

## **Comparison of Two Live-Animal Ultrasound Systems to Predict Carcase Intramuscular Fat and Marbling in Australian Angus Cattle.**

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### **Summary**

Genetic and phenotypic parameters were estimated to compare two ultrasound scan systems that predict carcase intramuscular fat (IMF) in Australian Angus cattle. The two ultrasound systems compared were the Pie Medical Esaote Aquila (PIE) and the Central Ultrasound Processing (CUP) technology. The data used in the study was generated from the Angus Sire Benchmarking Program (ASBP), also known as the Angus Beef Information Nucleus (BIN). The heritability of CUP ultrasound scan IMF (CUP\_IMF) and PIE ultrasound scan IMF (PIE\_IMF) were  $0.58 \pm 0.07$  and  $0.35 \pm 0.06$ , respectively. The genetic and phenotypic correlations between the two ultrasound systems were  $0.90 \pm 0.04$  and  $0.45 \pm 0.02$ , respectively. The genetic correlations between CUP\_IMF and the breeding objective traits of carcase IMF (CIMF), AUS-MEAT marbling scores (AMBL) and MSA marbling scores (MMBL) were  $0.70 \pm 0.07$ ,  $0.67 \pm 0.09$  and  $0.72 \pm 0.08$ , respectively. The genetic correlations between PIE\_IMF and CIMF, AMBL and MMBL were  $0.74 \pm 0.08$ ,  $0.69 \pm 0.10$  and  $0.70 \pm 0.09$ , respectively. This study indicates that with the higher heritability of CUP\_IMF compared to PIE\_IMF, coupled with similar phenotypic and genetic correlations to the objective traits of CIMF, AMBL and MMBL, the CUP ultrasound scan technology is most suitable for genetic evaluation of Angus cattle.

*Keywords: angus, intramuscular fat, marbling, ultrasound scanning*

### **Introduction**

A common breeding objective for Angus beef producers is to improve the carcase quality of animals used in breeding programmes. Traditionally, direct carcase traits like intramuscular fat (IMF) and marbling score have proved expensive and difficult, if not impossible, to measure on selection candidates. Due to this limitation, breeders typically use correlated ultrasound scan measurements of the live animal to increase selection accuracy during the selection stage. Since becoming available in the mid 1990s, this technology has been widely adopted by Angus seedstock producers. Currently, 501,213 animals with ultrasound scan records for IMF are included in the Trans-Tasman Angus BREEDPLAN analysis (mid-September 2017). In the most recent calving year to record a full set of performance data (2015), 30,335 animals had IMF ultrasound scan records, which is 41.2% of all calves registered with Angus Australia in that calving year.

Several authors have estimated genetic parameters using Angus cattle for carcase IMF based on ultrasound scan phenotypes (Borner *et al.*, 2013; Kemp *et al.*, 2002; Reverter *et al.*, 2000). However, few studies have compared the precision of different live animal ultrasound systems for predicting carcass IMF (Herring *et al.*, 1998) or the genetic parameters between the different systems, including their genetic relationships to carcase IMF and marbling score.

The most common ultrasound scanning technology used to predict carcase IMF 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 for the prediction of carcass IMF is the Central Ultrasound Processing (CUP) system. The CUP system uses unique software and algorithms to predict carcass IMF through a centralised image analysis laboratory based on images that are also captured crush-side through ultrasound scanning.

The purpose of this study was to estimate phenotypic and genetic parameters for two live-animal ultrasound systems (PIE and CUP) and to determine their relationship with carcass IMF and marbling scores.

## Materials and Methods

All phenotypic data, associated fixed effects and pedigree data used in this study were generated from the Angus Sire Benchmarking Program, also known as the Angus Beef Information Nucleus (BIN), described by Banks (2011). The animals in the study ( $n=2971$ ) were progeny of registered Angus sires ( $n=126$ ) from 5 different co-operator herds located in New South Wales and Victoria, Australia. The steer progeny ( $n=1508$ ) were ultrasound scanned following 95 days on feed at an average age of 614 days (SD 78.4) and killed at an average age of 795 days (SD 70.0) following a feeding period of 270 days. The heifer progeny ( $N=1463$ ) were ultrasound scanned on-farm at an average age of 521 days (SD 82.3).

Animals were ultrasound scanned crush-side at the 12<sup>th</sup> and 13<sup>th</sup> rib site by accredited technicians (Upton *et al.*, 1999) using the Esaote Aquila system (Pie Medical, Maastricht, The Netherlands) equipped with a 3.5-MHz, 18-cm transducer. IMF was predicted using an algorithm within the PIE software providing a real-time and crush-side prediction. At the same time, images using the same ultrasound hardware, from the same location on the animal, were captured using Central Ultrasound Processing (CUP) image capture software and sent to the CUP laboratory in Ames, Iowa, USA for image interpretation for IMF using proprietary software and algorithms. At the end of the feeding period steers were killed and on the following day the chilled carcasses were graded for AUS-MEAT marbling scores (AUS-Meat, 2005) and MSA marbling scores (Meat and Livestock Australia, 2017). Additionally, meat samples were collected from the grading site, in this case the 12<sup>th</sup> and 13<sup>th</sup> rib, and assessed for IMF using near infrared spectrophotometry (NIR), described by Perry *et al.* (2001). The number of records and descriptive statistics for all traits are shown in Table 1.

