PREDICTING LAMB CARCASE COMPOSITION FROM CARCASE WEIGHT AND GR TISSUE DEPTH

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Abstract – Twenty eight lamb datasets with carcase weight, GR tissue depth and computed tomography (CT) composition data were used to demonstrate how well the industry standard measurements of hot carcase weight and GR tissue depth predict carcase fatness. Models predicting carcase CT Fat% were derived in each of 28 datasets then validated in the other 27 datasets. It was shown that the accuracy and precision of prediction using hot carcase weight and GR tissue depth is highly variable when these models were transported between datasets highlighting the need for a more robust industry measurement of carcase composition.

Key Words – Computed Tomography, fatness.

I. INTRODUCTION

Lean meat yield is an important profit driver for the sheep meat industry. The current industry standard for determining carcase composition is based on carcase weight and a measurement of fat depth by palpation of the GR site (located over the 12th rib 110mm from the mid line), yet this has been shown to be a highly imprecise estimate of lean meat yield [1]. This precision can be markedly improved by manually measuring GR tissue depth in millimeters, however reliance upon a single point measurement is still likely to introduce significant bias in genetically diverse populations [2]. Furthermore, there is concern within the Australian lamb industry that these measures are prone to bias due to human operator error as well as variation in abattoir processing. There is little data available to quantify this error, with a key limitation being the method for determining carcase composition. Historically this has been reflected through carcase bone out data, yet this is problematic due to varying bone out specifications across data sets, as well as large human imposed operator effects [3]. In Australia, with the introduction of computed tomography (CT) scanning methodologies, datasets are now available to assess the efficiency of predicting carcase composition using carcase weight and GR tissue depth [4]. This study assesses the capacity of GR tissue depth and carcase weight to predict carcase CT fat% across multiple datasets, testing the hypothesis that the precision and accuracy of this prediction would vary.

II. MATERIALS AND METHODS

This study made use of 28 datasets totaling 2289 lambs where CT estimates of carcase fat% (CT fat%), carcase weight and GR tissue depth measurements had been collected over a 9 year period. One of these data sets (dataset 28, Table 1) consisted of lamb carcases that were sourced over a 45 minute period immediately following slaughter from a commercial abattoir near Bordertown, SA. These lambs were selected randomly across a broad range of fatness and carcase weight, hence their parentage is unknown. The remaining 27 of these datasets were individual slaughter groups of lambs from Meat and Livestock Australia's Nucleus Flock experiment, or from the Sheep Cooperative Research Centers Information Nucleus Flock experiment, the designs of which are detailed in Fogarty et al [5]. The lambs (Merino, Maternal x Merino, Terminal x Merino and Terminal x Border Leicester-Merino) were the progeny of 433 industry sires, representing the major sheep breeds used in the Australian industry. The siretypes included Terminal sires (Poll Dorset, Suffolk, Texel, White Suffolk), Maternal sires (Border Leicester, Coopworth, Dohne Merino), and Merino sires (Merino, Poll Merino). Each dataset represents a slaughter group which was balanced for sire breed. In all cases tissue depth at the GR site and hot carcase weight were measured within 1 hour of slaughter. CT scanned data was captured between 2 and 5 days post mortem using the scanning procedure and image analysis method described by Anderson et al [2].

General linear models were used to predict CT fat% from hot carcase weight and GR tissue depth using leave-one-out cross-validation (GLM Select procedure in SAS). To demonstrate transportability equations were derived in each dataset separately and then further validated in each of the remaining 27 datasets. Thus 28 models were tested, each across 27 datasets producing a total of 756 validation tests. For the relationship between actual versus predicted CT fat%, R-square (R^2) of the prediction and root mean square error of the prediction (RMSEP) are shown as indicators of precision, and slope of the relationship and bias estimates are shown to represent accuracy. Bias represents the difference between the predicted and actual values at the median of the dataset.

III. RESULTS AND DISCUSSION

Descriptive statistics for all 28 datasets are shown in Table 1. Within the training data across each of the 28 datasets the RMSE for predicting CT fat% varied markedly, ranging between 1.67 to 3.10 CT fat% units, describing as little as 15% and as much as 77% of the variation within these populations.

