	**-13.6 (-5.6)**

Bold $P < 0.1$

4.4.3 Other eating quality traits

In addition to testing the impact of HCWT and DXA bone R on MQ4, the traits used to calculate MQ4 (tenderness, juiciness, liking of flavour and overall liking) were also tested individually as dependent variables for each Flock. The same model structure has been followed as for MQ4, where 3 models were constructed: the first contained HCWT, IMF %, DXA lean % and DXA bone R; the second did not have DXA bone R and the third did not contain HCWT. F Value tables have been generated for predictions of the eating quality traits as well as the magnitude of the effect across the cut_cook combinations in the 4 Flocks. The impact of IMF % and lean % have not been reported for these other easting quality traits.

Tenderness

The F values, NDF and DDF for models predicting tenderness are shown in Table 8 with the 3 versions of the prediction models shown (Models 13, 14 and 15). The magnitude of effect of HCWT and DXA bone R, are shown for each of these models in Table 9. For tenderness, in Model 13, which contains HCWT, IMF %, DXA lean % and DXA bone R the same cuts demonstrated an effect. However, overall, the magnitude of these effects were increased. When DXA bone R was included without HCWT in the model (Table 9, Model 15), for Flock 1 the shoulder roast was not significant. Additionally, the outside grill was no longer significant for either HCWT or DXA bone R.

Juiciness

For juiciness, DXA bone R demonstrated a similar relation as when MQ4 was tested as the dependent variable (Table 10, Model 16). For Flock 1, the magnitude of effect of the shoulder roast was decreased, although for the rack cutlet roast and loin grill the magnitude of effect was increased compared to the impact on MQ4. Additionally, the juiciness of outside grill for Flock 1 had a negative association with DXA bone R of 12 scores ($P < 0.01$, Table 11).

For Flock 2 and 4, the results were similar when predicting tenderness, however the loin grill was no longer significant in a model containing all covariates (HCWT, IMF %, DXA lean % and DXA bone R) (Table 11, Model 14). However, for Flock 4, without HCWT in the model there was a negative association of DXA bone R with loin grill tenderness (Table 11, Model 15).

Liking of flavour

The impact of DXA bone R on flavour was somewhat diminished compared to the other individual traits and MQ4. When included along with HCWT, IMF % and DXA lean % it was significant across a range of cut_cook combinations ($P < 0.1$, Table 12). In Flock 1, the shoulder roast, rack cutlet roast and loin grill remined significant all the magnitude of the effects were slightly reduced (Table 13, Model 19). In Flock 2, the outside grill had a reduced magnitude of effect compared to MQ4, although the results for the eye of rack and topside grill were similar (Table 13, Model 19), with the loin and rump grill cuts no longer significant ($P > 0.1$). Within Flock 4 in the output from Model 19, there was not a significant relationship between DXA bone R and loin grill flavour, although without the inclusion of HCWT in the model a significant association was observed.

Overall liking

For overall liking the results were very similar to that of MQ4 (Table 14). For Flock 1, the shoulder roast, rack cutlet roast and loin grill all demonstrated a similar decrease in overall liking as DXA bone R increased (Table 15, Model 22). Without the inclusions of HCWT in this model (Table 15, Model 24), all cuts, with the exception of the knuckle grill, demonstrated a negative association with DXA bone R. For Flock 2, the loin grill overall liking was not predicted by DXA bone R or HCWT in models containing both terms or when included individually (Table 15). However, the outside, rump and topside grill demonstrated a negative relationship with DXA bone R. For Flock 4 the both the loin grill demonstrated demonstrate a negative association of DXA bone R, similar in magnitude to that seen with MQ4 (Table 15). In addition to this, the knuckle grill also demonstrated a decrease of 14 overall liking scores as DXA bone R increased. Similar to models predicting MQ4, the topside grill overall liking decreased, however this was only when HCWT was not include in the model (Table 15, Model 24). For Flock 3, overall liking was the only eating quality trait that demonstrated a negative relationship with DXA bone R (loin grill). There was an incongruous positive relationship with the eye of shoulder, as was observed with the other eating quality traits and in this case the knuckle grill also demonstrated a positive relationship with DXA bone R.

Table 8. F Values, numerator and denominator degrees of freedom (NDF, DDF) for models predicting tenderness scores in flocks (1, 2, 3, 4) using hot carcass weight (kg), loin IMF %, DXA lean % and DXA bone R. Random terms included animal identification and consumer within session.

Dependent variable: Tenderness	**Model 13: MSA model terms (HCWT, IMF %, lean %) & DXA bone R**		**Model 14: MSA model terms (HCWT, IMF %, lean %)**		**Model 15: IMF %, lean % & DXA bone R (no HCWT)**	
	NDF, DDF	**F-value**	**NDF, DDF**	**F-value**	**NDF, DDF**	**F-value**
Terms in models			**Flock 1**			
cut_cook	7, 8025	0.92	7, 7220	1.49	7, 7660	7.38***
Hot carcass weight	1, 108	0.01	1, 111	12.65***	NA	NA
Loin intramuscular fat %	1, 112	5.51**	1, 114	5.65**	1, 113	5.42**
DXA lean %	1, 111	2.03	1, 114	0.79	1, 113	2.31
DXA bone R	1, 110	3.02*	NA	NA	1, 112	15.74***
Hot carcass weight *cut_cook	7, 8246	1.43	7, 8021	9.41***	NA	NA
Loin intramuscular fat %*cut_cook	7, 7845	1.53	7, 7866	1.55	7, 7859	1.52
DXA lean %*cut_cook	7, 8078	0.59	7, 7858	0.41	7, 7923	0.78
Bone DXA R*cut_cook	7, 8114	1.10	NA	NA	7, 7878	9.01***
			Flock 2			
cut_cook	6, 6003	0.99	6, 6046	7.23***	6, 6073	2.33**
Hot carcass weight	1, 88	5.55**	1, 85	0.00	NA	NA
Loin intramuscular fat %	1, 88	4.64**	1, 88	5.78**	1, 88	4.55**
DXA lean %	1, 88	0.11	1, 88	0.95	1, 88	1.14
DXA bone R	1, 88	7.62***	NA	NA	1, 86	1.97
Hot carcass weight *cut_cook	6, 6004	1.01	6, 6083	2.66**	NA	NA
Loin intramuscular fat %*cut_cook	6, 5976	2.29**	6, 5987	2.53**	6, 5983	2.29**
DXA lean %*cut_cook	6, 6016	4.77***	6, 6037	5.82***	6, 6032	5.83***
Bone DXA R*cut_cook	6, 6010	1.43	NA	NA	6, 6089	3.07***
			Flock 3			
cut_cook	6, 4486	1.97*	6, 4570	0.97	6, 4600	1.76
Hot carcass weight	1, 68	0.02	1, 64	2.20	NA	NA
Loin intramuscular fat %	1, 63	0.11	1, 64	0.25	1, 64	0.13
DXA lean %	1, 67	1.66	1, 65	0.76	1, 65	1.94
DXA bone R	1, 68	0.89	NA	NA	1, 64	3.12*
Hot carcass weight *cut_cook	6, 4487	1.50	6, 4592	0.90	NA	NA
Loin intramuscular fat %*cut_cook	6, 4570	0.56	6, 4584	0.69	6, 4584	0.75
DXA lean %*cut_cook	6, 4504	0.24	6, 4569	0.98	6, 4556	0.22
Bone DXA R*cut_cook	6, 4479	1.79*	NA	NA	6, 4589	1.19
			Flock 4			
cut_cook	3, 6009	1.10	3, 6218	2.87**	3, 6138	4.38***
Hot carcass weight	1, 334	0.66	1, 361	2.61	NA	NA
Loin intramuscular fat %	1, 357	10.81***	1, 360	11.47***	1, 342	11.37***
DXA lean %	1, 339	7.41***	1, 255	25.52***	1, 354	10.90***
DXA bone R	1, 389	0.95	NA	NA	1, 504	1.52
Hot carcass weight *cut_cook	3, 5864	6.40***	3, 5853	8.86***	NA	NA
Loin intramuscular fat %*cut_cook	3, 5917	4.34***	3, 5926	4.43***	3, 6041	4.73***
DXA lean %*cut_cook	3, 6025	0.43	3, 6194	2.15*	3, 6342	0.79
Bone DXA R*cut_cook	3, 5990	0.95	NA	NA	3, 6145	4.17***

*P < 0.1; **P < 0.05; ***P<0.01

NA term not in the starting model

Table 9. Coefficients ± s.e. and magnitude of effect of hot carcass wight (kg) and DXA bone R for models predicting tenderness scores showing magnitude of the effect across a 4 standard deviation range of all animals combined and across a 4 SD within individual flocks shown in brackets.

