

SHOULD ANGUS BREEDERS LIVE-ANIMAL ULTRASOUND SCAN FOR INTRAMUSCULAR FAT IN THE GENOMICS ERA?

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SUMMARY

Accuracy of selection and response to selection for the breeding objective traits of carcass IMF, AUS-MEAT marbling score and MSA marbling score were generated by modelling seventeen different phenotyping and genotyping scenarios using selection index theory. The data used in the study was produced from the Angus Sire Benchmarking Program (ASBP). The study showed that the highest rates of selection accuracy and response (ΔG) were achieved through using a combination of ultrasound scan phenotyping for intramuscular fat (IMF) and genotyping with a reference population including carcass IMF and marbling score phenotypes. For phenotype only scenarios, Central Ultrasound Processing (CUP) showed substantially higher response to selection and accuracy of selection to the Esaote Aquila ultrasound system (PIE) for IMF resulting from the higher heritability and stronger genetic correlations to the direct carcass breeding objective traits. The value of ultrasound scan phenotyping diminishes as the prediction accuracy of the genomic breeding value (GBV) increases. The GBV only scenario surpassed phenotype only scenarios once GBV prediction accuracy was greater than 59% when compared to CUP IMF phenotyping and 46% when compared to the PIE IMF phenotyping.

INTRODUCTION

Improving meat quality is an important breeding objective for many Angus beef producers. Traditionally, meat quality traits measured on the carcass, like intramuscular fat (IMF) and marbling score, have proven expensive and difficult to measure on selection candidates. Consequently, breeders typically use correlated ultrasound scan measurements on the live animal to increase selection accuracy for these traits as outlined by Williams (2002). The most common ultrasound scanning technology used to predict carcass 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 proprietary 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. Selection for carcass traits can also be enhanced by using genomic information as derived from a reference population with IMF and marbling score phenotypes coupled with genotypes, as described by Goddard *et al.* (2010). This study models and compares different phenotyping and genotyping scenarios focussing on accuracy of selection and response to selection for the breeding objective traits of carcass IMF, AUS-MEAT marbling score and MSA marbling score.

MATERIALS AND METHODS

To estimate parameters for this study, all phenotypes, associated fixed effects and pedigree were generated from the Angus Sire Benchmarking Program (ASBP). The animals in the study ($n=1,622$) were steer progeny of registered Angus sires ($n=173$) from 7 different co-operator herds located in

New South Wales and Victoria, Australia. At feedlot intake, at an average age of 502 days (SD 74.1), the steers were ultrasound scanned crush-side at the 12th and 13th rib site by experienced technicians 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 assessment. 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. The steers were then killed at an average age of 795 days (SD 70.0) following an average feeding period of 293 days. Their carcasses were graded (MSA and AUS-MEAT) and meat samples collected for laboratory assayed IMF measurement.

ASReml software (Gilmour *et al.* 2015) was used to fit an 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 and dam age. Age at measurement was fitted for ultrasound scan traits, while carcass weight was fitted for direct carcass traits. The contemporary group included a concatenation of 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 estimated from the resulting variance components.

With the resulting phenotypic and genetic parameters, the GenSel program (van der Werf 2019) was used to calculate selection accuracy and response using selection index theory and deterministically optimizing generation intervals by truncation selection across age classes. Seventeen different phenotyping and genotyping scenarios were compared, focussing on the breeding objective traits of carcass IMF (CIMF), AUS-MEAT marbling score (AMBL) and MSA marbling score (MMBL). The herd structure was based on a self-replacing Angus breeding herd with 500 females, mating ratio of 2.5% and a 90% weaning rate. The first two scenarios included phenotype only cases with PIE IMF (scenario 1) or CUP IMF (scenario 2) where all males and females bred in the herd are measured as yearlings with the specified ultrasound scan technology. In scenarios 3 to 7, being genotype only cases, genomic breeding values (GBV) were estimated from a reference population with the traits CIMF, AMBL and MMBL measured. GBV accuracies were 17%, 47%, 70%, 85% or 95%, resulting from the single trait GBV accuracies of 10%, 30%, 50%, 70% and 90%. Scenarios 8 to 17 included combinations of the abovementioned cases by combining one phenotyping with one genotyping scenario.