Table 1. Descriptive statistics including animal numbers (n), and mean ± standard deviation (minimum, maximum) for CT fat %, GR tissue depth and hot standard carcase weight.

	n	CT fat %		GR tissue depth (mm)		Hot Standard Carcase Weight (kg)	
Dataset 1	95	23.19 ± 3.09	(16.37 , 30.28)	10.91 ± 3.52	(4 , 22)	21.5 ± 2.5	(16.0 , 29.6)
Dataset 2	72	22.12 ± 2.74	(17.06 , 28.88)	9.65 ± 2.50	(3 , 17)	20.9 ± 1.7	(17.4 , 24.6)
Dataset 3	63	23.83 ± 3.18	(17.54 , 32.57)	11.02 ± 2.43	(6 , 17)	20.0 ± 1.2	(17.6 , 22.8)
Dataset 4	97	29.33 ± 3.70	(21.09 , 37.63)	18.93 ± 4.56	(7 , 30)	27.8 ± 3.7	(19.2 , 39.6)
Dataset 5	99	33.48 ± 3.09	(26.73 , 41.27)	24.88 ± 3.84	(14 , 30)	31.8 ± 3.3	(23.0 , 40.0)
Dataset 6	98	23.22 ± 3.85	(13.53 , 33.15)	9.07 ± 3.89	(3 , 22)	19.7 ± 2.8	(15.4 , 28.8)
Dataset 7	96	31.03 ± 3.61	(22.96 , 38.30)	20.17 ± 5.02	(9 , 30)	27.7 ± 3.4	(18.8 , 34.8)
Dataset 8	95	27.96 ± 3.91	(19.03 , 37.17)	17.32 ± 5.58	(4 , 30)	23.6 ± 4.8	(13.5 , 35.0)
Dataset 9	93	22.85 ± 3.23	(15.65 , 31.77)	9.38 ± 3.58	(2 , 17)	20.0 ± 3.3	(13.5 , 29.0)
Dataset 10	98	27.32 ± 3.52	(20.16 , 34.56)	15.30 ± 5.14	(6 , 28)	23.5 ± 4.6	(13.0 , 34.2)
Dataset 11	93	29.53 ± 4.53	(18.41 , 39.53)	19.76 ± 7.72	(5 , 44)	26.2 ± 6.1	(13.2 , 39.3)
Dataset 12	99	25.99 ± 4.00	(18.62 , 36.55)	14.33 ± 5.49	(5 , 30)	21.3 ± 4.9	(12.3 , 33.5)
Dataset 13	99	27.68 ± 4.21	(17.11 , 36.47)	15.71 ± 6.03	(2 , 36)	22.1 ± 5.4	(10.9 , 37.1)
Dataset 14	59	28.76 ± 3.49	(18.15 , 35.21)	17.64 ± 5.46	(5 , 27)	24.2 ± 3.5	(15.6 , 29.6)
Dataset 15	57	28.55 ± 3.11	(22.96 , 38.05)	18.67 ± 3.58	(11 , 28)	26.9 ± 2.1	(22.6 , 31.6)
Dataset 16	56	26.49 ± 3.46	(17.26 , 33.36)	16.48 ± 3.60	(7 , 24)	25.7 ± 2.4	(19.8 , 30.6)
Dataset 17	94	29.14 ± 4.09	(20.57 , 39.69)	15.52 ± 5.36	(2 , 25)	24.1 ± 4.3	(15.3 , 33.5)
Dataset 18	68	29.50 ± 3.31	(21.83 , 38.85)	16.10 ± 4.13	(7 , 25)	26.2 ± 3.5	(19.3 , 33.6)
Dataset 19	93	25.14 ± 3.54	(18.81 , 33.89)	11.05 ± 3.63	(3 , 21)	22.2 ± 2.8	(16.1 , 29.6)
Dataset 20	58	26.14 ± 3.74	(17.44 , 33.42)	11.70 ± 3.73	(5 , 25)	23.2 ± 2.2	(18.7 , 29.7)
Dataset 21	60	23.94 ± 2.60	(17.44 , 30.19)	10.90 ± 3.34	(4 , 19)	21.4 ± 2.5	(16.0 , 27.9)
Dataset 22	52	29.68 ± 3.19	(22.39 , 37.74)	22.44 ± 3.16	(13 , 29)	28.6 ± 2.6	(23.3 , 36.0)
Dataset 23	78	25.79 ± 4.03	(16.60 , 37.51)	13.68 ± 4.45	(3 , 24)	22.3 ± 2.9	(14.3 , 27.4)
Dataset 24	95	23.99 ± 3.31	(16.09 , 32.57)	9.99 ± 4.40	(3 , 25)	20.9 ± 2.7	(13.5 , 27.4)
Dataset 25	88	25.26 ± 2.88	(18.87 , 31.37)	15.64 ± 3.77	(9 , 25)	24.6 ± 1.7	(20.8 , 29.0)
Dataset 26	99	23.86 ± 2.98	(17.70 , 30.16)	10.15 ± 3.68	(3 , 21)	21.0 ± 2.0	(16.2 , 25.8)
Dataset 27	87	20.55 ± 2.55	(15.42 , 28.17)	7.90 ± 2.90	(3 , 16)	19.8 ± 2.2	(16.5 , 26.6)
Dataset 28	48	21.74 ± 3.99	(12.70 , 33.81)	14.63 ± 5.40	(5 , 27)	24.7 ± 4.4	(17.4 , 32.2)

