Contributed paper

THE VALUE OF LIVE-ANIMAL ULTRASOUND SCANNING OF BREEDING CANDIDATES FOR CARCASE TRAITS IN THE AGE OF GENOMICS

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SUMMARY

A common question from Angus seedstock producers is "what is the value of live-animal ultrasound scanning of breeding candidates for carcase traits, particularly young bulls, if they are already genomic tested for genetic evaluation and underpinned by a reference population with carcase data". To help answer this question, 3 ultrasound scan phenotyping scenarios were analysed through the Trans-Tasman Angus Cattle Evaluation (TACE) to produce and compare the subsequent eye muscle area (EMA), intramuscular fat (IMF), rib fat (RIB) and rump fat (RUMP) Estimated Breeding Values (EBVs) and their accuracies. This study shows that ultrasound scanning of genotyped bulls does provide some "value" for breeding programs in terms of increasing accuracy to carcase EBVs across all traits and scenarios. However, the value differs by trait (e.g. more influence on EMA EBV compared to IMF EBV) and by scenario (e.g. more influence from heifer scans, particularly on IMF, RIB and RUMP EBVs, compared to bull scans, because of the differences in genetic parameters for the bull and heifer ultrasound scan traits). Further work is required to understand at a herd and population level the impact of a reduction in ultrasound scan phenotyping, particularly on genotyped bulls, coupled with an increasing number of direct carcase phenotypes in the Angus Australia genomics reference population.

INTRODUCTION

A common breeding objective for beef producers is to improve carcase traits of animals used in breeding programs. Traditionally, carcase 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 to increase selection accuracy for breeding objective 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 carcase attributes has been widely adopted in beef cattle breeding programs. For example, over 650,000 animals have live-animal ultrasound scan records in the Angus Australia performance database. These phenotypes are included in the Trans-Tasman Angus Cattle Evaluation (TACE) and, as correlated traits, are used to inform the carcase Estimated Breeding Values (EBVs).

A recent alternative method for carcase trait selection is through genomic testing selection candidates and including the genomic profiles in single-step genetic evaluation programs (Johnston *et al*. 2019), such as TACE. The value of the genomic information is directly related to the underlying reference population of phenotypes coupled with genotypes, as described by Goddard *et al*. (2010). With these alternative methods for selection now available, a common question from Angus seedstock producers is "what is the value of live-animal ultrasound scanning of breeding candidates for carcase traits, particularly young bulls, if they are already genomic tested for genetic evaluation and underpinned by a reference population with carcase data". This was modelled for the carcase intra-muscular (IMF) and marbling traits by Duff *et al.* (2019) and concluded that the value of ultrasound scan phenotyping for IMF diminishes as the prediction accuracy of the genomic breeding value (GBV) increases.

This study further explores the answer to this question in the commercial genetic evaluation environment by comparing carcase EBVs and accuracies for defined groups of genotyped Angus

breeding cattle under three phenotyping scenarios.

MATERIALS AND METHODS

In collaboration with the Agriculture Business Research Institute (ABRI), 3 separate research analyses (herein reported as scenarios) of TACE were undertaken to produce a range of Estimated Breeding Values (EBV) and accuracies. TACE is underpinned by the BREEDPLAN software as described by Graser *et al.* (2005), and the single-step component to incorporate genomic information as outlined by Johnston *et al.* (2019). These analyses utilised the phenotype, pedigree and genotype extracts provided by Angus Australia for the mid-August 2020 TACE. The 3 scenarios were:

- Scenario 1: All data available included in the analysis (i.e. standard analysis).
- Scenario 2: As with scenario 1, but with exclusion of bull ultrasound scan phenotypes for eye muscle area (UEMA), rib fat (URIB), rump fat (URUMP) and intramuscular fat (UIMF) recorded from 1st January 2019 onwards.
- Scenario 3: As with scenario 1, but with exclusion of bull, heifer and steer ultrasound scan phenotypes for SEMA, SRIB, SRUMP and SIMF recorded from 1st January 2019 onwards.

The number of ultrasound scan phenotypes, direct carcase phenotypes and genotypes included in each scenario is listed in Table 1, showing scenario 2 and scenario 3 having approximately 20,000 and 40,000 less ultrasound scan records analysed respectively, per trait, compared to scenario 1, while the number of carcase phenotypes and genotypes remained constant. Additionally, approximately 4,000 animals have both a genotype and a direct carcase phenotype, forming an effective segment of the Angus Australia genomics refence population and influencing the EBVs and accuracies of all genotyped animals.

Table 1. Count of ultrasound scan phenotypes, carcase phenotypes and genotypes included in each scenario based on mid-August 2020 TACE extract

	Ultrasound Scan Phenotypes				Direct Carcase Phenotypes				
Scenario	UEMA	UIMF	URIB	URUMP	CEMA	CIMF	CRIB	CRUMP	Genotypes
1	643,153	594,372	642,217	642,005	7,392	13,092	5,319	14,793	95,180
2	622,795	573,808	621,932	622,055	7,392	13,092	5,319	14,793	95,180
3	603,814	554,749	603,295	602,832	7,392	13,092	5,319	14,793	95,180

The resulting EBVs for EMA, IMF, RIB and RUMP and their accuracies were compared across the 3 scenarios, focussing on young bulls, born in 2018 and 2019, that had genotypes included in all scenarios and additionally had ultrasound scan phenotypes included in scenario 1 (n=9,089).

RESULTS AND DISCUSSION

For the 3 scenarios, the mean and standard deviation for the carcase EBVs and accuracies, along with EBV correlations are shown in Tables 2 to 5 (one table per trait).

