Proc. Assoc. Advmt. Anim. Breed. Genet: 24: 467-470

INVESTIGATING THE POTENTIAL TO UTILISE COMMERCIAL CARCASS TRAITS IN GENETIC EVALUATION

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SUMMARY

This project sought to explore whether targeted beef carcass records from commercial production systems in southern Australia were suitable for use in genetic evaluation. The motivation to do so was to increase the number of carcass records in reference population. The project team liaised with Hereford and Angus bull breeders and their clients to identify potentially suitable records from their production systems. In total, a dataset comprised of 1406 records from Hereford and Angus steers and heifers from 23 management groups was established. Records were classified as either High-Quality (HQ) or Medium-Quality (MQ) based on ability to describe fixed effects. This data was compared against a research dataset of 642 Angus and Hereford x Angus carcasses finished to a similar carcass weight end point. Traits analysed include MSA Marble, ossification, rib fat depth and eye muscle area, MSA Index and hot standard carcass weight. Heritability estimated for HQ and the research herd dataset were moderate indicating potential to use high quality commercial carcass records in genomic evaluation. Heritability estimates for the same traits for MQ were very low indicating lack of knowledge on fixed effects severely impeded the utility of such records in genomic evaluation.

INTRODUCTION

The Australian beef grading system to ensure eating quality is Meat Standards Australia (MSA, Polkinghorne *et al*. 2008). There are currently close to zero carcasses from commercial production systems that are being used for genetic evaluation. Reverter *et al*. (2000) reported that in Australian Angus and Hereford cattle, the genetic correlation between ultrasound and carcass traits was variable, but averaged 0.46 for EMA and 0.54 for IMF. These correlations are important as they provide the upper limit to accuracy of selection for the carcass traits based on ultrasound measurement. As industry adopts objective measurements of eating quality, it is becoming increasingly important to be able to record the traits in the breeding objective directly rather than relying on correlated ultrasound measures.

In the past, there has been multiple limitations to using commercial carcass data. The first problem has been to get pedigree information. However, the impact of genomics (Meuwissen *et al*. 2001) means that genomic relationships on commercial animals can be established. In addition, if the property has been using bulls with high genetic merit, then their animals will likely be genetically related to leading animals in the breed. Thus, scope exists for commercial performance to be integrated into genetic evaluation programs like BREEDPLAN (Graser *et al*. 2005) and can provide valuable information which is currently difficult for studs to record.

A problem often encountered with commercial data is maintenance of contemporary groups. However, increasingly cattle are grazed in large mobs (>100) and this is becoming less of an issue. Most genetic evaluation systems require birth date of calves so adjustments can be made for age which is important for early growth traits. Another common problem is that of drafting cattle for sale where cattle are weighed and the heaviest potentially grazed in a separate mob for 1-4 weeks, then transported to a feedlot or abattoir for slaughter. However, Pitchford (2016) demonstrated that for genetic evaluation of carcass traits, such as loin eye muscle area and intramuscular fat, when

they are adjusted for carcass weight, the effect of drafting on genetic evaluation of these traits is minimal.

Pitchford (2018) quantified the loss of precision for commercial cattle when less information (fixed effects) are collected than commonly recorded in seedstock herd recording programs. Pitchford (2018) found for the carcass weight that the correlation between EBVs between a reduced and full model of fixed effects had a correlation of 0.93. For all other traits (loin eye muscle area, P8 rump fat depth and intramuscular fat content), correlations between EBVs for a reduced model with a full model were much more highly correlated (>0.96) indicating little re-ranking due to fitting reduced fixed effects. Pitchford (2018) concluded that there are many commercial herds that have sufficient control of contemporary groups so their data should be utilised for genomic selection of carcass quality traits.

Based on the above findings, this project sought to evaluate the scope to use MSA grading records from commercial groups of steers and heifers for genomic evaluation for data where fewer fixed effects were known on the groups of animals.

