Comparison of two live-animal ultrasound systems for genetic evaluation of carcass traits in Angus cattle

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ABSTRACT: The improvement of carcass traits is an important breeding objective in beef cattle breeding programs. The most common way of selecting for improvement in carcass traits is via indirect selection using ultrasound scanning of selection candidates which are submitted to genetic evaluation programs. Two systems used to analyze ultrasound images to predict carcass traits are the Pie Medical Esaote Aquila (**PIE**) and Central Ultrasound Processing (**CUP**). This study compared the ability of the two systems to predict carcass traits for genetic evaluation in Australian Angus cattle. Genetic and phenotypic parameters were estimated using data from 1,648 Angus steers which were ultrasound scanned twice with both systems, first at feedlot entry and then following 100 d in the feedlot. The traits interpreted from ultrasound scanning included eye muscle area (**EMA**), rib fat (**RIB**) rump fat (**RUMP**), and intramuscular fat (**IMF**). Abattoir carcass data were collected on all steers following the full feedlot feeding period of 285 d. For all ultrasound scan traits, CUP resulted in higher phenotypic and genetic variances compared to the PIE. For IMF, CUP had higher heritability at feedlot intake (0.51 for CUP compared to 0.37 for PIE) and after 100 d feeding (0.54 for CUP compared to 0.45 PIE). CUP predicted IMF also tended to have stronger correlations with the breeding objective traits of carcass IMF and marbling traits, both genetically (ranging from 0.59 to 0.75 for CUP compared to 0.45–0.63 for PIE) and phenotypically (ranging from 0.27 to 0.43 for CUP compared to 0.19–0.28 for PIE). Ultrasound scan EMA was the only group of traits in which the heritabilities were higher for PIE (0.52 for PIE compared to 0.40 for CUP at feedlot intake and 0.46 for PIE compared to 0.43 for CUP at 100 d of feeding), however with similar relationships to the breeding objective carcass EMA observed. For subcutaneous fat traits of ultrasound RIB and RUMP, the heritabilites and genetic correlations to the related carcass traits were similar, with the exception being the higher heritability observed for CUP predicted RUMP at feedlot intake at 0.52 compared to 0.38 for PIE. The results from this study indicates that the CUP system, compared to PIE, provides an advantage for genetic evaluation of carcass traits in Angus cattle, particularly for the IMF and associated marbling traits.

Key words: Angus, beef cattle, carcass, genetic parameters, phenotypic parameters ultrasound

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INTRODUCTION

A common breeding objective for beef producers is to improve carcass traits of animals used

in breeding programs. Traditionally, carcass traits have proven expensive and difficult to measure and they cannot be measured on selection candidates. Due to this limitation, breeders use correlated ultrasound scan measurements on the live animal, submitted to genetic evaluation programs, to increase selection accuracy for carcass traits related to meat quantity and quality, including eye muscle area (**EMA**), rib fat (**RIB**) rump fat (**RUMP**) and intramuscular fat (**IMF**). Since becoming available in the mid-1990s, ultrasound scanning for carcass traits has been widely adopted in beef cattle breeding programs. During this period, ultrasound scan records on over 640,000 animals have been recorded in the Angus Australia performance database and included in genetic evaluation and the production of Estimated Breeding Values for carcass traits (A Byrne, Angus Australia, pers. comm., August 31, 2020).

The most common ultrasound scanning technology used to predict carcass traits in Australian Angus herds is the Esaote Aquila system produced by Pie Medical (PIE). This technology facilitates crush-side and real-time image capture, interpretation and analysis using inbuilt software and algorithms. An alternative approach, which is commonly used in the United States of America, is the Central Ultrasound Processing (**CUP**) system. The CUP system uses different software, algorithms and processes to predict carcass traits through a centralized image analysis laboratory based on images that are also captured crush-side through ultrasound scanning.

Previous studies have published estimates of genetic and phenotypic parameters using Angus cattle for carcass traits based on ultrasound scan records (Reverter et al., 2000; Kemp et al., 2002; Boerner et al., 2013), but none of these compared different ultrasound scan systems. Herring et al. (1998) compared four ultrasound scan systems, but focused solely on the phenotypic prediction of carcass IMF. No other comparisons have been published describing the precision of different live animal ultrasound systems for predicting carcass traits, or the genetic parameters between the different systems, including their relationships to the direct carcass traits.

The objective of this study was to estimate phenotypic and genetic parameters for the ultrasound scan measured traits (IMF, EMA, RIB, and RUMP) to compare the two live-animal ultrasound systems (PIE and CUP) and determine their genetic relationships with the direct carcass breeding objective traits for genetic evaluation programs.

MATERIALS AND METHODS

Animal Care

Records collected during the feedlot feeding period were subject to animal ethics approval AEC12-082. Data for carcass traits were collected as part of routine commercial animal management and, therefore, not subject to animal care and animal ethics committee approval.

Animals, Phenotypes, and Pedigree

All phenotypic data, associated fixed effects and pedigree data used in this study were supplied by Angus Australia and generated from the Angus Sire Benchmarking Program, also known as the Angus Beef Information Nucleus (BIN), described by Parnell et al. (2019). The animals in the study (n = 1,648), born across 2011–2015 calving years, were straightbred steer progeny of Angus sires (n = 173) and Angus dams (n = 1,448) from seven different co-operator herds located in New South Wales and Victoria, Australia. Of the dams, the majority had a single progeny represented, while 190 had two or more progeny included in the study.