Dependent variable: Tenderness		Model 13: MSA terms (HCWT, IMF%, lean%) & DXA bone R				Model 14: MSA terms (HCWT, IMF%, lean%)		Model 15: IMF%, lean % & DXA bone R	
Covariate tested		**Hot carcass weight**		**DXA bone R**		**Hot carcass weight**		**DXA bone R**	
Cut	**Cook**	**coefficient ± s.e.**	**Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)**	**coefficient ± s.e.**	**Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)**	**coefficient ± s.e.**	**Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)**	**coefficient ± s.e.**	**Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)**
					Flock 1				
Shoulder	**RST**	0.34 ± 0.4	5.8 (5.9)	**-139.55 ± 71.6**	**-14.2 (-15.3)**	**1.11 ± 0.2**	**18.6 (19.1)**	-189.50 ± 32.5	-19.3 (-20.8)
Rack cutlet	**RST**	0.19 ± 0.4	3.2 (3.2)	**-181.78 ± 72.4**	**-18.5 (-19.9)**	**1.19 ± 0.2**	**19.9 (20.4)**	**-209.06 ± 32.8**	**-21.3 (-22.9)**
Loin	**GRL**	-0.45 ± 0.4	-7.5 (-7.7)	**-123.67 ± 73.6**	**-12.6 (-13.6)**	0.22 ± 0.2	3.8 (3.8)	**-57.91 ± 34.1**	**-5.9 (-6.3)**
Knuckle	**GRL**	-0.42 ± 0.4	-7.0 (-7.2)	-49.48 ± 73.1	-5.0 (-5.4)	-0.15 ± 0.2	-2.5 (-2.5)	11.39 ± 33.4	1.2 (1.2)
Outside	**GRL**	0.01 ± 0.4	0.1 (0.1)	-39.03 ± 73.1	-4.0 (-4.3)	0.22 ± 0.2	3.7 (3.8)	-39.57 ± 33.4	-4.0 (-4.3)
Rump	**GRL**	0.64 ± 0.4	10.7 (11.0)	-39.02 ± 73.1	-4.0 (-4.3)	**0.85 ± 0.2**	**14.3 (14.6)**	**-131.18 ± 33.4**	**-13.3 (-14.4)**
Topside	**GRL**	-0.39 ± 0.4	-6.5 (-6.6)	-111.77 ± 73.1	-11.4 (-12.2)	**0.23 ± 0.2**	**3.8 (3.9)**	**-55.72 ± 33.4**	**-5.7 (-6.1)**
Topside	**RST**	0.29 ± 0.4	4.9 (5.0)	-22.90 ± 71.7	-2.3 (-2.5)	0.42 ± 0.2	7.0 (7.2)	**-65.51 ± 32.5**	**-6.7 (-7.2)**
Eye shoulder					**Flock 2**				
Eye of rack	**GRL**	-0.11 ± 0.6	-1.8 (-1.2)	-55.57 ± 158.4	-5.7 (-2.5)	0.08 ± 0.3	1.4 (1.0)	-31.03 ± 81.2	-3.2 (-1.4)
Loin	**GRL**	**-1.57 ± 0.6**	**-26.3 (-18.0)**	**-272.61 ± 158.2**	**-27.7 (-12.3)**	**-0.63 ± 0.3**	**-10.6 (-7.2)**	65.49 ± 81.3	6.7 (2.9)
Knuckle	**GRL**	**-1.11 ± 0.6**	**-18.6 (-12.7)**	**-281.48 ± 158.5**	**-28.6 (-12.7)**	-0.15 ± 0.3	-2.4 (-1.7)	-40.92 ± 81.4	-4.2 (-1.8)
Outside	**GRL**	-0.52 ± 0.6	-8.8 (-6.0)	-173.07 ± 158.2	-17.6 (-7.8)	0.08 ± 0.3	1.4 (0.9)	-60.97 ± 81.1	-6.2 (-2.7)
Rump	**GRL**	-0.98 ± 0.6	-16.5 (-11.3)	**-509.17 ± 158.5**	**-51.8 (-22.9)**	**0.77 ± 0.3**	**12.9 (8.8)**	**-296.04 ± 81.2**	**-30.1 (-13.3)**
Topside	**GRL**	**-1.37 ± 0.6**	**-22.9 (-15.7)**	**-432.14 ± 158.3**	**-44.0 (-19.4)**	0.12 ± 0.3	2.0 (1.4)	**-137.13 ± 81.3**	**-14.0 (-6.2)**
	GRL	**-1.25 ± 0.6**	**-21.0 (-14.4)**	**-304.34 ± 158.1**	**-31.0 (-13.7)**	-0.20 ± 0.3	-3.4 (-2.3)	-33.78 ± 81.3	-3.4 (-1.5)
Eye shoulder									
Eye of rack					**Flock 3**				
Loin	**GRL**	0.70 ± 0.5	11.8 (13.8)	**512.94 ± 230.1**	**52.2 (28.1)**	-0.26 ± 0.2	-4.4 (-5.2)	**229.01 ± 110.2**	**23.3 (12.5)**
Knuckle	**GRL**	0.55 ± 0.5	9.2 (10.8)	247.01 ± 229.0	25.1 (13.5)	0.09 ± 0.2	1.5 (1.7)	22.60 ± 110.0	2.3 (1.2)
Outside	**GRL**	-0.53 ± 0.5	-9.0 (-10.5)	-163.40 ± 228.3	-16.6 (-9.0)	-0.23 ± 0.2	-3.9 (-4.6)	52.57 ± 109.7	5.3 (2.9)
Rump	**GRL**	0.22 ± 0.5	3.7 (4.4)	373.48 ± 230.1	38.0 (20.5)	**-0.48 ± 0.2**	**-8.1 (-9.5)**	**285.35 ± 109.7**	**29.0 (15.6)**
Topside	**GRL**	-0.52 ± 0.5	-8.7 (-10.2)	-83.75 ± 229.0	-8.5 (-4.6)	-0.37 ± 0.2	-6.2 (-7.3)	127.60 ± 109.9	13.0 (7.0)
	GRL	-0.18 ± 0.5	-3.0 (-3.5)	25.55 ± 229.9	2.6 (1.4)	-0.23 ± 0.2	-3.8 (-4.5)	97.39 ± 109.9	9.9 (5.3)
Eye of rack	**GRL**	0.04 ± 0.5	0.6 (0.8)	73.51 ± 229.9	7.5 (4.0)	-0.10 ± 0.2	-1.6 (-1.9)	55.82 ± 109.9	5.7 (3.1)
Loin									
Knuckle					**Flock 4**				
Topside	**GRL**	0.75 ± 0.7	12.6 (6.8)	158.75 ± 255.4	16.2 (6.7)	0.65 ± 0.7	10.8 (5.9)	168.18 ± 220.5	17.1 (7.1)
Shoulder	**GRL**	0.35 ± 0.3	5.9 (3.2)	**-236.85 ± 101.1**	**-24.1 (-10.0)**	**0.73 ± 0.3**	**12.2 (6.6)**	**-292.74 ± 78.6**	**-29.8 (-12.3)**
Rack cutlet	**GRL**	**-0.67 ± 0.3**	**-11.2 (-6.1)**	-140.41 ± 100.8	-14.3 (-5.9)	-0.43 ± 0.3	-7.3 (-3.9)	-47.90 ± 76.8	-4.9 (-2.0)
Loin	**GRL**	**0.59 ± 0.3**	**9.8 (5.3)**	-164.25 ± 100.4	-16.7 (-6.9)	**0.86 ± 0.3**	**14.4 (7.8)**	**-216.59 ± 76.4**	**-22.0 (-9.1)**

Bold P < 0.1

Table 10. F Values, numerator and denominator degrees of freedom (NDF, DDF) for models predicting juiciness scores in flocks (1, 2, 3, 4) using hot carcass weight (kg), loin IMF %, DXA lean % and DXA bone R. Random terms included animal identification and consumer within session.

Dependent variable: Juiciness	Model 16: MSA model terms (HCWT, IMF %, lean %) & DXA bone R		Model 17: MSA model terms (HCWT, IMF %, lean %)		Model 18: IMF %, lean % & DXA bone R (no HCWT)	
	NDF, DDF	F-value	NDF, DDF	F-value	NDF, DDF	F-value
Terms in models			**Flock 1**			
cut_cook	7, 8083	1.55	7, 7277	1.52	7, 7846	4.95***
Hot carcass weight	1, 108	0.01	1, 111	19.45***	NA	NA
Loin intramuscular fat %	1, 113	13.92***	1, 115	13.69***	1, 114	13.95***
DXA lean %	1, 111	2.96*	1, 115	0.95	1, 113	3.13*
DXA bone R	1, 110	5.80**	NA	NA	1, 112	26.17***
Hot carcass weight *cut_cook	7, 8216	2.00*	7, 8096	6.30***	NA	NA
Loin intramuscular fat %*cut_cook	7, 7977	2.20**	7, 7991	2.28**	7, 7987	2.22**
DXA lean %*cut_cook	7, 8109	1.86*	7, 7968	1.76*	7, 8012	1.79*
Bone DXA R*cut_cook	7, 8145	1.65	NA	NA	7, 8029	5.89***
			Flock 2			
cut_cook	6, 5946	0.55	6, 5993	3.89***	6, 6030	2.12**
Hot carcass weight	1, 87	6.16**	1, 83	0.01	NA	NA
Loin intramuscular fat %	1, 88	10.54***	1, 88	12.07***	1, 89	10.20***
DXA lean %	1, 87	0.61	1, 87	2.11	1, 87	2.47
DXA bone R	1, 88	8.54***	NA	NA	1, 85	2.31
Hot carcass weight *cut_cook	6, 5946	1.02	6, 6033	2.32**	NA	NA
Loin intramuscular fat %*cut_cook	6, 5918	2.51**	6, 5928	2.57**	6, 5923	2.51**
DXA lean %*cut_cook	6, 5959	3.74***	6, 5980	4.30***	6, 5976	4.68***
Bone DXA R*cut_cook	6, 5954	0.74	NA	NA	6, 6041	2.03*
			Flock 3			
cut_cook	6, 4409	2.34**	6, 4488	0.56	6, 4515	2.04*
Hot carcass weight	1, 65	1.72	1, 59	0.01	NA	NA
Loin intramuscular fat %	1, 58	0.01	1, 58	0.04	1, 58	0.02
DXA lean %	1, 63	3.14*	1, 59	1.06	1, 61	1.58
DXA bone R	1, 65	2.05	NA	NA	1, 59	0.31
Hot carcass weight *cut_cook	6, 4412	1.51	6, 4513	0.80	NA	NA
Loin intramuscular fat %*cut_cook	6, 4480	1.10	6, 4494	1.15	6, 4494	1.12
DXA lean %*cut_cook	6, 4420	0.90	6, 4486	0.55	6, 4472	0.40
Bone DXA R*cut_cook	6, 4402	2.32**	NA	NA	6, 4505	1.60
			Flock 4			
cut_cook	3, 5713	0.15	3, 5989	0.51	3, 5887	1.25
Hot carcass weight	1, 364	2.20	1, 398	3.83*	NA	NA
Loin intramuscular fat %	1, 413	12.26***	1, 417	12.58***	1, 371	10.57***
DXA lean %	1, 382	4.04**	1, 272	13.00***	1, 386	5.87**
DXA bone R	1, 455	0.21	NA	NA	1, 577	0.82
Hot carcass weight *cut_cook	3, 5544	1.26	3, 5526	1.96	NA	NA
Loin intramuscular fat %*cut_cook	3, 5639	4.72***	3, 5644	4.80***	3, 5808	4.85***
DXA lean %*cut_cook	3, 5728	0.07	3, 5972	0.38	3, 6105	0.23
Bone DXA R*cut_cook	3, 5689	0.15	NA	NA	3, 5892	1.23