When the 28 trained models were validated across each of the other datasets the precision and accuracy indicators showed marked variation. Across the 756 validation tests the RMSEP values averaged 2.36, yet ranged between 1.67 to 3.33 CT fat% units, with a standard deviation of the RMSEP values of 0.30 CT fat% units (Table 2). Similarly the R^2 values averaged 0.52, yet ranged between 0.12 and 0.77, with a standard deviation of the R^2 values of 0.15. This highlights substantial variation in precision. The accuracy indicators also varied, with bias values ranging between 6.83 to -6.95 and a standard deviation of 2.08 CT fat% units (Table 2). Furthermore, the slope of these relationships also deviated markedly from 1, ranging between 0.51 to 2.00, with a standard deviation in slope values of 0.25 (Table 2), implying that the bias would change markedly if it were estimated at a value higher or lower than the median CT fat%.

Table 2. Precision and accuracy estimates for the relationship between actual CT fat % and predicted CT fat % from models containing hot carcase weight (kg) and GR tissue depth (mm). Precision estimates include R-square and root mean square error of the prediction, and accuracy estimates include slope of the relationship and bias at the median. Values are shown for the mean, standard deviation, minimum and maximum from testing 28 models across 27 datasets, a total of 756 validation tests.

	Mean	Standard Deviation	Minimum	Maximum
R^2	0.52	0.15	0.12	0.77
RMSEP	2.36	0.30	1.67	3.33
Slope	1.00	0.25	0.51	2.00
Bias	1.60*	2.08	-6.95	6.83

*The average of the absolute values of bias is reported.