In contemporary groups, the progeny were ultrasound scanned twice, first at feedlot entry at an average age of 511 d (SD 72.4), then following an average of 103 d in a feedlot at an average age of 614 d (SD 78.4). The steers were then harvested for slaughter, staying in their contemporary groups (i.e., no selective harvesting), at an average age of 795 d (SD 70.0) following the full feeding period of approximately 285 d.

The first feedlot phase (initial 103 d on average) was undertaken at Tullimba, Kingstown, NSW, Australia, where the steers had ad libitum access to a ration composed of 74.8% tempered barley, 4.6% cotton hulls, 6% cottonseed, 5% mill run, 4.6% chopped hay, and 5% liquid mineral supplement. Here, they were fed utilizing the GrowSafe feeding system (GrowSafe Systems Ltd., Airdrie, Alberta, Canada). Following this first feedlot phase, the steers were relocated for phase two (final 182 d on average) to Rangers Valley Feedlot, Rangers Valley, NSW to finish the feeding program. Here, they were fed a similar ration under a normal, controlled commercial feeding program.

All animals were ultrasound scanned at the 12th and 13th rib site and P8 site by one accredited and experienced technician (Upton et al., 1999). All steers within a contemporary group were scanned on the same day with the

Esaote Aquila system (Pie Medical, Maastricht, The Netherlands) equipped with a 3.5-MHz, 18-cm transducer. EMA, RIB, RUMP, and IMF were measured using the PIE software providing a real-time prediction at feedlot intake (InP-EMA InP-RIB, InP-RUMP, and InP-IMF, respectively) and repeated after 103 d on average in the feedlot (100dP-EMA 100dP-RIB, 100dP-RUMP, and 100dP-IMF, respectively). At the same time, images using the same ultrasound hardware, from the same physiological locations on the animal, were captured using CUP image capture software and sent to the CUP laboratory (Ames, Iowa, USA) for image interpretation and prediction of the same traits as the PIE system. Being EMA, RIB, RUMP, and IMF at feedlot intake (InC-EMA InC-RIB, InC-RUMP, and InC-IMF, respectively) and after 103 d on average in the feedlot (100dC-EMA 100dC-RIB, 100dC-RUMP, and 100dC-IMF, respectively). The phenotypes returned from CUP compared to PIE were reported to an extra decimal place (e.g., two compared to one) which may be considered additional precision.

At the end of the feeding period, steers were harvested, on the same day, within contemporary groups (i.e., no selective harvesting). On the day of harvest, hot standard carcass weight (C-WT) and hot rump fat (C-RUMP) measured on the P8 site were collected. The following day the chilled carcasses were graded by experienced Meat Standards Australia (MSA) graders (Polkinghorne et al., 2008) for eye muscle area (C-EMA), rib fat (C-RIB), MSA marbling score (C-MMBL) and AUS-MEAT marbling score (C-AMBL) (AUS-MEAT, 2020). All carcass grade data was collected by the one grader on each steer carcase. Additionally, meat samples were collected from the grading site, at the 12th and 13th rib, and assessed for IMF (C-IMF) using soxhlet calibrated near-infrared spectrophotometry (NIR), described by Perry et al. (2001). To ensure consistency and data quality, experienced Angus Australia staff oversaw all collection on the live steers and their carcasses in the abattoir.

The EMA trait measured in this study by PIE, CUP, and on the carcass, is also commonly referred to as rib eye area (REA). Furthermore, in Australian abattoirs, hot carcasses are routinely measured for subcutaneous fat depth at the P8 site, also referred to as rump fat, as an indicator of sealable meat yield and market suitability. The P8 site is defined as the point of intersection of a line from the dorsal tuberosity of the tripartite tuber ischii parallel with the chine, and a line at 90° to the sawn chine centered on the crest of the spinous process of the third sacral vertebrae (AUS-MEAT, 2020).

Additionally, all animals in this study with CUP phenotypes also had the matching PIE phenotype recorded. Some steers with PIE phenotypes did not have the matching CUP phenotype, mainly due to the CUP image capture system not being available at three scanning events accounting for 173 steers at feedlot intake and 66 steers at 100 d of feeding. A smaller number of animals could not have phenotypes provided by CUP due to the image quality not meeting the required standards for phenotype interpretation. This ranged from 10 to 22 steers across the ultrasound scan traits and events. The number of records and descriptive statistics for all traits are shown in Table 1.