*P < 0.1; **P < 0.05; ***P<0.01

NA term not in the starting model

Table 11. Coefficients ± s.e. and magnitude of effect of hot carcass wight (kg) and DXA bone R for models predicting juiciness scores showing magnitude of the effect across a 4 standard deviation range of all animals combined and across a 4 SD within individual flocks shown in brackets.

Dependent variable: Juiciness		Model 16: MSA terms (HCWT, IMF%, lean%) & DXA bone R				Model 17: MSA terms (HCWT, IMF%, lean%)		Model 18: IMF%, lean % & DXA bone R	
Covariate tested		**Hot carcass weight**		**DXA bone R**		**Hot carcass weight**		**DXA bone R**	
Cut	**Cook**	**coefficient ± s.e.**	**Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)**	**coefficient ± s.e.**	**Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)**	**coefficient ± s.e.**	**Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)**	**coefficient ± s.e.**	**Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)**
		Flock 1							
Shoulder	RST	0.56 ± 0.4	9.4 (9.7)	**-114.87 ± 60.8**	**-11.7 (-12.6)**	**1.19 ± 0.2**	**20.0 (20.5)**	**-196.15 ± 27.6**	**-20.0 (-21.5)**
Rack cutlet	RST	-0.19 ± 0.4	-3.3 (-3.3)	**-173.48 ± 61.9**	**-17.7 (-19.0)**	**0.76 ± 0.2**	**12.7 (13.0)**	**-145.30 ± 27.9**	**-14.8 (-15.9)**
Loin	GRL	-0.46 ± 0.4	-7.8 (-7.9)	**-168.12 ± 62.8**	**-17.1 (-18.4)**	**0.45 ± 0.2**	**7.5 (7.7)**	**-100.78 ± 29.2**	**-10.3 (-11.0)**
Knuckle	GRL	-0.48 ± 0.4	-8.1 (-8.3)	-102.54 ± 62.3	-10.4 (-11.2)	0.07 ± 0.2	1.2 (1.2)	-32.09 ± 28.4	-3.3 (-3.5)
Outside	GRL	-0.29 ± 0.4	-4.8 (-4.9)	**-119.54 ± 62.3**	**-12.2 (-13.1)**	**0.36 ± 0.2**	**6.1 (6.3)**	**-77.76 ± 28.4**	**-7.9 (-8.5)**
Rump	GRL	**0.64 ± 0.4**	**10.8 (11.0)**	10.49 ± 62.3	1.1 (1.1)	**0.58 ± 0.2**	**9.8 (10.0)**	**-82.96 ± 28.4**	**-8.4 (-9.1)**
Topside	GRL	0.27 ± 0.4	4.6 (4.7)	-14.76 ± 62.3	-1.5 (-1.6)	**0.35 ± 0.2**	**5.9 (6.0)**	**-54.46 ± 28.4**	**-5.5 (-6.0)**
Topside	RST	-0.20 ± 0.4	-3.3 (-3.4)	-57.70 ± 60.9	-5.9 (-6.3)	0.12 ± 0.2	2.0 (2.0)	-29.42 ± 27.6	-3.0 (-3.2)
		Flock 2							
Eye shoulder	GRL	-0.19 ± 0.5	-3.2 (-2.2)	-87.38 ± 133.7	-8.9 (-3.9)	0.12 ± 0.3	1.9 (1.3)	-46.24 ± 68.5	-4.7 (-2.1)
Eye of rack	GRL	**-1.54 ± 0.5**	**-25.9 (-17.7)**	**-242.21 ± 133.5**	**-24.6 (-10.9)**	**-0.71 ± 0.3**	**-11.9 (-8.1)**	89.92 ± 68.6	9.2 (4.0)
Loin	GRL	-0.32 ± 0.5	-5.4 (-3.7)	-138.88 ± 133.8	-14.1 (-6.2)	0.15 ± 0.3	2.6 (1.8)	-67.80 ± 68.7	-6.9 (-3.1)
Knuckle	GRL	-0.48 ± 0.5	-8.1 (-5.6)	-193.80 ± 133.6	-19.7 (-8.7)	0.19 ± 0.3	3.2 (2.2)	-91.20 ± 68.4	-9.3 (-4.1)
Outside	GRL	**-0.93 ± 0.5**	**-15.7 (-10.7)**	**-399.82 ± 133.8**	**-40.7 (-18.0)**	**0.44 ± 0.3**	**7.4 (5.1)**	**-198.08 ± 68.5**	**-20.2 (-8.9)**
Rump	GRL	-0.78 ± 0.5	-13.2 (-9.0)	**-248.17 ± 133.6**	**-25.3 (-11.2)**	0.07 ± 0.3	1.2 (0.8)	-79.13 ± 68.6	-8.1 (-3.6)
Topside	GRL	**-1.10 ± 0.5**	**-18.4 (-12.6)**	**-268.66 ± 133.4**	**-27.3 (-12.1)**	-0.17 ± 0.3	-2.9 (-2.0)	-32.17 ± 68.6	-3.3 (-1.4)
		Flock 3							
Eye shoulder	GRL	0.69 ± 0.4	11.6 (13.6)	**426.61 ± 198.0**	**43.4 (23.4)**	-0.11 ± 0.2	-1.9 (-2.2)	141.53 ± 94.4	14.4 (7.8)
Eye of rack	GRL	**0.82 ± 0.4**	**13.8 (16.2)**	315.66 ± 196.5	32.1 (17.3)	0.23 ± 0.2	3.9 (4.5)	-21.22 ± 94.2	-2.2 (-1.2)
Loin	GRL	-0.17 ± 0.4	-2.9 (-3.4)	-212.72 ± 195.8	-21.6 (-11.7)	0.21 ± 0.2	3.6 (4.2)	-144.87 ± 93.8	-14.7 (-7.9)
Knuckle	GRL	0.64 ± 0.4	10.7 (12.6)	**435.96 ± 198.3**	**44.4 (23.9)**	-0.19 ± 0.2	-3.2 (-3.7)	**173.29 ± 93.9**	**17.6 (9.5)**
Outside	GRL	0.38 ± 0.4	6.4 (7.5)	177.94 ± 196.6	18.1 (9.8)	0.03 ± 0.2	0.5 (0.6)	23.00 ± 94.1	2.3 (1.3)
Rump	GRL	-0.36 ± 0.4	-6.1 (-7.2)	-140.92 ± 197.7	-14.3 (-7.7)	-0.11 ± 0.2	-1.8 (-2.1)	2.41 ± 94.1	0.2 (0.1)
Topside	GRL	0.33 ± 0.4	5.5 (6.5)	173.22 ± 197.9	17.6 (9.5)	0.01 ± 0.2	0.1 (0.2)	32.00 ± 94.1	3.3 (1.8)
		Flock 4							
Eye of rack	GRL	0.30 ± 0.7	5.1 (2.7)	-5.80 ± 242.8	-0.6 (-0.2)	0.33 ± 0.6	5.5 (3.0)	63.70 ± 210.9	6.5 (2.7)
Loin	GRL	**0.67 ± 0.3**	**11.3 (6.1)**	-86.43 ± 87.8	-8.8 (-3.6)	**0.81 ± 0.3**	**13.6 (7.4)**	**-183.66 ± 70.1**	**-18.7 (-7.7)**
Knuckle	GRL	0.09 ± 0.3	1.6 (0.9)	-33.51 ± 87.4	-3.4 (-1.4)	0.15 ± 0.2	2.6 (1.4)	-55.34 ± 68.3	-5.6 (-2.3)
Topside	GRL	**0.51 ± 0.3**	**8.6 (4.6)**	-29.79 ± 87.0	-3.0 (-1.3)	**0.56 ± 0.2**	**9.5 (5.1)**	-78.72 ± 67.9	-8.0 (-3.3)

Bold $P < 0.1$

Table 12. F Values, numerator and denominator degrees of freedom (NDF, DDF) for models predicting liking of flavour scores in flocks (1, 2, 3, 4) using hot carcass weight (kg), loin IMF %, DXA lean % and DXA bone R. Random terms included animal identification and consumer within session.