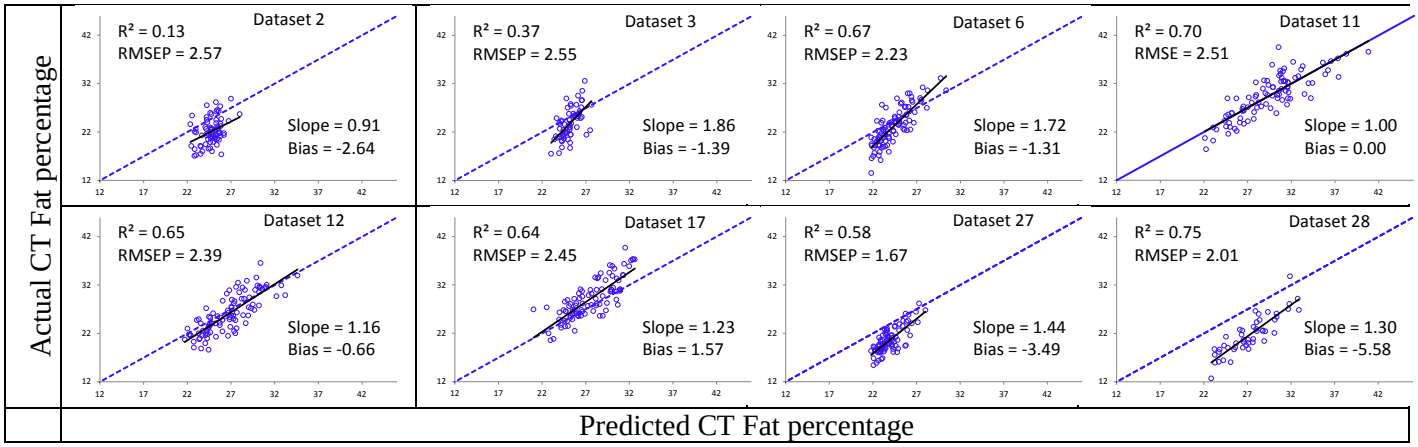

Figure 1. Relationship between actual CT fat % and predicted CT fat % from a model containing hot carcase weight (kg) and GR tissue depth (mm). A small number of datasets are selected to demonstrate how the model was trained (in this case in dataset 11) and then validated in the other data sets. Dashed lines represent a perfect prediction; solid lines show the average prediction in the validation dataset.

Figure 1 provides an example of the process of training the model, in this case in dataset 11 with an RMSE of 2.51 and R^2 of 0.70, and then validating it across the remaining datasets. In this example validation tests are shown for only 7 of the remaining 27 datasets as examples.

In support of our hypothesis, these results highlight the substantial variation in prediction precision and accuracy when using carcase weight and a single point measure of tissue depth to reflect carcase fatness. This work aligns well with previous studies where carcase weight and GR tissue depth demonstrated poor precision [1] and limited ability to differentiate between genetically diverse lines of sheep [6]. In part this variability in precision and accuracy would be driven by differences in data range between the datasets, potentially causing some extrapolation beyond the range of the training data. However the datasets used (see Table 1) all had broad variation with data ranges that substantially overlapped, hence in most cases there was relatively little extrapolation. As such, the variability in prediction is likely due to a number of other factors. Firstly use of a single measure of tissue depth to reflect carcase fatness relies upon accurate and consistent measurement. Although these are experimental datasets in which great care has been taken during the collection of GR tissue depth, there are still likely to be processing and operator effects which would show up most strongly between datasets. Furthermore, under commercial conditions within those abattoirs that measure GR tissue depth there is likely to be even greater variability due to operator error when working at speed. Alternatively, it should be noted that most Australian abattoirs don't measure GR tissue depth directly, instead using palpation of the carcase to estimate this measure. Hence under commercial conditions the prediction of carcase fatness would be even more variable than that demonstrated in this study. Secondly the prediction of carcase fat composition relies upon a strong correlation between GR tissue depth at its site of measurement with fat composition elsewhere in the carcase. However, there is evidence that suggests that genetics can strongly influence this correlation, redistributing bone, muscle and fat within the carcase [2, 4]. Therefore the genetic differences present across datasets may offer an additional source of error contributing to the bias and variable precision. In the present study this effect may be limited as the datasets used are derived from nucleus flock slaughters, with strong genetic linkage between these groups through common sires or common dams. The only exception to this was for dataset 28 which consisted entirely of randomly sourced animals of unknown parentage, thus it is not surprising that this group demonstrated substantial bias (example shown in Figure 1). Therefore, based on the genetic variation present in Australian sheep flocks, and the

likely increase in measurement error under commercial conditions, we conclude that the variation in bias and precision demonstrated in this study could well be understating that present in commercial reality.

IV. CONCLUSION

These results demonstrate the variability in estimating carcase fat composition from carcase weight and GR tissue depth. Factors influencing this prediction include restricted range of training data, measurement and processing error, and genetic differences between groups. This illustrates why the Australian sheep industry has little confidence in these measurements to reflect carcase composition and highlights the need for a whole carcase composition measurement that is independent of breed, processing and operator error.

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