Analysis Models

ASReml software (Gilmour et al., 2009) was used to model each trait and to estimate parameters based on univariate and bivariate mixed model analysis including up to three generations of pedigree. Maternal grandparents of the steers were unknown from five of the seven co-operator herds. Fixed effects fitted in all models included the contemporary group and dam age. Age at measurement was fitted by linear regression for ultrasound scan traits, while carcass weight was fitted by linear regression for each of the other carcass traits. The contemporary group included animals from the same herd, year of birth, birth type (twin v single), breeder-defined management group, and observation date (ultrasound scan or harvest date). This resulted in 54 unique contemporary groups for the ultrasound scan traits including an average of 30 animals and 53 unique contemporary groups for the carcass traits including an average of 26.4 animals. In all cases, contemporary group was a significant fixed effect ($P < 0.001$), while the level of significance varied for the other fixed effects. For consistency, the fixed effects as described above were included in all models. The univariate animal models are expressed as

$$y = Xb + Zu + e$$

where $\boldsymbol{y}$ is the vector of the trait phenotype; $\boldsymbol{X}$ is the matrix which relates to the fixed effects; $\boldsymbol{b}$ is the vector of the fixed effect of the traits analysed; $\boldsymbol{Z}$ is the matrix which relates to the animal effect; $\boldsymbol{u}$ is the vector of the random additive genetic effect of the animal; and $\boldsymbol{e}$ is the vector of residual effects for the traits analysed. The expectations and variance matrices for random vectors are described as

Table 1. Descriptive statistics

Trait	Unit of measure	*n*	Mean	SD	Minimum	Maximum	CV (%)
Ultrasound scan at feedlot intake*							
InP-IMF	%	1,622	4.5	1.2	1.3	7.7	26.5
InC-IMF	%	1,457	4.9	1.8	1.1	10.3	35.8
InP-EMA	cm^2	1,647	59.7	5.6	41.0	79.0	9.4
InC-EMA	cm^2	1,457	61.0	7.1	42.6	93.5	11.7
InP-RIB	mm	1,648	4.4	1.8	1.0	11.0	40.9
InC-RIB	mm	1,460	5.3	2.3	1.0	16.8	43.4
InP-RUMP	mm	1,648	5.7	2.5	1.0	17.0	43.9
InC-RUMP	mm	1,458	5.3	2.6	0.8	17.0	49.1
Ultrasound scan at 100 d feeding†							
100dP-IMF	%	1,508	7.2	1.0	3.5	8.3	13.3
100dC-IMF	%	1,432	6.0	1.8	1.3	11.9	29.8
100dP-EMA	cm^2	1,508	80.7	8.0	46.0	104.0	9.9
100dC-EMA	cm^2	1,420	83.5	8.6	58.7	115.5	10.3
100dP-RIB	mm	1,508	10.5	2.1	5.0	22.0	20.0
100dC-RIB	mm	1,429	13.6	3.3	5.3	26.4	24.3
100dP-RUMP	mm	1,508	14.0	3.3	5.0	31.0	23.6
100dC-RUMP	mm	1,432	14.0	3.5	4.6	30.5	25.0
Carcass‡							
C-IMF	mm	1,475	10.1	3.3	3.2	25.1	32.6
C-AMBL	score	1,473	2.7	1.2	0.0	8.0	46.4
C-MMBL	score	1,474	514.4	120.2	160.0	1030.0	23.4
C-EMA	cm^2	1,460	90.2	9.6	66.0	124.0	10.6
C-RIB	mm	1,450	18.7	5.5	6.0	40.0	29.4
C-RUMP	mm	1,462	23.2	6.3	10.0	50.0	27.2
C-WT	kg	1,462	460.2	37.4	334.9	568.6	8.1

*Steers ultrasound scanned at feedlot intake at an average age of 511 d (SD 72.4).

†Steers ultrasound scanned after an average of 103 d on feed, at an average age of 614 d (SD 78.4).

‡Steers harvested and graded at an average age of 796 d (SD 70.0) following an average feedlot period of 285 d.

$$E\begin{bmatrix} y \\ u \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \end{bmatrix}; V\begin{bmatrix} u \\ e \end{bmatrix}$$

The bivariate animal models are expressed as

$$Y = Xb + Zu + e$$

where $\boldsymbol{Y}$ is the vector of the trait phenotypes; $\boldsymbol{X}$ is the matrix which relates to the fixed effects; $\boldsymbol{b}$ is the vector of the fixed effects of the traits analysed; $\boldsymbol{Z}$ is the matrix which relates to the animal effect; $\boldsymbol{u}$ is the vector of the random animal effects; and $\boldsymbol{e}$ is the vector of residual effects for the traits analyzed. The expectations and variance matrices for random vectors are described as

$$E\begin{bmatrix} y \\ u \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \end{bmatrix}; V\begin{bmatrix} u \\ e \end{bmatrix} = \begin{bmatrix} G \\ R \end{bmatrix} = \begin{bmatrix} A \otimes G & 0 \\ 0 & I \otimes R \end{bmatrix}$$

Where $\boldsymbol{G}$ and $\boldsymbol{R}$ denote the 2 × 2 matrices containing additive genetic and residual variance components; $\boldsymbol{A}$ is the numerator relationship matrix; $\boldsymbol{I}$ is an identity matrix for the total number of observations; and ⊗ is the Kronecker product.

Heritability estimates from the univariate models, as well as phenotypic and genetic correlations from the bivariate models, were calculated from the resulting variance components.