Dependent variable: Liking of flavour	**Model 19: MSA model terms (HCWT, IMF %, lean %) & DXA bone R**		**Model 20: MSA model terms (HCWT, IMF %, lean %)**		**Model 21: IMF %, lean % & DXA bone R (no HCWT)**	
	NDF, DDF	**F-value**	**NDF, DDF**	**F-value**	**NDF, DDF**	**F-value**
Terms in models			**Flock 1**			
cut_cook	7, 7874	1.00	7, 7260	1.42	7, 7601	3.29***
Hot carcass weight	1, 108	0.17	1, 111	23.11***	NA	NA
Loin intramuscular fat %	1, 114	20.02***	1, 115	19.73***	1, 115	20.04***
DXA lean %	1, 111	0.51	1, 114	0.00	1, 114	0.75
DXA bone R	1, 110	4.18**	NA	NA	1, 113	27.90***
Hot carcass weight *cut_cook	7, 8090	0.78	7, 8025	4.34***	NA	NA
Loin intramuscular fat %*cut_cook	7, 7621	0.82	7, 7624	0.87	7, 7630	0.83
DXA lean %*cut_cook	7, 7939	1.32	7, 7582	0.95	7, 7725	1.40
Bone DXA R*cut_cook	7, 7986	1.23	NA	NA	7, 7915	4.73***
			Flock 2			
cut_cook	6, 5904	1.65	6, 5954	3.65***	6, 5991	2.50**
Hot carcass weight	1, 87	3.30*	1, 85	0.47	NA	NA
Loin intramuscular fat %	1, 88	6.40**	1, 88	7.57***	1, 89	6.38**
DXA lean %	1, 87	0.02	1, 88	0.53	1, 87	0.52
DXA bone R	1, 88	6.28**	NA	NA	1, 85	3.41*
Hot carcass weight *cut_cook	6, 5903	1.78*	6, 5996	2.06*	NA	NA
Loin intramuscular fat %*cut_cook	6, 5875	2.85***	6, 5886	2.98***	6, 5882	2.85***
DXA lean %*cut_cook	6, 5917	4.11***	6, 5939	4.45***	6, 5935	5.03***
Bone DXA R*cut_cook	6, 5912	1.83*	NA	NA	6, 6002	2.10**
			Flock 3			
cut_cook	6, 4406	1.27	6, 4486	0.43	6, 4517	0.67
Hot carcass weight	1, 66	0.54	1, 60	0.32	NA	NA
Loin intramuscular fat %	1, 59	0.00	1, 59	0.07	1, 59	0.03
DXA lean %	1, 65	2.20	1, 61	0.94	1, 62	1.67
DXA bone R	1, 66	1.25	NA	NA	1, 60	1.05
Hot carcass weight *cut_cook	6, 4407	1.23	6, 4510	0.54	NA	NA
Loin intramuscular fat %*cut_cook	6, 4483	0.87	6, 4498	0.95	6, 4497	0.98
DXA lean %*cut_cook	6, 4421	0.53	6, 4485	0.43	6, 4472	0.27
Bone DXA R*cut_cook	6, 4400	1.23	NA	NA	6, 4505	0.53
			Flock 4			
cut_cook	3, 5624	0.28	3, 5919	0.71	3, 5748	2.16*
Hot carcass weight	1, 376	1.37	1, 412	3.14*	NA	NA
Loin intramuscular fat %	1, 432	9.95***	1, 436	10.38***	1, 397	10.42***
DXA lean %	1, 399	5.04**	1, 280	17.86***	1, 412	8.31***
DXA bone R	1, 477	0.48	NA	NA	1, 627	1.23
Hot carcass weight *cut_cook	3, 5439	1.57	3, 5423	2.24*	NA	NA
Loin intramuscular fat %*cut_cook	3, 5553	3.00**	3, 5562	3.04**	3, 5670	3.20**
DXA lean %*cut_cook	3, 5640	0.21	3, 5905	0.97	3, 5968	0.08
Bone DXA R*cut_cook	3, 5599	0.20	NA	NA	3, 5751	1.82

*P < 0.1; **P < 0.05; ***P<0.01

NA term not in the starting model

Table 13. Coefficients ± s.e. and magnitude of effect of hot carcass wight (kg) and DXA bone R for models predicting liking of flavour scores showing magnitude of the effect across a 4 standard deviation range of all animals combined and across a 4 SD within individual flocks shown in brackets.

Dependent variable: Liking of flavour		**Model 19: MSA terms (HCWT, IMF%, lean%) & DXA bone R**				**Model 20: MSA terms (HCWT, IMF%, lean%)**		**Model 21: IMF%, lean % & DXA bone R**	
Covariate tested		**Hot carcass weight**		**DXA bone R**		**Hot carcass weight**		**DXA bone R**	
Cut	**Cook**	**coefficient ± s.e.**	**Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)**	**coefficient ± s.e.**	**Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)**	**coefficient ± s.e.**	**Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)**	**coefficient ± s.e.**	**Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)**
					Flock 1				
Shoulder	**RST**	0.29 ± 0.3	4.8 (4.9)	**-121.48 ± 55.1**	**-12.4 (-13.3)**	**0.95 ± 0.2**	**16.0 (16.4)**	**-162.96 ± 25.0**	**-16.58 (-17.9)**
Rack cutlet	**RST**	0.18 ± 0.3	3.0 (3.1)	**-100.36 ± 56.3**	**-10.2 (-11.0)**	**0.73 ± 0.2**	**12.3 (12.6)**	**-126.36 ± 25.4**	**-12.86 (-13.8)**
Loin	**GRL**	-0.35 ± 0.3	-5.9 (-6.0)	**-153.42 ± 56.8**	**-15.6 (-16.8)**	**0.48 ± 0.2**	**8.0 (8.2)**	**-102.03 ± 26.4**	**-10.38 (-11.2)**
Knuckle	**GRL**	-0.25 ± 0.3	-4.2 (-4.3)	-58.85 ± 56.3	-6.0 (-6.4)	0.07 ± 0.2	1.2 (1.2)	-22.84 ± 25.6	-2.32 (-2.5)
Outside	**GRL**	0.27 ± 0.3	4.5 (4.6)	-17.01 ± 56.4	-1.7 (-1.9)	**0.35 ± 0.2**	**6.0 (6.1)**	**-55.16 ± 25.6**	**-5.61 (-6.0)**
Rump	**GRL**	0.32 ± 0.3	5.3 (5.4)	-16.85 ± 56.3	-1.7 (-1.8)	**0.40 ± 0.2**	**6.8 (7.0)**	**-62.54 ± 25.6**	**-6.36 (-6.9)**
Topside	**GRL**	-0.08 ± 0.3	-1.3 (-1.4)	-49.61 ± 56.3	-5.0 (-5.4)	0.19 ± 0.2	3.2 (3.2)	-37.95 ± 25.6	-3.86 (-4.2)
Topside	**RST**	0.28 ± 0.3	4.7 (4.8)	-3.23 ± 55.2	-0.3 (-0.4)	**0.29 ± 0.2**	**4.9 (5.0)**	**-43.41 ± 24.9**	**-4.42 (-4.8)**
					Flock 2				
Eye shoulder	**GRL**	-0.04 ± 0.5	-0.6 (-0.4)	-25.12 ± 127.7	-2.6 (-1.1)	0.05 ± 0.3	0.9 (0.6)	-16.62 ± 65.2	-1.7 (-0.7)
Eye of rack	**GRL**	**-1.06 ± 0.5**	**-17.8 (-12.2)**	**-225.17 ± 127.6**	**-22.9 (-10.1)**	-0.29 ± 0.3	-4.8 (-3.3)	3.53 ± 65.3	0.4 (0.2)
Loin	**GRL**	-0.54 ± 0.5	-9.1 (-6.2)	-183.93 ± 127.8	-18.7 (-8.3)	0.09 ± 0.3	1.4 (1.0)	-65.11 ± 65.3	-6.6 (-2.9)
Knuckle	**GRL**	0.33 ± 0.5	5.5 (3.8)	-42.37 ± 127.6	-4.3 (-1.9)	0.48 ± 0.3	8.1 (5.6)	-114.18 ± 65.1	-11.6 (-5.1)
Outside	**GRL**	**-0.99 ± 0.5**	**-16.7 (-11.4)**	**-449.97 ± 127.9**	**-45.8 (-20.2)**	0.55 ± 0.3	9.3 (6.4)	-235.02 ± 65.1	-23.9 (-10.6)
Rump	**GRL**	-0.24 ± 0.5	-4.1 (-2.8)	-99.77 ± 127.6	-10.2 (-4.5)	0.11 ± 0.3	1.8 (1.2)	-46.97 ± 65.2	-4.8 (-2.1)
Topside	**GRL**	**-1.26 ± 0.5**	**-21.1 (-14.4)**	**-288.87 ± 127.5**	**-29.4 (-13.0)**	-0.26 ± 0.3	-4.3 (-2.9)	-18.75 ± 65.2	-1.9 (-0.8)
					Flock 3				
Eye shoulder	**GRL**	**0.71 ± 0.4**	**11.9 (14.0)**	**450.15 ± 187.3**	**45.8 (24.7)**	-0.14 ± 0.2	-2.3 (-2.7)	**160.67 ± 89.8**	**16.3 (8.8)**
Eye of rack	**GRL**	0.44 ± 0.4	7.4 (8.7)	142.59 ± 186.2	14.5 (7.8)	0.17 ± 0.2	2.9 (3.4)	-37.90 ± 89.6	-3.9 (-2.1)
Loin	**GRL**	-0.10 ± 0.4	-1.7 (-2.0)	17.00 ± 185.6	1.7 (0.9)	-0.14 ± 0.2	-2.3 (-2.7)	57.28 ± 89.3	5.8 (3.1)
Knuckle	**GRL**	-0.07 ± 0.4	-1.2 (-1.4)	5.80 ± 187.4	0.6 (0.3)	-0.09 ± 0.2	-1.5 (-1.8)	36.26 ± 89.4	3.7 (2.0)
Outside	**GRL**	-0.37 ± 0.4	-6.2 (-7.3)	-111.01 ± 186.2	-11.3 (-6.1)	-0.17 ± 0.2	-2.9 (-3.4)	39.07 ± 89.5	4.0 (2.1)
Rump	**GRL**	0.04 ± 0.4	0.7 (0.9)	82.79 ± 187.1	8.4 (4.5)	-0.12 ± 0.2	-2.0 (-2.4)	64.99 ± 89.7	6.6 (3.6)
Topside	**GRL**	0.52 ± 0.4	8.7 (10.2)	233.83 ± 187.1	23.8 (12.8)	0.07 ± 0.2	1.2 (1.5)	23.64 ± 89.5	2.4 (1.3)
					Flock 3				
Eye of rack	**GRL**	0.45 ± 0.7	7.6 (4.1)	35.13 ± 228.0	3.6 (1.5)	0.44 ± 0.6	7.4 (4.0)	66.87 ± 197.6	6.8 (2.8)
Loin	**GRL**	**0.48 ± 0.3**	**8.1 (4.4)**	-113.31 ± 81.0	-11.5 (-4.8)	**0.67 ± 0.2**	**11.2 (6.1)**	**-206.77 ± 63.9**	**-21.0 (-8.7)**
Knuckle	**GRL**	-0.12 ± 0.3	-2.0 (-1.1)	-73.27 ± 80.7	-7.5 (-3.1)	0.00 ± 0.2	0.0 (0.0)	-86.93 ± 62.2	-8.8 (-3.7)
Topside	**GRL**	0.32 ± 0.3	5.3 (2.9)	-62.87 ± 80.2	-6.4 (-2.6)	**0.42 ± 0.2**	**7.1 (3.9)**	-56.11 ± 61.7	-5.7 (-2.4)