For all carcase EBVs, the mean EBV remained constant across scenarios, with an associated reduction in EBV standard deviation from scenarios 1 to 2 and 2 to 3, being the lowest in all cases for scenario 3. This is also matched with a reduction in EBV accuracy from scenario 1 to 2 and 2 to 3, being again the lowest in scenario 3. The correlations between carcase EBVs were strong and positive in all cases (>0.92) with the weakest correlation observed between scenarios 1 to 3. This is expected as the largest portion of ultrasound scan phenotypes were excluded from scenario 3.

Comparing the carcase traits, the least amount of change was observed for the carcase IMF EBV between scenario 1 and 2, reflected in both for change in EBV accuracy, from 59.5% to 58.6%, and high EBV correlation of 0.989. The carcase trait with the most change in EBV was EMA, between

scenario 1 and 2, the change in EBV accuracy was 60.0% to 58.2%, and EBV correlation of 0.957. This is partly explained by differences in the genetic parameters used in TACE for bull ultrasound scan traits, with a bull UIMF heritability of 0.17 being lower than bull UEMA heritability of 0.24. Additionally, bull UIMF has a weaker genetic correlation with CIMF of 0.60, compared to bull UEMA to CEMA correlation of 0.70. In general, this means that bull UIMF phenotypes have less influence on the IMF EBVs and accuracies compared to the bull UEMA influence on the EMA EBVs and accuracies. The results for RIB and RUMP EBVs were closer to those observed for the EMA EBV.

Table 2. EMA EBV and accuracy means, standard deviations and EBV correlations

	EMA EBV (cm^2)			Accuracy (%)		
Scenario	1	2	3	1	2	3
Mean	+6.2	+6.2	+6.1	60.0	58.2	56.7
SD	2.89	2.73	2.67	3.97	4.67	4.92
Correlation to Scenario 1	1.00	0.957	0.944	-	-	-

Table 3. IMF EBV and accuracy means, standard deviations and EBV correlations

	IMF EBV (%)			Accuracy (%)		
Scenario	1	2	3	1	2	3
Mean	+2.3	+2.3	+2.3	59.5	58.6	56.9
SD	1.03	1.02	1.01	4.38	4.64	4.91
Correlation to Scenario 1	1.00	0.989	0.980	-	-	-

Table 4. RIB EBV and accuracy means, standard deviations and EBV correlations

	Rib Fat EBV (mm)			Accuracy (%)		
Scenario	1	2	3	1	2	3
Mean	+0.0	+0.0	+0.0	63.9	62.9	61.6
SD	1.52	1.45	1.43	3.75	4.05	4.34
Correlation to Scenario 1	1.00	0.964	0.947	-	-	-

Table 5. RUMP EBV and accuracy means, standard deviations and EBV correlations

	Rump Fat EBV (mm)			Accuracy (%)		
Scenario	1	2	3	1	2	3
Mean	-0.4	-0.4	-0.4	61.5	59.8	58.6
SD	1.76	1.63	1.60	3.64	4.28	4.59
Correlation to Scenario 1	1.00	0.941	0.929	-	-	-

While changes in EBV spread, accuracy and correlation between scenarios are informative, for breeding candidate selection, understanding the change in EBVs for traits in the breeding objective can be more useful. To illustrate this, the distribution of change for the EMA EBV and IMF EBV are shown in Figures 1 and 2 respectively. This shows that for the IMF EBV, comparing scenario 1 to 2, 70% of bulls did not change by more than ±0.1 % units (or approximately $1/10^{th}$ of the IMF EBV SD), while for scenario 1 to 3, this decreases to 51% of bulls. In contrast, for EMA EBV, comparing scenario 1 to 2, 35% of bulls did not change by more than ±0.3 % cm^2 units (or approximately 1/10th of the EMA EBV SD), while for scenario 1 to 3, this decreases to 30% bulls. This demonstrates that there is less change and associated re-ranking of breeding candidates for the

IMF EBV, across scenarios, compared to the changes observed for EMA EBV. There is also more re-ranking when comparing scenario 1 to 3, compared to scenarios 1 to 2.

Figure 1. Change in EMA EBVs comparing scenario 1 to 2 and 1 to 3

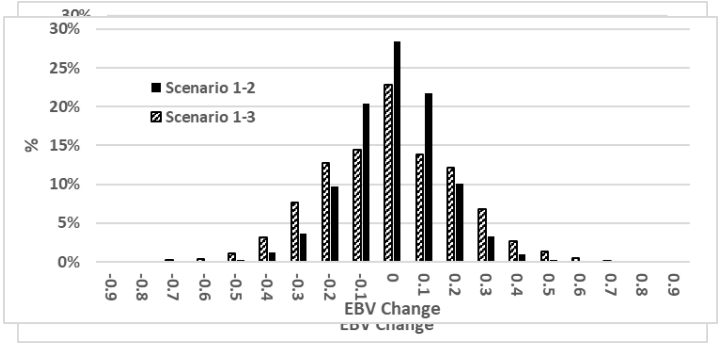

Figure 2. Change in IMF EBVs (%) comparing scenario 1 to 2 and 1 to 3

CONCLUSIONS

This study shows that ultrasound scanning of genotyped bulls does provide some "value" for breeding programs in terms of increasing accuracy to carcase EBVs across all scenarios. However, the value differs by trait (e.g. ultrasound scanning had more influence on EMA EBV compared to IMF EBV) and by scenario (e.g. ultrasound scanning heifers had more influence, particularly on IMF, RIB and RUMP EBVs, compared to bull scans, because of the differences in the genetic parameters for bull and heifer ultrasound scan traits). Before breeding program design advice can be confidently provided, additional research is required, at both a herd and population level, to further understand the cost:benefit relationship and the overall impact of a reduction in ultrasound scan phenotyping, particularity on genotyped bulls, coupled with an increasing number of direct carcase phenotypes in the Angus Australia genomics reference population.

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