RESULTS AND DISCUSSION

Summary Statistics

Summary statistics for the ultrasound scan measurements and carcass traits are shown in Table 1. Comparing scanning systems, CUP consistently produced more variation as indicated by higher standard deviations and higher coefficients of variation. This was most noticeable for the IMF ultrasound scan trait, for example, 100dC-IMF had a 0.8 higher standard deviation and 16.5% higher coefficient of variation compared to 100dP-IMF.

Across all ultrasound scan trait traits, there were consistently fewer animals measured using the CUP system mainly due to the image capture technology not being available for some scanning events. There

was also a decrease in the number of steers between scanning and harvest due to the normal attrition during the lot feeding and pre-harvest phase. This was also a function of the time between scanning events and harvest with the steers being an average of 511 d of age at feedlot intake, 614 d of age for the second ultrasound scanning event, and 796 d of age at harvest.

Variance Component and Heritability Estimates

Variance components and heritability estimates for the intramuscular fat and marbling traits, eye muscle area, rib fat and rump fat are shown in Tables 2, 3, 4, and 5, respectively.

All heritabilities were moderate to high, confirming that ultrasound scan and direct carcass traits provide valuable information for genetic evaluation of beef cattle. This finding is consistent with previous studies that have estimated variance components and heritabilities of ultrasound scan traits and direct carcass traits on Angus and Angus influenced beef cattle populations (Reverter et al., 2000; Kemp et al., 2002; Boerner et al., 2013; Walkom et al., 2015; Kelly et al., 2019).

Comparing the two ultrasound scanning systems, CUP resulted in higher phenotypic and genetic variances compared to PIE for all ultrasound scan traits of IMF, EMA, RIB, and RUMP at both steer feedlot intake and after 100 d of feeding.

Heritability estimates of InC-IMF and 100dC-IMF were consistently higher than InP-IMF and 100dP-IMF, with a 0.14 increase at steer feedlot intake and a 0.09 increase after 100 d of feeding. Ultrasound EMA, at both feedlot intake and 100 d of feeding, were the only group of traits in which the heritabilities were higher for PIE (0.52 for InP-EMA compared to 0.40 for InC-EMA and 0.46 for 100dP-EMA compared to 0.43 100dC-EMA). For subcutaneous fat traits of ultrasound RIB and RUMP, the heritabilities were similar across systems, with the exception being the higher heritability observed for InC-RUMP at feedlot intake at 0.52 compared to 0.38 for InP-RUMP.

The heritability estimates for InC-IMF and 100dC-IMF were noticeably higher than found in previous studies. For example, Walkom et al. (2015) obtained heritability estimates for ultrasound scan IMF of 0.28 in heifers and 0.20 for bulls, based on phenotypes collected mainly on the PIE system in primarily Angus breeding animals. Similarly, Kelly et al. (2019) estimated the heritability of ultrasound scan IMF as 0.25 from a combined dataset of bulls, steers and heifers measured using the PIE system. The heritability estimates of InC-IMF and 100dC-IMF from the current study were similar to the estimates from Kemp et al. (2002) of 0.51. This is a more comparable study as it was undertaken on Angus steers, rather than bulls or heifers, and with the ultrasound scan images interpreted in a laboratory setting rather than crush-side in real-time.

The heritability estimates for InP-IMF and 100dP-IMF in the current study were closer to most previous studies from Australian cattle populations, particularly heifers, which was expected as most phenotypic data analyzed in those studies were based on the PIE ultrasound technology. Estimates of IMF from bull phenotypes from the previous studies found lower heritability which is likely to be the result of lower mean intramuscular fat, and therefore genetic differences expressed to a lesser degree in bulls compared to heifers and steers (Reverter et al., 2000; Boerner et al., 2013; Walkom et al., 2015).

For ultrasound scan EMA, this study showed higher heritability compared to previous studies (Reverter et al., 2000; Kemp et al., 2002; Boerner et al., 2013; Kelly et al., 2019). For the

Table 2. Heritabilities, additive genetic variances, phenotypic variances, genetic, and phenotypic correlations for IMF and carcass marbling traits (standard errors in parenthesis)

Variance/trait*	InP-IMF	InC-IMF	100dP-IMF	100dC-IMF	C-IMF	C-AMBL	C-MMBL
h^2	0.37 (0.08)	0.51 (0.09)	0.45 (0.09)	0.54 (0.09)	0.62 (0.09)	0.42 (0.09)	0.46 (0.09)
σ^2a	0.25	0.73	0.13	1.16	5.91	0.57	5,872
σ^2p	0.68	1.45	0.29	2.13	9.46	1.35	12,794
InP-IMF	–	0.79 (0.09)	0.73 (0.10)	0.71 (0.11)	0.64 (0.11)	0.45 (0.14)	0.46 (0.14)
InC-IMF	0.34 (0.03)	–	0.78 (0.10)	0.98 (0.06)	0.75 (0.09)	0.59 (0.12)	0.64 (0.12)
100dP-IMF	0.39 (0.02)	0.30 (0.02)	–	0.76 (0.09)	0.59 (0.10)	0.62 (0.12)	0.63 (0.12)
100dC-IMF	0.30 (0.02)	0.49 (0.02)	0.43 (0.02)	–	0.66 (0.09)	0.68 (0.10)	0.74 (0.09)
C-IMF	0.27 (0.03)	0.36 (0.02)	0.28 (0.03)	0.43 (0.02)	–	0.97 (0.04)	0.96 (0.03)
C-AMBL	0.19 (0.03)	0.27 (0.03)	0.24 (0.03)	0.34 (0.03)	0.56 (0.02)	–	0.99 (0.01)
C-MMBL	0.21 (0.03)	0.30 (0.03)	0.25 (0.03)	0.38 (0.03)	0.62 (0.02)	0.94 (0.01)	–

*For traits genetic correlations above diagonal, phenotypic correlation below diagonal.