Bold P < 0.1

Table 14. F Values, numerator and denominator degrees of freedom (NDF, DDF) for models predicting overall liking scores in flocks (1, 2, 3, 4) using hot carcass weight (kg), loin IMF %, DXA lean % and DXA bone R. Random terms included animal identification and consumer within session.

Dependent variable: Overall liking	**Model 22: MSA model terms (HCWT, IMF %, lean %) & DXA bone R**		**Model 23: MSA model terms (HCWT, IMF %, lean %)**		**Model 24: IMF %, lean % & DXA bone R (no HCWT)**	
	NDF, DDF	**F-value**	**NDF, DDF**	**F-value**	**NDF, DDF**	**F-value**
Terms in models			**Flock 1**			
cut_cook	7, 7930	1.13	7, 7211	1.85*	7, 7665	5.26***
Hot carcass weight	1, 109	0.11	1, 111	24.42***	NA	NA
Loin intramuscular fat %	1, 113	13.99***	1, 115	13.81***	1, 114	13.87***
DXA lean %	1, 111	1.18	1, 114	0.15	1, 114	1.53
DXA bone R	1, 110	4.92**	NA	NA	1, 112	30.09***
Hot carcass weight *cut_cook	7, 8101	1.55	7, 7996	7.35***	NA	NA
Loin intramuscular fat %*cut_cook	7, 7763	1.37	7, 7775	1.42	7, 7769	1.38
DXA lean %*cut_cook	7, 7965	1.26	7, 7753	0.99	7, 7821	1.40
Bone DXA R*cut_cook	7, 8010	1.29	NA	NA	7, 7920	6.99***
			Flock 2			
cut_cook	6, 5931	2.03*	6, 5981	4.84***	6, 6018	3.75***
Hot carcass weight	1, 89	4.19**	1, 87	0.19	NA	NA
Loin intramuscular fat %	1, 90	4.57**	1, 90	5.61**	1, 90	4.52**
DXA lean %	1, 89	0.01	1, 89	0.48	1, 89	0.52
DXA bone R	1, 90	6.90**	NA	NA	1, 87	2.84*
Hot carcass weight *cut_cook	6, 5931	1.27	6, 6025	2.68**	NA	NA
Loin intramuscular fat %*cut_cook	6, 5902	2.50**	6, 5915	2.61**	6, 5909	2.50**
DXA lean %*cut_cook	6, 5944	4.27***	6, 5967	5.05***	6, 5963	5.51***
Bone DXA R*cut_cook	6, 5939	2.50**	NA	NA	6, 6029	3.91***
			Flock 3			
cut_cook	6, 4416	1.47	6, 4495	0.67	6, 4525	2.09*
Hot carcass weight	1, 69	0.17	1, 62	1.13	NA	NA
Loin intramuscular fat %	1, 61	0.02	1, 62	0.00	1, 62	0.01
DXA lean %	1, 66	1.93	1, 63	0.84	1, 64	1.85
DXA bone R	1, 69	1.07	NA	NA	1, 62	2.07
Hot carcass weight *cut_cook	6, 4418	0.82	6, 4519	1.01	NA	NA
Loin intramuscular fat %*cut_cook	6, 4493	0.92	6, 4508	1.09	6, 4507	1.09
DXA lean %*cut_cook	6, 4430	0.29	6, 4494	0.70	6, 4480	0.27
Bone DXA R*cut_cook	6, 4409	1.38	NA	NA	6, 4513	1.56
			Flock 4			
cut_cook	3, 5766	0.41	3, 6034	0.99	3, 5892	1.72
Hot carcass weight	1, 359	1.59	1, 392	4.30**	NA	NA
Loin intramuscular fat %	1, 403	12.60***	1, 407	13.27***	1, 377	13.16***
DXA lean %	1, 375	4.80**	1, 271	19.01***	1, 392	7.46***
DXA bone R	1, 444	0.91	NA	NA	1, 585	1.86
Hot carcass weight *cut_cook	3, 5601	2.00	3, 5594	2.25*	NA	NA
Loin intramuscular fat %*cut_cook	3, 5688	3.50**	3, 5702	3.50**	3, 5808	3.48**
DXA lean %*cut_cook	3, 5783	0.72	3, 6015	1.63	3, 6109	0.20
Bone DXA R*cut_cook	3, 5743	0.33	NA	NA	3, 5897	1.43

*P < 0.1; **P < 0.05; ***P<0.01

NA term not in the starting model

Table 15. Coefficients ± s.e. and magnitude of effect of hot carcass wight (kg) and DXA bone R for models predicting overall liking scores showing magnitude of the effect across a 4 standard deviation range of all animals combined and across a 4 SD within individual flocks shown in brackets.