RESULTS AND DISCUSSION

The characteristics of the traits included in this study are summarised in Table 1. Heritabilities were moderate to high for all traits. The heritability for CUP IMF was significantly higher than PIE IMF at 0.51 and 0.37, respectively, displaying similar standard errors (0.09, 0.08). The genetic and phenotypic correlations with the objective traits CIMF, AMBL and MMBL tended to be stronger for CUP IMF compared to PIE IMF (Table 2). The heritabilities are comparable to those reported by Duff *et al.* (2018), however the genetic correlations are more favourable for CUP IMF to the objective traits in this study.

From the GenSel analysis, comparing phenotyping only scenarios, selection on CUP IMF showed substantially higher response to selection and accuracy of selection compared to using PIE IMF. Selecting on CUP IMF resulted in a 29%, 50% and 54% increase in selection response for CIMF, AMBL and MMBL, respectively (Table 3). The genotyping only scenarios surpassed the phenotype only scenarios once GBV prediction accuracy was greater than 59% when compared to CUP IMF phenotype selection and 46% when compared to PIE IMF (Figure 1).

Table 1. Number of records and the descriptive statistics for carcass weight, IMF and marbling score

| Trait ¹ | n | Mean | SD ² | Minimum | Maximum | CV (%) ³ |
|--------------------|------|-------|-----------------|---------|---------|---------------------|
| PIE IMF | 1622 | 4.5 | 1.2 | 1.3 | 7.7 | 26.5 |
| CUP IMF | 1457 | 4.9 | 1.8 | 1.1 | 10.3 | 35.8 |
| CIMF | 1475 | 10.1 | 3.3 | 3.2 | 25.1 | 32.6 |
| AMBL | 1473 | 2.7 | 1.2 | 0.0 | 8.0 | 46.4 |
| MMBL | 1474 | 514.4 | 120.2 | 160.0 | 1030.0 | 23.4 |
| CWT | 1462 | 460.2 | 37.4 | 334.9 | 568.6 | 8.1 |

¹ PIE IMF: Ultrasound Scan IMF using PIE (%); CUP IMF: Ultrasound scan IMF using CUP (%); CIMF: Carcass Intramuscular Fat by Near Infrared Spectrophotometry; AMBL: AUS-MEAT Marbling Score; MMBL: MSA Marbling Score; CWT: Hot Standard Carcass Weight (kg). ²SD: Standard Deviation; ³CV: Coefficient of Variation.

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

| Trait ¹ | PIE IMF | CUP IMF | CIMF | AMBL | MMBL |
|--------------------|--------------------|--------------------|--------------------|--------------------|-------------|
| PIE IMF | 0.37 (0.08) | 0.79 (0.09) | 0.64 (0.11) | 0.45 (0.14) | 0.46 (0.14) |
| CUP IMF | 0.34 (0.03) | 0.51 (0.09) | 0.75 (0.09) | 0.59 (0.12) | 0.64 (0.12) |
| CIMF | 0.27 (0.03) | 0.36 (0.02) | 0.62 (0.09) | 0.97 (0.04) | 0.96 (0.03) |
| AMBL | 0.19 (0.03) | 0.27 (0.03) | 0.56 (0.02) | 0.42 (0.09) | 0.99 (0.01) |
| MMBL | 0.21 (0.03) | 0.30 (0.03) | 0.62 (0.02) | 0.94 (0.01) | 0.46 (0.09) |

¹ Heritabilities on diagonal, genetic correlations above diagonal, phenotypic correlation below diagonal