Table 3. Heritabilities, additive genetic variances, phenotypic variances, genetic and phenotypic correlations for EMA traits (standard errors in parenthesis)

Variance/trait*	InP-EMA	InC-EMA	100dP-EMA	100dC-EMA	C-EMA
h^2	0.52 (0.09)	0.40 (0.09)	0.46 (0.09)	0.43 (0.08)	0.60 (0.10)
σ^2a	10.01	12.27	13.48	24.55	37.91
σ^2p	19.43	30.82	29.41	56.85	62.92
InP-EMA	–	0.94 (0.06)	0.80 (0.07)	0.92 (0.06)	0.83 (0.07)
InC-EMA	0.76 (0.01)	–	0.84 (0.08)	0.94 (0.07)	0.90 (0.07)
100dP-EMA	0.52 (0.02)	0.49 (0.02)	–	0.94 (0.04)	0.86 (0.07)
100dC-EMA	0.51 (0.02)	0.50 (0.02)	0.71 (0.01)	–	0.78 (0.08)
C-EMA	0.35 (0.03)	0.36 (0.02)	0.38 (0.03)	0.38 (0.03)	–

*For traits genetic correlations above diagonal, phenotypic correlation below diagonal.

Table 4. Heritabilities, additive genetic variances, phenotypic variances, genetic and phenotypic correlations for Rib Fat traits (standard errors in parenthesis)

Variance/trait*	InP-RIB	InC-RIB	100dP-RIB	100dC-RIB	C-RIB
h^2	0.42 (0.08)	0.44 (0.09)	0.50 (0.09)	0.59 (0.10)	0.40 (0.09)
σ^2a	0.56	1.24	1.70	4.47	10.35
σ^2p	1.35	2.83	3.39	7.56	26.00
InP-RIB	–	0.98 (0.03)	0.75 (0.08)	0.58 (0.10)	0.42 (0.08)
InC-RIB	0.75 (0.01)	–	0.75 (0.08)	0.58 (0.11)	0.33 (0.15)
100dP-RIB	0.48 (0.02)	0.49 (0.02)	–	0.83 (0.04)	0.58 (0.11)
100dC-RIB	0.40 (0.02)	0.42 (0.03)	0.75 (0.01)	–	0.60 (0.11)
C-RIB	0.33 (0.03)	0.26 (0.03)	0.41 (0.02)	0.41 (0.03)	–

*For traits genetic correlations above diagonal, phenotypic correlation below diagonal.

Table 5. Heritabilities, additive genetic variances, phenotypic variances, genetic and phenotypic correlations for Rump Fat traits (standard errors in parenthesis)

Variance/trait*	InP-RUMP	InC-RUMP	100dP-RUMP	100dC-RUMP	C-RUMP
h^2	0.38 (0.08)	0.52 (0.10)	0.61 (0.10)	0.61 (0.10)	0.50 (0.09)
σ^2a	0.99	1.59	4.97	5.78	14.71
σ^2p	2.58	3.04	8.12	9.52	29.10
InP-RUMP	–	0.80 (0.09)	0.85 (0.06)	0.84 (0.06)	0.55 (0.11)
InC-RUMP	0.85 (0.01)	–	0.86 (0.06)	0.87 (0.07)	0.55 (0.11)
100dP-RUMP	0.62 (0.02)	0.61 (0.02)	–	0.99 (0.05)	0.75 (0.07)
100dC-RUMP	0.59 (0.02)	0.59 (0.02)	0.94 (0.01)	–	0.71 (0.07)
C-RUMP	0.41 (0.02)	0.41 (0.02)	0.55 (0.02)	0.55 (0.02)	–

*For traits genetic correlations above diagonal, phenotypic correlation below diagonal.

subcutaneous fat ultrasound scan traits of RIB and RUMP, the heritability results were like previous studies.

The heritability estimates for the carcass marbling and EMA traits were higher than the scan traits with estimates of 0.62, 0.42, 0.46, and 0.60 for C-IMF, C-AMBL, C-MMBL, and C-EMA, respectively. For the marbling traits, the higher heritability for C-IMF is expected given the objective NIR assay used to precisely measure this trait, compared to the subjective scoring by a human grader and categorical nature of both C-AMBL and C-MMBL. For the subcutaneous fat traits of C-RIB and C-RUMP the heritability estimates where similar to the associated ultrasound scan traits.