Dependent variable: Overall liking		**Model 22: MSA terms (HCWT, IMF%, lean%) & DXA bone R**				**Model 23: MSA terms (HCWT, IMF%, lean%)**		**Model 24: IMF%, lean % & DXA bone R**	
Covariate tested		**Hot carcass weight**		**DXA bone R**		**Hot carcass weight**		**DXA bone R**	
Cut	**Cook**	**coefficient ± s.e.**	**Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)**	**coefficient ± s.e.**	**Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)**	**coefficient ± s.e.**	**Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)**	**coefficient ± s.e.**	**Magnitude of effect: all flocks 4 SD range (individual flock 4 SD range)**
					Flock 1				
Shoulder	**RST**	0.45 ± 0.4	7.6 (7.8)	**-133.56 ± 58.8**	**-13.6 (-14.6)**	**1.18 ± 0.2**	**19.9 (20.4)**	**-199.38 ± 26.7**	**-20.29 (-21.9)**
Rack cutlet	**RST**	0.25 ± 0.4	4.1 (4.2)	**-133.15 ± 59.9**	**-13.5 (-14.6)**	**0.98 ± 0.2**	**16.4 (16.8)**	**-168.64 ± 27.0**	**-17.16 (-18.5)**
Loin	**GRL**	-0.56 ± 0.4	-9.4 (-9.7)	**-173.11 ± 60.6**	**-17.6 (-19.0)**	**0.37 ± 0.2**	**6.3 (6.4)**	**-90.95 ± 28.1**	**-9.25 (-10.0)**
Knuckle	**GRL**	-0.40 ± 0.4	-6.7 (-6.9)	-79.28 ± 60.1	-8.1 (-8.7)	0.03 ± 0.2	0.5 (0.6)	-21.18 ± 27.4	-2.16 (-2.3)
Outside	**GRL**	0.10 ± 0.4	1.8 (1.8)	-44.96 ± 60.1	-4.6 (-4.9)	**0.35 ± 0.2**	**5.8 (6.0)**	**-59.49 ± 27.4**	**-6.05 (-6.5)**
Rump	**GRL**	0.45 ± 0.4	7.6 (7.8)	-28.34 ± 60.1	-2.9 (-3.1)	**0.60 ± 0.2**	**10.1 (10.4)**	**-93.65 ± 27.4**	**-9.53 (-10.3)**
Topside	**GRL**	0.00 ± 0.4	0.1 (0.1)	-55.75 ± 60.2	-5.7 (-6.1)	**0.31 ± 0.2**	**5.1 (5.2)**	**-56.15 ± 27.4**	**-5.71 (-6.2)**
Topside	**RST**	0.31 ± 0.4	5.2 (5.3)	-21.35 ± 58.8	-2.2 (-2.3)	**0.43 ± 0.2**	**7.2 (7.3)**	**-66.55 ± 26.6**	**-6.77 (-7.3)**
					Flock 2				
Eye shoulder	**GRL**	0.12 ± 0.5	2.1 (1.4)	11.18 ± 136.1	1.1 (0.5)	0.09 ± 0.3	1.5 (1.0)	-14.71 ± 69.6	-1.5 (-0.7)
Eye of rack	**GRL**	-1.06 ± 0.5	-17.9 (-12.2)	-180.31 ± 135.9	-18.3 (-8.1)	-0.44 ± 0.3	-7.4 (-5.1)	48.98 ± 69.6	5.0 (2.2)
Loin	**GRL**	-0.76 ± 0.5	-12.9 (-8.8)	-219.35 ± 136.2	-22.3 (-9.9)	-0.01 ± 0.3	-0.2 (-0.2)	-52.75 ± 69.7	-5.4 (-2.4)
Knuckle	**GRL**	-0.10 ± 0.5	-1.7 (-1.1)	-94.95 ± 136.0	-9.7 (-4.3)	0.24 ± 0.3	4.0 (2.7)	-75.05 ± 69.5	-7.6 (-3.4)
Outside	**GRL**	**-1.14 ± 0.5**	**-19.1 (-13.1)**	**-561.81 ± 136.2**	**-57.2 (-25.3)**	**0.80 ± 0.3**	**13.4 (9.1)**	**-316.15 ± 69.5**	**-32.2 (-14.2)**
Rump	**GRL**	**-0.90 ± 0.5**	**-15.2 (-10.4)**	**-257.12 ± 136.0**	**-26.2 (-11.6)**	-0.01 ± 0.3	-0.2 (-0.2)	-62.56 ± 69.6	-6.4 (-2.8)
Topside	**GRL**	**-1.07 ± 0.5**	**-17.9 (-12.3)**	**-276.86 ± 135.8**	**-28.2 (-12.5)**	-0.11 ± 0.3	-1.8 (-1.3)	-46.95 ± 69.6	-4.8 (-2.1)
					Flock 3				
Eye shoulder	**GRL**	0.60 ± 0.4	10.1 (11.8)	**494.70 ± 194.4**	**50.3 (27.1)**	**-0.33 ± 0.2**	**-5.5 (-6.4)**	**250.16 ± 93.2**	**25.5 (13.7)**
Eye of rack	**GRL**	0.45 ± 0.4	7.5 (8.8)	151.04 ± 193.4	15.4 (8.3)	0.16 ± 0.2	2.8 (3.2)	-31.33 ± 93.0	-3.2 (-1.7)
Loin	**GRL**	-0.27 ± 0.4	-4.5 (-5.2)	**-119.09 ± 192.8**	**-12.1 (-6.5)**	-0.05 ± 0.2	-0.8 (-0.9)	-12.17 ± 92.8	-1.2 (-0.7)
Knuckle	**GRL**	0.09 ± 0.4	1.5 (1.8)	**197.45 ± 194.4**	**20.1 (10.8)**	-0.28 ± 0.2	-4.7 (-5.6)	**160.41 ± 92.8**	**16.3 (8.8)**
Outside	**GRL**	-0.12 ± 0.4	-2.0 (-2.3)	56.38 ± 193.3	5.7 (3.1)	-0.23 ± 0.2	-3.9 (-4.6)	104.67 ± 93.0	10.7 (5.7)
Rump	**GRL**	-0.18 ± 0.4	-3.0 (-3.5)	-9.05 ± 194.2	-0.9 (-0.5)	-0.16 ± 0.2	-2.8 (-3.2)	62.14 ± 92.9	6.3 (3.4)
Topside	**GRL**	0.13 ± 0.4	2.2 (2.6)	59.68 ± 194.3	6.1 (3.3)	0.02 ± 0.2	0.4 (0.5)	3.76 ± 93.1	0.4 (0.2)
Eye of rack					**Flock 4**				
Loin	**GRL**	0.80 ± 0.7	13.5 (7.3)	91.03 ± 231.5	9.3 (3.8)	0.75 ± 0.6	12.6 (6.8)	93.93 ± 200.2	9.6 (3.9)
Knuckle	**GRL**	0.37 ± 0.3	6.3 (3.4)	**-139.67 ± 85.1**	**-14.2 (-5.9)**	**0.60 ± 0.2**	**10.1 (5.5)**	**-219.53 ± 66.7**	**-22.3 (-9.2)**
Topside	**GRL**	-0.21 ± 0.3	-3.4 (-1.9)	**-135.72 ± 84.7**	**-13.8 (-5.7)**	0.02 ± 0.2	0.3 (0.2)	-98.17 ± 65.0	-10.0 (-4.1)
Shoulder	**GRL**	0.34 ± 0.3	5.6 (3.1)	-128.66 ± 84.3	-13.1 (-5.4)	**0.55 ± 0.2**	**9.2 (5.0)**	**-140.94 ± 64.6**	**-14.3 (-5.9)**

Bold P < 0.1

4.5 Hot versus cold DXA

When the mean R and STD of all carcass R, soft tissue R and bone R from the carcasses scanned hot was compared to the cold scanned carcasses there was a significant difference ($P < 0.01$). This was also true when the mean and STD of the soft tissue R and bone R values were compared ($P < 0.01$). This indicates, in this particular data set of 48 animals that scanning carcasses hot will yield a different result to scanning the same carcasses cold.

5. Discussion

5.1 The association of DXA bone R with eating quality traits

5.1.1 The impact of DXA bone R on cuts within individual flocks

The findings in this report demonstrate a negative association between DXA bone R in lamb scanned at commercial processing plants and their subsequent eating quality. This finding is the first time that the association has been demonstrated using AUS-MEAT accredited DXA devices with an improved algorithm for detecting bone in the images. The relationship between DXA bone R and eating quality align with a previous experiment where lambs were shown to have reduced overall liking scores associated with increasing DXA bone values as measured in the abattoir (Anderson et al., 2021). In previous studies when DXA bone variables were used to predict overall liking (Anderson et al., 2021) the inclusion of IMF %, lean % and DXA bone concurrently resulted in many cases the DXA term no longer being significant. This current experiment where the predictive power of DXA bone R was more powerful likely reflects the improved algorithm and calibration of the DXA system to better isolate bone pixels in the DXA images, making the DXA bone R term more independent of both IMF % and DXA lean %.

This is the first experiment to assess the relationship between DXA bone R values and MQ4 scores. A recent publication on the sheepmeat MSA eating quality prediction model (Pannier et al., 2025) has demonstrated the appropriate proportions to include the individual eating quality traits and allow for a better assessment of eating quality. Additionally, the individual traits (tenderness, juiciness, liking of flavour and overall liking) have been analysed in relation to DXA bone R, with earlier experiments focussing only on overall liking (Anderson et al., 2021). A key outcome of this experiment was to determine the relationship between DXA bone R and eating quality in the presence of supply chain measurements currently included in the MSA prediction model such as HCWT, IMF % and lean % (Pannier et al., 2025). In order to compare the magnitude of effect of DXA bone R on eating quality traits it was necessary to analyse each of the 4 flocks independently.

The strongest association of DXA bone R was observed in the saddle region of the carcass. The MQ4 of two cuts arising from the *Longissimus thoracis et lumborum* demonstrated a negative association with DXA bone R: the loin grill (Flocks 1, 2 and 4); rack cutlet roast (Flock 1); rack grill (Flock 2). The loin grill has previously shown a similar relationship with DXA bone R (Anderson et al., 2021), however the rack grill and rack cutlet roast have not been tested previously. It is difficult to compare the results of this experiment using DXA bone R with experiments investigating the impact of ossification in beef. However, Bonny et al. (2016) demonstrated more effects of ossification in the leg muscles.

For MQ4 scores there was a relatively consistent negative relationship between DXA bone R and loin grill scores. When comparing the magnitude of effect on MQ4 across the entire range 4 SD range of DXA bone R, there was a decrease of 15, 23 and 16 scores in Flocks 1, 2, and 4 which demonstrates the variation in the strength of the effect in different flocks. If this magnitude was only expressed across the 4 SD range within the flock this equated to 16, 10 and 7 in Flocks 1, 2 and 4. As an important comparison, the impact of IMF % which is a main driver of MQ4 within these flocks on loin grill MQ4 was 11, 10 and 11. Additionally DXA lean % had a less consistent effect on MQ4 in the loin grill than either DXA bone R or IMF %.

A moderate to high negative correlation existed between HCWT and DXA bone R, therefore it was important to determine if DXA bone R contributed more than HCWT alone. DXA bone R appears not to simply be a proxy for HCWT and describes eating quality variation across cut_cook combinations beyond what HCWT can describe alone in many instances and importantly in the loin cut.