ASReml software (Gilmour *et al.*, 2015) was used to fit the animal model to each trait to estimate parameters based on univariate and bivariate mixed model analysis using three generations of pedigree. Fixed effects fitted in all models included the contemporary group (as defined by BREEDPLAN) and dam age. Age at measurement was fitted for ultrasound scan traits, while carcass weight was fitted for carcass traits. The contemporary group included herd, year of birth, sex, birth type (twin v single), breeder-defined management group, observation date (ultrasound scan or kill date) and management group history (Graser *et al.*, 2005). Heritabilities, as well as phenotypic and genetic correlations were calculated from the resulting variance components.

## Results and Discussion

The characteristics of the traits included in this study are summarised in Table 1. The estimated heritabilities, genetic correlations and phenotypic correlations are given in Table 2.

*Table 1. Number of records and the descriptive statistics for Carcass Weight, IMF and*

marbling score data.

| Trait <sup>1</sup> | No.  | Mean   | SD     | Min   | Max   |
|--------------------|------|--------|--------|-------|-------|
| All                |      |        |        |       |       |
| PIE_IMF            | 2971 | 6.32   | 1.59   | 0.50  | 8.30  |
| CUP_IMF            | 2773 | 5.47   | 1.75   | 0.96  | 11.92 |
| Steers             |      |        |        |       |       |
| PIE_IMF            | 1508 | 7.23   | 0.96   | 3.50  | 8.30  |
| CUP_IMF            | 1432 | 5.98   | 1.78   | 1.32  | 11.92 |
| CWT                | 1462 | 460.21 | 37.44  | 334.9 | 568.6 |
| CIMF               | 1475 | 10.05  | 3.28   | 3.20  | 25.1  |
| AMBL               | 1473 | 2.67   | 1.24   | 0     | 8     |
| MMBL               | 1474 | 514.40 | 120.21 | 160   | 1030  |
| Heifers            |      |        |        |       |       |
| PIE_IMF            | 1463 | 5.39   | 1.57   | 0.50  | 8.20  |
| CUP_IMF            | 1341 | 4.91   | 1.52   | 0.96  | 9.77  |

<sup>1</sup> PIE\_IMF: Ultrasound Scan IMF using PIE (%); CUP\_IMF: Ultrasound scan IMF using CUP (%); CWT: Hot Standard Carcase Weight (kg); CIMF: Carcase Intramuscular Fat by NRI; AMBL: AUS-MEAT Marbling Score; MMBL: MSA Marbling Score.

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

| Trait <sup>1</sup> | PIE_IMF            | CUP_IMF            | CIMF               | AMBL               | MMBL               |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| PIE_IMF            | <b>0.35 (0.06)</b> | 0.90 (0.04)        | 0.74 (0.08)        | 0.69 (0.10)        | 0.70 (0.09)        |
| CUP_IMF            | 0.45 (0.02)        | <b>0.58 (0.07)</b> | 0.70 (0.07)        | 0.67 (0.09)        | 0.72 (0.08)        |
| CIMF               | 0.42 (0.03)        | 0.42 (0.02)        | <b>0.62 (0.09)</b> | 0.97 (0.04)        | 0.96 (0.03)        |
| AMBL               | 0.36 (0.03)        | 0.32 (0.03)        | 0.56 (0.02)        | <b>0.42 (0.09)</b> | 0.99 (0.01)        |
| MMBL               | 0.38 (0.03)        | 0.36 (0.02)        | 0.62 (0.02)        | 0.94 (0.01)        | <b>0.46 (0.09)</b> |

<sup>1</sup> Heritabilities on diagonal, genetic correlations above diagonal, phenotypic correlation below diagonal

Heritabilities were moderate to high for all traits. The heritability for CUP\_IMF was significantly higher than PIE\_IMF at 0.58 and 0.35, respectively, displaying similar standard errors (0.06, 0.07). CUP\_IMF heritability was higher than those reported by Reverter *et al.* (2000), and Borner *et al.* (2013). PIE\_IMF heritability in our study was closer to previous estimates, which was expected as most phenotypic data analysed in those studies are based on PIE ultrasound technology. The heritability for CIMF of 0.62 was higher than the values reported by Reverter *et al.* (2000) and Borner *et al.* (2013). In our study, steers were killed at an older age and greater carcass weight than previous studies, resulting in higher means and standard deviations for all carcass traits. The heritability for MMBL of 0.46 corresponds with the value reported by Jeyruban *et al.* (2017).

The genetic and phenotypic correlations of PIE\_IMF and CUP\_IMF with CIMF, AMBL and MMBL were similar in sign, magnitude and direction as shown in Table 2. Both PIE\_IMF and CUP\_IMF have a moderate to strong positive genetic correlation to CIMF (0.74, 0.70), AMBL (0.69, 0.67) and MMBL (0.70, 0.72). The genetic correlations of PIE\_IMF and CUP\_IMF to CIMF were higher than those observed by Reverter *et al.* (2000), and Borner *et al.* (2013). Phenotypic correlations between the scan and carcass traits were moderate and positive, but lower than those observed by Herring *et al.* (1998), particularly for the CUP system. In our study, the interval between ultrasound scan and carcass data was on average 181 days, while in the Herring *et al.* (1998) study the interval ranged from 8 to 14 days.

## Conclusions

The significantly higher heritability of CUP\_IMF compared to PIE\_IMF, coupled with similar phenotypic and genetic correlations to the objective traits of CIMF, AMBL and MMBL, indicates that CUP ultrasound scan technology is most suitable for genetic evaluation of Angus cattle. Further research is required to compare the genetic parameters for the full suite of ultrasound scan traits including eye muscle area, rib fat and rump fat.

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