The heritability estimates for the carcass traits were generally higher in the current study compared to some previous reports. For example, Borner et al. (2013) estimated heritabilities for carcass IMF, carcass rump fat, carcass rib fat and carcass eye muscle area of 0.33, 0.36, 0.23, and 0.39, respectively. In the current study, steers were killed at an older age and higher carcass weight resulting in higher means and variances for all carcass traits. However, several other reports, based on similar

cattle and production systems, showed comparable heritabilities to this study. For example, the Torres-Vázquez et al. (2018), Jeyaruban et al. (2017), and Kemp et al. (2002) obtained heritability estimates for carcass IMF at 0.61, MSA marbling score at 0.48 and USDA marbling score at 0.40, respectively.

In most genetic evaluation programs, it is more common for bulls and heifers to be ultrasound scanned for the correlated carcass traits, rather than steers as in the current study. For example, from the 593,376 ultrasound scan IMF records on the Angus Australia database, 49.8% are from bulls, 45.6% from heifers, and 4.6% from steers (A Byrne, Angus Australia 2020, pers. comm., January 28, 2020). While this should be a consideration in the interpretation and application of the results from this study, a similar study (Duff et al., 2018) of combined steer and heifer data showed comparable results to this study, particularly the higher heritability for CUP IMF compared to PIE IMF.

It is common practice to combine heifer and steer ultrasound scan data for parameter estimation and genetic evaluation. For example, Walkom et al. (2015) observed substantially higher genetic variance and heritabilties for ultrasound scan IMF from the combined heifer and steer phenotypes, compared to bull phenotypes. There are no known previous reports where Angus bulls have been ultrasound scanned for IMF, EMA, RIB, and RUMP with both the PIE and CUP systems.

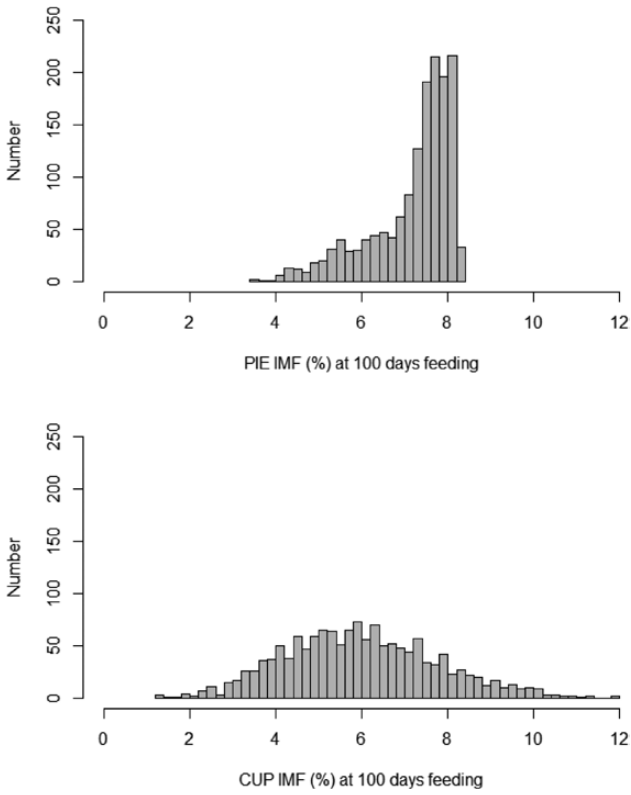

Figure 1. Distribution of ultrasound scan intramuscular fat (IMF) steer phenotypes for the PIE (top) and CUP (bottom) systems at 100 d feeding.

Genetic Correlations

Genetic correlations for the intramuscular fat and marbling traits, eye muscle area, rib fat and rump fat are shown in Tables 2, 3, 4, and 5, respectively.

The genetic correlations between ultrasound scan traits and the direct breeding objective carcass traits presented were positive and moderate to strong. This is consistent with previous studies (Reverter et al., 2000; Kemp et al., 2002; Borner et al., 2013; Walkom et al., 2015), showing that ultrasound scanning is a valuable indirect carcass measurement for informing genetic evaluation programs of beef cattle.

Comparing the two ultrasound scanning systems, the genetic correlations of ultrasound scan IMF and the breeding objective carcass IMF (C-IMF) and marbling traits (C-AMBL and C-MMBL) tended to be higher for CUP compared to PIE, at both ultrasound scanning events, however, also acknowledging that the standard errors of these estimates indicate the differences are not significant. For example, the genetic correlation with C-IMF was 0.11 higher for InC-IMF and 0.07 higher for 100dC-IMF compared to the PIE estimates at the same event. A possible explanation for this may be the narrower range of IMF prediction for PIE compared to CUP. The PIE system, and its in-built algorithm used to predict IMF, is known to be most effective between 2.0% and 8.0% IMF range (R. Evans, Bovine Scanning Services Pty Ltd, pers. comm., January 6, 2021). For this reason, we observed few records in this study that are less than 2.0% or greater than 8.0% from PIE, compared to CUP, particularly in the 100-d scan (Figure 1) where we expect to observe a higher proportion of IMF values greater than 8%. The CUP system can predict IMF to a wider range (Table 1) and can more precisely determine genetic merit by explaining greater genetic variance (Table 2). This is evident and consistent at both steer intake and 100 d on feed. This finding also highlights the difference observed in the genetic correlations between the same ultrasound scan system at steer intake and 100 d feeding, being 0.98 for CUP and 0.73 for PIE. In contrast, the genetic correlations with the breeding objective carcass traits tended to be similar when

comparing CUP to PIE for the ultrasound scan traits of EMA, RIB, and RUMP.