There is generally a high correlation between eating quality traits (tenderness, juiciness, liking of flavour and overall liking) through the halo effect. Therefore, it is not unexpected that relationships between DXA bone R and the eating quality traits that the MQ4 score is comprised. One of the strongest effects was observed with tenderness which is not surprising given that this is considered a maturity effect.

For all eating quality traits, the strongest effects were seen in Flock 1 and Flock 2 and 4, however in contrast there was almost no association of MQ4 with DXA bone R in Flock 3. Flock 1 contained a large number of mutton and some lambs in the data and demonstrated a large range in DXA bone R which is likely reflecting the animal age. Flock 2 were a group of MLA Resource Flock hoggets that were held over until they were approximately 12 months of age and also underwent some degree of nutritional stress over the winter. Although having a small age range, being older and subjected to nutritional stress may have driven variation in both DXA bone R and their eating quality. Flock 4 were animals from an experiment that represented sheep from the general farming population representing a range of genetics, nutritional background and age. In contrast, Flock 3 although similar to Flock 2 being a single kill group from the MLA Resource Flock, were young with a small range in HCWT, IMF %, DXA lean % and SF. When this Flock was analysed there were very few traits which demonstrated an association with eating quality, with even the SF range small with only a moderate effect on MQ4.

The variation in the associations of DXA bone R with eating quality in different cuts is not surprising. In the beef MSA model ossification score, which is designed to reflect the impact of maturity on eating quality has a variable impact on different cut by cooking combinations (Watson et al., 2008). There are some cuts where the impact of ossification is large, however others where the impact of ossification is negligible. For sheep, animal age impacted eating quality to a greater magnitude in certain muscles (Pethick, Hopkins, et al., 2005) which may be due to the differences in collagen content (Hopkins et al., 2013) and cross linkage in muscles across the carcass. These studies in lamb indicate that age may be more influential on the higher quality muscles. This is in contrast to our findings where DXA bone R as a proxy for age had the most consistent effect on the loin. However ossification, although related to age may be more reflective of maturity at a given weight and therefore a better predictor of eating quality than age alone and therefore a good inclusion in future MSA prediction models.

5.1.2 The potential to include DXA bone R in an MSA prediction model

To align with the principles of establishing an eating quality prediction model an analysis was performed where all 4 flocks were combined. This analysis included flock as a random term in order to combine all the available data to predict various cut_cook combinations. Similarly to when individual flocks were analysed, MQ4 was predicted using the key variable include in the current MSA prediction model HCWT, IMF % and lean % were included in models alongside DXA bone R. When data was analysed with flock as a random term, most of the effects within cut_cook combinations remained significant, though magnitude of coefficient diminished. Similarly, when the covariates included were allowed to interact with the term cut_cook_flock. The effects of DXA bone R were not diminished, although notably the HCWT term decreased in significance as in the initial analysis. This is not surprising as we are combining data sets where there were minimal effects given they were young lambs with a minimal range in age and DXA bone R with a data sets with large age range and bone R.

These analysis demonstrated that DXA bone R was a significant predictor of MQ4 in cuts across the carcass with the other MSA predictors included in the models. The inclusion of DXA bone R alongside a measure of lean % such as GR tissue depth support the notion that the use of DXA bone R is not dependent on the inclusion of other DXA generated variables. Additionally, there are some situations where processing plants may sort carcasses based on GR tissue depth hot, then through the use of DXA in the boning room sort based on prediction of eating quality through DXA bone R and other variables.

As an additional test, SF was included in models along with DXA bone R and both terms remained significant. It has been demonstrated that increasing SF has a strong negative association with eating quality of lamb cuts (Hopkins et al., 2006; Hopkins et al., 2007). Therefore, although it is considered that DXA bone R is related to eating quality by representing increased maturity, it is not a proxy for SF. Therefore in the event that future measurement devices can be developed to predict shear force, they are unlikely to displace the use of DXA bone R from an eating quality prediction model.

There is confidence that, with the exception of Flock 3, animals in this current analysis represent a broad range of animals slaughtered at this abattoir having a wide range of HCWT, IMF % and lean %. Additionally, the DXA bone R range in these Flocks appear to be representative of the sheep population slaughtered at this processing plant as they fall within the range of DXA bone R from 35,585 animals slaughtered and scanned at this same processing plant over a period of 8 months (*Willimas per comms*).

There is further experimental work required before the DXA bone R trait could be considered for inclusion in an MSA eating quality model. Firstly, there is consideration about developing a “gold standard”, which in this case is difficult as the predicted trait is eating quality directly. This means that it would be difficult to calibrate individual DXA systems, beyond the standard calibration for prediction of DXA lean and fat %. Similar to other prediction traits such as IMF % and lean %, it can be difficult to apply a single “coefficient” across all data. Collection and analysis of more data is required to better understand the magnitude of the effects in different cuts and populations of animals.

5.2 The biology of the association of DXA bone R with eating quality

To date, the biology behind the association of DXA bone R and eating quality has not been determined. Advancing age is associated with reductions in eating quality as reviewed by Pannier et al. (2018). It is thought that increasing DXA bone R may be a reflection of animal age and/or maturity and is the reason DXA bone R demonstrates generally a negative relationship with sheepmeat eating quality. In humans, DXA has been well established as a measure of changes in bone mineral density (Bachrach, 2000; Pouilles et al., 1991; Syed & Khan, 2002) and has been used to assess bone mineral density in different age classes of beef cattle (López-Campos et al., 2018).

Within the beef MSA model, ossification is used in reference to the manual grading post slaughter of the calcification of the sacral and dorsal vertebrae (Polkinghorne et al., 2008). Beef cattle with increased ossification at a given carcass weight will incur an adjustment to their predicted MQ4 scores for some cuts (Watson et al., 2008). In beef it has demonstrated a better relationship with eating quality than age, prior to skeletal maturity (Bonny et al., 2016). The mechanism for the effect of ossification on eating quality is thought to be related to older animals having less soluble collagen (Young & Braggins, 1993) and increased cross linking (Bailey, 1985; Light et al., 1985). This experiment, however indicated that although increasing DXA bone R has a negative association with eating quality it is not directly linked to shear force with only moderate correlation between these two traits. Additionally, when SF was included in prediction models for eating quality both SF and DXA bone R remained significant in the models. This indicates that should a technology be developed that can adequately predict SF it is unlikely to displace the use of DXA bone R.

An increase in DXA bone R is thought to be associated with increased mineralisation of the bones and maturity. There is evidence that bone mineral content changes as sheep mature with Cake et al. (2006) demonstrating bone magnesium decreased during the growth period. There is limited data relating bone mineral content to DXA bone R and/or eating quality. A study by Payne et al. (2022) demonstrated a weak positive relationship between DXA bone R of the lumbar bones and magnesium, however this was linked to lean % of the carcasses. It is hard to draw conclusions from this work as it represented lambs that were processed and scanned using a different bone algorithm and further work on bone mineral content and DXA bone R is recommended. Bone mineralisation occurs as animals mature, however rather than resulting in a strong relationship between DXA bone R and bone mineral concentration, it may be that the structure of the bone represents the changes in maturity better. As such it may be useful to collect bones in future experiments not only for mineral analysis but also for histological examination.

5.3 Hot versus cold DXA scanning

The data available to analyse included 48 animals which had been scanned both hot and cold. The results of this analysis indicated that scanning carcasses hot will yield a different result to scanning the same carcasses cold. However, the carcasses used in this experiment were generated at a time when the calibration between days and within days was less sophisticated and prior to the development of the more advanced bone detection methods. It has previously been determined that the day and time within the day of scanning influences the R values. These calibration issues have been resolved sine the time of collection of the data analysed in this experiment, however the corrections are unable to be applied to this data set. As such it is necessary to obtain a new data set where carcasses are scanned both hot and cold using the current DXA scanning protocols. This will provide evidence around whether there is a difference in R values between hot and cold carcasses and whether this influences the determination of DXA fat and lean %.

5.4 Workshop – Industry Calibration Working Group

On June 10th- 11th 2025 there was a meeting of the Industry Calibration Working Group. At this meeting, the main results from this report were presented and discussed with key industry and scientific representatives relevant to the project. In addition to the results presented in this report, some further analysis of phenotypic data was presented as part of the working group objectives. In particular the presentation of the range of DXA bone R values from 35,585 animals slaughtered at a commercial processing plant over a period of 8 months. A small subset of these animals originated from the Meat and Livestock Resource Flock, which means there is information on their genetics and a range of production and phenotypic measurements at slaughter. This enabled a preliminary analysis of factors that may impact on DXA bone R which assists in the design of future experiments. Feedback from this workshop in part informs the design of future work on the DXA bone R trait to investigate the feasibility of introducing it into an MSA eating quality prediction model.

6 Conclusion

6.1 Key findings

This analysis demonstrates that DXA images obtained at chain speed in sheep processing plants can be used to generate DXA bone R, which represent the mean of the pixel values identified as carcass bone. DXA bone R demonstrates a relationship with eating quality through prediction of MQ4 in various cut and cook combinations across the carcass. The relationship between DXA bone R and MQ4 was demonstrated best when there was a large range in animal age. The negative relationship between DXA bone R and eating quality has good biological basis as largely indicates that with increased animal maturity there is a decrease in eating quality.