Table 3. Accuracy of selection (Acc), and response to selection (ΔG) per year for breeding objective traits of CIMF, AMBL and MMBL

| Scenario | Abbreviation | Acc CIMF | ΔG CIMF (%) | Acc AMBL | ΔG AMBL (Score) | Acc MMBL | ΔG MMBL (Score) |
|----------|--------------|----------|---------------------|----------|-------------------------|----------|-------------------------|
| 1 | PIE IMF | 0.46 | 0.75 | 0.32 | 0.16 | 0.33 | 16.95 |
| 2 | CUP IMF | 0.59 | 0.97 | 0.47 | 0.24 | 0.51 | 26.13 |
| 3 | GBV 17% | 0.17 | 0.28 | 0.17 | 0.09 | 0.17 | 8.90 |
| 4 | GBV 47% | 0.47 | 0.79 | 0.47 | 0.24 | 0.47 | 24.85 |
| 5 | GBV 70% | 0.70 | 1.16 | 0.70 | 0.36 | 0.70 | 36.81 |
| 6 | GBV 85% | 0.85 | 1.42 | 0.85 | 0.44 | 0.85 | 44.93 |
| 7 | GBV 95% | 0.95 | 1.59 | 0.95 | 0.49 | 0.95 | 50.25 |
| 8 | 1+3 | 0.48 | 0.78 | 0.36 | 0.18 | 0.36 | 18.64 |
| 9 | 1+4 | 0.61 | 1.00 | 0.53 | 0.27 | 0.53 | 27.92 |
| 10 | 1+5 | 0.75 | 1.25 | 0.71 | 0.37 | 0.72 | 37.62 |
| 11 | 1+6 | 0.87 | 1.46 | 0.85 | 0.44 | 0.86 | 45.06 |
| 12 | 1+7 | 0.96 | 1.60 | 0.96 | 0.49 | 0.96 | 50.34 |
| 13 | 2+3 | 0.60 | 0.99 | 0.48 | 0.25 | 0.52 | 26.96 |
| 14 | 2+4 | 0.68 | 1.12 | 0.59 | 0.30 | 0.62 | 32.11 |
| 15 | 2+5 | 0.78 | 1.30 | 0.73 | 0.37 | 0.75 | 38.98 |
| 16 | 2+6 | 0.88 | 1.47 | 0.86 | 0.44 | 0.87 | 45.18 |
| 17 | 2+7 | 0.96 | 1.60 | 0.95 | 0.49 | 0.96 | 50.03 |

Combining information of scanned phenotype and GBV showed the highest selection responses overall. However, the value of phenotyping with CUP IMF or PIE IMF diminished as the GBV accuracy increases (Figure 1). Based on Goddard *et al.* (2011), with the effective number of chromosome segments calculated according to Daetwyler *et al.* (2008) and an assumed effective population size for Angus of 90 (Clark *et al.* 2019), we expect a GBV accuracy of 48% for CIMF, given the current Angus Australia reference population size of approximately 3,300 animals with carcass IMF phenotypes and genotypes. When the reference population number doubles, the GBV accuracy increases to 61%.

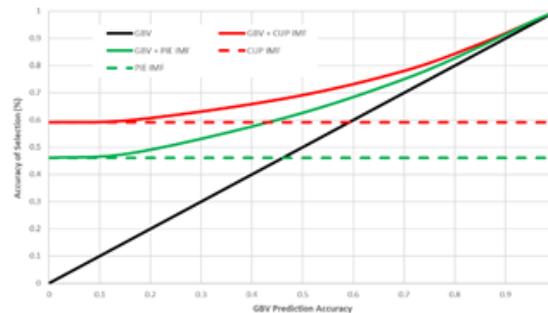


Figure 1. Accuracy of selection of CIMF comparing phenotyping and genotyping scenarios

CONCLUSIONS

The study showed, for Australian Angus breeders, the highest rates of selection accuracy and response (ΔG) will be achieved through using a combination of CUP 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.

This study also confirmed the potential benefit of utilising the CUP ultrasound scan technology for genetic analysis and selection for carcass IMF. This will be achieved through higher selection accuracy resulting from higher heritability and stronger genetic correlations to the direct carcass breeding objective traits.

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