The genetic correlations for the ultrasound IMF traits with the carcass IMF and marbling traits were generally stronger than reported in previous studies. For example, Reverter et al. (2000), obtained genetic correlation estimates for carcass IMF to bull IMF ultrasound of 0.47 and heifer IMF ultrasound of 0.46. Kemp et al. (2002), reported a much stronger genetic correlation of 0.90 in steers, but the time interval in that study was much shorter between ultrasound scanning and harvest of i.e. 52 d, compared to a 285 and 182-d interval in the current study.

For EMA, the genetic correlations of PIE and CUP ultrasound to carcass EMA were stronger in this study than those reported in previous studies (Kemp et al., 2002; Reverter et al. 2000; Borner et al., 2013). The high correlations observed in the current study may have been a function of the use of highly experienced ultrasound scanning technicians on the live steers, experienced carcass graders in the abattoir and controlled data collection, whereas field data from large scale bull breeding herds were mostly utilized in other studies.

In contrast, for the fat traits, genetic correlations of ultrasound rib and rump fat to the respective carcass measures were weaker than those observed in previous studies. The possible reason being unintended abattoir effects, such as hide puller damage on the fat distribution on the long-fed steer carcasses. With more subcutaneous fat observed on the long-fed steer carcass compared to shorter fed steers, there is higher probability of damage to the subcutaneous fat which may lead to reduced precision of measurement in the chiller. For example, in this study steers averaged 18.7 mm for carcass rib fat at an average of 460.2 kg carcass weight. In contrast, in the Reverter et al. (2000), Borner et al. (2013) and Kemp et al. (2002) studies the carcass rib fat measurements were leaner at 6.2, 9.0, and 14.1 mm, respectively, and with lighter carcasses.

The genetic correlations between the three carcass traits of C-IMF, C-AMBL, and C-MMBL were very strong and positive ranging from 0.96 to 0.99. A study with temperate beef cattle by Johnston (2001) showed similar genetic correlations between carcass IMF to MSA Marbling and AUS-meat marbling score of 1.00 and 0.96, respectively, supporting the findings in this study.

Phenotypic Correlations

Phenotypic correlations for the intramuscular fat and marbling traits, eye muscle area, rib fat and rump fat are listed in Tables 2, 3, 4, and 5, respectively.

Like the genetic parameters, the phenotypic correlations for the CUP system for IMF to C-IMF, C-AMBL, and C-MMBL were higher than for the PIE system. While for ultrasound scan EMA, RIB, and RUMP the phenotypic correlations to the associated breeding objective traits tended to be similar between systems. An exception being the 0.33 correlation for InP-RIB with C-RIB, compared to 0.26 for InC-RIB with C-RIB.

Herring et al. (1998) reported stronger phenotypic correlations for the ultrasound predicted IMF traits with carcass IMF and marbling score across four different ultrasound systems, including CUP (described as CVIS) and PIE in crossbred beef steers. They reported phenotypic correlations for CUP IMF with carcass IMF and marbling score of 0.61 and 0.74, respectively. While for PIE IMF to carcass IMF and marbling score, the reported estimates were 0.31 and 0.39, respectively. The contrasting results between studies is likely to be due to the different time intervals between ultrasound scanning steers and their harvest followed by carcass data collection. The interval was much shorter in the Herring et al. (1998) study ranging from 8 to 14 d.

The results from the current study are more likely to reflect industry practice, as phenotypic selection (e.g., drafting pre-harvest) with short time intervals between ultrasound scanning and harvest is unlikely due to the associated stressors having negative impacts on meat quality through dark cutting (Ponnampalam et al., 2017) or welfare implications of increased injury risk. It is more practical, and therefore more likely, to ultrasound scan animals on-farm or at feedlot induction, well before harvest.

For the carcass traits, the correlations between C-IMF with C-AMBL and C-MMBL were moderate at 0.56 and 0.62, respectively. These estimates were lower than those reported by Lee et al. (2019) of 0.87 in a different breed and production system having higher mean carcass IMF and marbling scores with greater variability. Konarska et al. (2017) reported a closer correlation between MSA marbling score and carcass IMF by NIR in *M. longissimus thoracis*, the same muscle as measured in the current study, of 0.75. The phenotypic correlation of C-AMBL with C-MMBL was high at 0.94. This was expected as both scores were assessed by the same grader, albeit on different scales.

Breeding Program Design

Comparing ultrasound scan methods to predict carcass traits is an important step in understanding strategies, particularly breeding program design, aimed at increasing accuracy of selection and genetic gain for carcass traits in breeding objectives. In a companion study (Duff et al., 2019), we modeled several phenotyping and genotyping scenarios focused on the breeding objective traits of C-IMF, C-AMBL, and C-MMBL. The study investigated how breeding programs may be enhanced by using genomic-based information as derived from a reference population with direct carcass IMF and marbling score phenotypes coupled with genotypes, as described by Goddard et al. (2010). This study found the highest rates of selection accuracy and response would be achieved through a combination of CUP ultrasound scan phenotyping for IMF and genotyping with a reference population of related animals with carcass IMF and marbling score phenotypes. However, the value of ultrasound scan phenotyping diminishes as the GBV prediction accuracy increases, which is mainly a function of the reference population size.