The saddle section of the lamb carcass showed the strongest relationships with DXA bone R with a negative relationship demonstrated in the rack cutlet roast (Flock 1), eye of rack grill (Flock 2) and the loin grill (Flock 1 and 2). There were other cuts that demonstrated an association with DXA bone R, however this varied by cut cook and flock combinations with a lack of consistency between the results. This can be partly explained by the nature of the data sets, whereby in some flocks the animals were young with minimal age range.

Importantly, DXA bone R remined significant in models when included alongside key traits measured in a sheep meat eating quality (HCWT, IMF % and carcass lean %). This indicates that it may provide an independent input into a cut by cook eating quality prediction model.

The mechanism behind the association of DXA bone R and MQ4 to date has not been elucidated. The relationship may partially reflect correlations with other traits such as HCWT, and DXA bone %. Future work is needed to review the equations that generate the DXA bone R values to determine if this can be further refined to decrease the associations and make bone R more independent of the other phenotypic traits.

Although the association of DXA bone R with eating quality is thought to reflect increased maturity, it appears to be largely independent of SF. To better elucidate the mechanism for the association of DXA bone R with eating quality it is necessary to identify associated environmental production, genetic and non-genetic factors (sex, phenotypic data).

Finally, the historical data set used to analyse the differences between hot and cold DXA scanning was not able to have the current algorithms applied to the images. Despite the analysis demonstrating differences between hot and cold scanning it will be necessary to undertake further experiments to make appropriate comparisons.

6.2 Benefits to industry

The red meat industry stands to benefit significantly from the use of DXA technology in predicting eating quality. It can provide rapid, objective assessments of carcass composition, and enables processors to better sort and grade meat based on its potential eating quality. This not only improves consistency and consumer satisfaction but could supports premium branding and pricing strategies. Additionally, integrating DXA into processing workflows can streamline operations and enhance data-driven decision making across the supply chain.

This research provides 3 keys benefits:

1. Enable supply chains to more confidently underpin premium and elite meat brands with eating quality claims. By integrating these insights into branding strategies, processors and marketers can differentiate their products in domestic and international markets.
2. Facilitate accelerated adoption for any processors utilising a hot DXA system among processors. This technology allows for real-time carcass assessment, improving processing speed and accuracy. By reducing barriers to adoption, processors can enhance operational efficiency, reduce costs, and improve consistency in meat quality grading.
3. Contributes to the refinement of the MSA Sheepmeat cuts-based model, potentially introducing greater precision in eating quality prediction. This sets Australia apart from other countries by offering a more robust system for lamb quality assessment. The improved model supports better decision-making across supply chain, from producers to retailers.

7 Future research and recommendations

7.1 Requirements to achieve DXA bone R as an AUS-MEAT trait

To establish a new trait for the Sheep Meat trading language, we forecast the need for several steps:

1. Construct a carefully designed dataset that would enable the robust estimation of DXA Bone R coefficients for inclusion in the MSA Cuts-Based Eating Quality Prediction Model.

2. Fundamental biology research to understand the link between DXA Bone R and the bone/muscle characteristics that underpin this linkage. This would enhance future experimental designs, helping to inform the production factors that need to be accounted for when generating the eating quality data.

3. Construct and test a calibration and reference standard methodology that ensures the existing and future DXA systems align with this original data set and the associated prediction coefficients. In particular this should be structured in a way that enable multiple DXA provider companies to seek accreditation to predict this trait.

4. Through analysis of the data acquired in Step 1 and 3 above, define a set of accreditation and auditing standards. This would have required accuracies that must be met, and an auditing protocol that could be routinely scrutinised by AUSMEAT.

5. Compilation of components 1 to 4 above would represent the basis for industry communication, Task Force and MSA Pathways approval, and ultimately an Australian Meat Industries Language and Standards Committee submission to establish this as a new trait in the Sheep Meat trading language.

7.2 A proposed experiment to establish coefficients for DXA Bone R to predict eating quality

The following experimental proposal would enable the initial estimation of DXA Bone R coefficients that could be integrated into the sheep meat MSA model for the prediction of eating quality. This structure is required to robustly estimate these coefficients. The design is described as the "ideal scenario", which we expect may be limited by the availability of suitable flocks.

7.2.1 Experimental design requirements

This experiment would make use of commercial sheep that vary in age. Resource Flock slaughter groups are not appropriate for this work, as each individual kill group represents only a narrow age range (approximately 10 to 20 days) due to the tightly controlled joining period of the ewes.

To assess how DXA bone R values vary, a preliminary analysis has been performed on 9 kill groups of Resource Flock lambs with known genetics and where DXA bone R and carcass data has been collected. Results indicate sire type differences in DXA bone R in lambs which have been corrected for HCWT (*Anderson pers comm)*. This indicates that future experiments need to include a balance of genotypes and ensure that animals were "finished" together prior to slaughter to give them similar nutritional and environmental conditions with balanced genotypes.

To date, there is no indication that there are differences in DXA bone R between sex, however given the potential for sex and parity to influence ossification at a given age (Scheffler et al., 2003; Waggoner et al., 1990) future experiments should be balanced for sex. If the parity and number of lambs born to ewes was known then it could be incorporated into the experimental design to assess their influence on DXA bone R and eating quality.

7.2.2 Selection of animals and data collection

Ideally, commercial sheep would be sourced from at least 6 different farms enabling us to assess the effect of environment within the design structure. From each farm we would source sheep ranging in age from young lambs (4-5 month wethers and ewes, n=24), older lambs (6-12 month wethers and ewes, n=24), yearlings (12 – 24 month wethers and ewes, n=24), 4-tooth wethers and ewes (2.5 years of age, n=24), and mature ewes of up to 8 years of age (n=24). These age-classes selected from each farm would be as genetically homogeneous as possible.

Sheep from all 6 farms would be transported to one "finishing farm", maintained as one flock for a period of at least 3 weeks, and then transported to slaughter at an abattoir with a functioning hot DXA system. These sheep would be slaughtered across at least 6 kill groups each separated by 1 week, balanced for equal representation of farm, age class, and sex.

This design would be repeated at least twice across the year to build a fragmented data set with multiple replications. Bone mass in sheep has been shown to change between seasons (summer v winter) (Arens et al., 2007) and a better understanding of how this may influence DXA bone R needs to be investigated.

This entire structure should be replicated in both the East (GMP) and West (WAMMCO) of Australia.

7.2.3 Selection of cuts

The range of cuts collected should include those from across the fore, saddle and hind sections, and should be assessed under both grill and roast cook method as previous work has shown that the effect of DXA bone R differs within the same cut when grilled or roasted. The impact that ageing of cuts has on the relationship between DXA bone R and eating quality also needs to be determined. A small preliminary analysis has been performed on animals that were eaten at 5 days and 70 days. The number of cuts and animals was small, however it appears that the relationship between DXA bone R and MQ4 may be diminished in cuts that have been aged for 70 days (A*nderson pers comms)*.

7.2.4 Carcass sampling

The biology of the DXA bone R trait has not been elucidated. Therefore, some biological benchmarking must be incorporated into future experiments. This would include, but is not limited to, HCWT, IMF%, carcass lean %, Shear Force and GR tissue depth. Although in this experiment Shear Force was only moderately correlated with DXA bone R, it is important to assess this relationship in future experiments as it seems mechanistically the most likely to show objective associations. In order to measure other parameters of maturity, we would also collect muscle samples for collagen content and collagen cross linkages.

Bone samples would be acquired from a range of anatomical locations for analysis of minerals (e.g. calcium, magnesium and phosphorus). Additionally, bone samples could be collected for histology to determine if structural changes to the bone better align with maturity compared to bone mineral content. Future work would incorporate the use of markers associated with the formation of bone (Camassa et al., 2017) which could potentially describe the relationships between maturity, DXA bone R and eating quality.

7.2.5 DXA scanning of animals

A robust experiment would include at least 2 DXA systems with numerous slaughter days, enabling us to account for environmental, seasonal, and site effects. All DXA images will be stored, along with phantom and clear field images to ensure accurate calibration across days, months, and sites. Additionally, reference standards for the DXA devices will be incorporated into the design of the experiment and image acquisition.

There is the opportunity to explore the methods for defining bone and soft tissue containing pixels. The isolation of bone pixels enables the generation of carcass DXA bone R values, which represent the mean value of these bone pixels. Further improving the identification of these bone-containing pixels may reduce the existing strong correlation between DXA bone R value and animal size (HCWT). This in-turn may improve the strength of the relationship between DXA bone R and eating quality and enhance the independence of its effect from animal size/HCWT. Any adaptations to the algorithms used to generate DXA bone R from the DXA images will not interfere with the ability of DXA to predict carcass composition or the DXA accreditation. However, it should be noted that if the enhanced bone identification techniques were to generate markedly superior prediction of carcass composition then there may be the potential to update algorithms and re-accredit the device.

In the current analysis DXA bone R is comprised of the average R value of the bone from the entire carcass. Future work could investigate isolating individual bones from across the carcass to determine if the individual bones are better predictors of eating quality compared to the entire carcass bone. Additionally, the bones at sites in close locality to individual cuts may demonstrate a stronger association with the eating quality of these cuts.

7.3 Hot versus cold DXA

Finally, to better compare hot versus cold scanning of carcasses a new data set needs to be obtained. The carcasses scanned both hot and cold should be selected across a range in weights, and fatness. The images obtained would be analysed using the modern processing methods which involves calibration adjustments to account for scan variation within and between days as well as a superior bone detection method. There is currently an experiment planned with these experimental design considerations in mind.

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