CONCLUSIONS

This study compared the phenotypic and genetic parameters for the ultrasound scan measured traits (IMF, EMA, RIB, and RUMP) for two live-animal ultrasound systems (PIE and CUP) and estimated their relationship with the direct carcass traits. The results showed substantial genetic variation in carcass performance can be measured using either ultrasound scan system, even when there is a considerable interval (e.g., 285 d) between the ultrasound scanning event and harvest. This is based on the moderate to high heritabilities observed, coupled with moderate to strong relationships with the related breeding objective carcass traits. A noticeable difference was the CUP system explaining more variation, particularly for ultrasound scan IMF, resulting in a higher heritability and stronger correlations with the carcass IMF and marbling traits in the breeding objective. This indicates that the CUP system, compared to PIE, provides an advantage for genetic evaluation of carcass traits in Angus cattle. This advantage should be considered with knowledge of possible additional costs involved with interpreting ultrasound images through a centralized laboratory. Furthermore, there is also a turn-around time of 24–48 h in receiving the phenotype measurement results from CUP, compared to the crush-side and real-time process of PIE.

To benefit from the results of this study, beef cattle genetic evaluation programs could consider transitioning all live animal ultrasound phenotype recording to the CUP system or similar systems using a centralized processing approach and prediction algorithms. An alternative, but more complex, approach is to receive ultrasound phenotypes from a range of systems (e.g., both PIE and CUP) and model each specifically to recognize the differences in trait variances, heritabilities and genetic correlations to the breeding objective traits.

Consistent with Kemp et al. (1998), this study confirmed that ultrasound scanning can be used to effectively predict carcass phenotypes in Angus steers, including those from progeny test programs, to inform genetic evaluation programs, particularly where collection of effective carcass data from the abattoir is not possible or difficult.

A unique feature of this study was the inclusion of three measurements of marbling traits on each carcass, being C-IMF, C-AMBL, and C-MMBL. The results indicate that these measures are all strongly and positively correlated, both phenotypically and genetically. As a result, for beef cattle genetic evaluation, the collection of just one of the marbling traits is likely to be sufficient. Additional benefit is attained from measuring C-IMF due to the higher heritability of this trait and stronger genetic correlations with live animal ultrasound scan IMF, but there are added cost and sample collection considerations associated with the C-IMF phenotype.

It is also recognized that the ultrasound scanning hardware used in the study, which is still commonly used to phenotype live animals for carcass traits for genetic evaluation, was developed in the 20th century. More sophisticated ultrasound scan systems are available today which can capture higher quality images and potentially predict more precise phenotypes, if coupled with appropriate prediction algorithms. A study to understand potential benefits of modern ultrasound scan systems for beef cattle genetic evaluation programs is recommended.

Further research is also warranted to understand genotyping and phenotyping strategies for beef herds with carcass traits included in the breeding objective. As it is more common for breeding candidates to scanned for the correlated carcass traits, rather than steers as in this study, the future research also needs to better understand the

genetic and phenotypic relationship between bull, heifer, and steer measurements.

ABBREVIATIONS

100dC-EMA, 100 days on feed eye muscle area using CUP; 100dC-IMF, 100 days on feed intramuscular fat using CUP; 100dC-RIB, 100 days on feed rib fat depth using CUP; 100dC-RUMP, 100 days on feed rump fat depth using CUP; 100dP-EMA, 100 days on feed eye muscle area using PIE; 100dP-IMF, 100 days on feed intramuscular fat using PIE; 100dP-RIB, 100 days on feed rib fat depth using PIE; 100dP-RUMP, 100 days on feed rump fat depth using PIE; ASBP, Angus Sire Benchmarking Program; BIN, Beef Information Nucleus; C-AMBL, carcass measured AUS-MEAT marbling score; C-EMA, carcass measured eye muscle area; C-IMF, carcass measured intramuscular fat by near-infrared spectrophotometry; C-MMBL, carcass measured Meat Standards Australia marbling score; C-RIB, carcass measured cold rib fat; C-RUMP, carcass measured hot P8 fat; CUP, Central Ultrasound Processing ultrasound scan system; C-WT, carcass measured hot carcass weight; EMA, eye muscle area; GBV, Genomic Breeding Value; IMF, intramuscular fat; InC-EMA, feedlot intake eye muscle area using CUP; InC-IMF, feedlot intake intramuscular fat using CUP; InC-RIB, feedlot intake rib fat depth using CUP; InC-RUMP, feedlot intake rump fat depth using CUP; InP-EMA, feedlot intake eye muscle area using PIE; InP-IMF, feedlot intake intramuscular fat using PIE; InP-RIB, feedlot intake rib fat depth using PIE; InP-RUMP, feedlot intake rump fat depth using PIE; MSA, Meat Standards Australia; PIE, Pie Medical Esaote Aquila ultrasound Scan system; RIB, rib fat; RUMP, rump fat

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Conflicts of interest statement. The authors declare that there are no conflicts of interest to disclose that relate to the research described in this paper.

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