METHODS

This project was a collaboration between Herefords Australia, Hereford and Angus bull breeders and their commercial clients with the aim of identifying mobs of cattle that were managed together from birth to slaughter, processed in large mobs and MSA records could be accessed from the supply chain. Eight bull breeders were approached to participate in the project, of which five were active participants. These bull breeders approached 15 clients to identify eight commercial producers who were likely to meet the data recording requirements and had animals with expecting processing dates within the timeframe of the project. There were 1406 carcass records included in the analysis. These animals were from 23 management groups (a concatenation of on-farm management group, feedlot groups and processing date). Mean management group size was 61 (range 11-210, standard deviation 51). Over 2400 animals were identified for carcass outcomes to be included in the study but approximately 40% of records were excluded due to not meeting minimum data quality criteria. In addition to exclusion above, a data quality factor was developed (high quality, HQ vs. moderate quality, MQ). This was based on information provided by commercial producers on:

- Length of calving - progeny from calving periods less than 8 weeks were considered high quality, whereas >8 weeks (maximum 12 weeks) were classed as moderate quality.
- Confidence in defining lifetime management groups (some groups came from > 1 calving paddock but Pitchford (2018) showed this to be of likely low importance when omitted).

In total there were 627 HQ records and 779 MQ records.

All feedlots and processors approached to collaborate in the project were highly supportive and accommodating. This is important as it highlights commitment to further improvements in carcass quality. Contribution to the project included provision of feedlot information (feedlots), provision of carcass grading information, limiting carcass grader to one or few graders for a cohort, access to carcasses for collection of sample for DNA testing.

The comparison data for the project was sourced from “Hereford Black Baldy BIN: Improving productivity of commercial cattle through utilising superior sires within and across breeds (P.PSH.0716)”, herein referred to as Black Baldy dataset. In total 642 steers had carcass records, from 11 processing dates, i.e. 11 contemporary groups with average management group size was 58 (range 1 -112, standard deviation 43). The steers were a mix of Angus and Hereford x Angus. All steers were finished on pasture with a mean hot standard carcass weight 292kg (minimum 181kg – maximum 353kg, standard deviation, 30kg). The Black Baldy data is part of a structured progeny test, and thus lifetime management groups are well defined. As such, it provides a point of comparison point for heritability compared with commercial data collected. All carcases were

graded using the Meat Standard Australia grading system. AUS-MEAT certified MSA graders measured hot standard carcass weight, marbling, ossification, fat colour and subcutaneous rib fat.

Overall there were 2,850 animals with genotypes used to develop a genomic relationship matrix between datasets. These comprised 1,406 genotypes and 1,458 genotypes from Black Baldy, for the 642 steers with carcass records, and the remainder being their relatives (e.g. heifers and bulls) that are part of the Black Baldy project. All genotypes were generated on a variety of Illumina genotyping chips. All of the animals and SNPs were merged to generate a matrix of genotypes, containing 2,850 animals and 157,665 SNPs. FImpute (Sargolzaei *et al*. 2014) was used to impute all genotypes to a set of 40,683 SNPs. Using the genomic relationship matrix from 40,683 SNPs, data was analysed with a general linear mixed model using ASreml-R 4.0 (Butler *et al*. 2017). The model used across all traits was the same and presented random terms of known and heterogeneous variance structures. The known variance structure was the additive relationships between individuals represented through a Genomic Relationship Matrix constructed as per Van Raden Method 1 (2008) and the heterogeneous variance structure was a diagonal variance model for Dataset Quality Factor (Black Baldy vs. HQ vs. MQ). Direct sum structures were also obtained for the residual error term. This allowed variance components and hence heritabilities to be estimated for the same trait between datasets of different quality. The model also included fixed effects of dataset Quality factor (3 levels: Black Baldy, HQ, MQ), contemporary group adjusted for processing date and grader as well as HSCW as a covariate, except where HSCW was itself the trait of interest.

RESULTS AND DISCUSSION

Phenotypic and additive genetic variance components together with estimated heritability are reported by dataset (HQ, MQ, Black Baldy) in Table 1. Heritability estimates for HQ were moderate for EMA, Rib, MSA Marble, Ossification and MSA Index. In general, MQ had similar phenotypic variance to HQ but lower additive variance resulting in lower heritability estimates. For MSA Marble, phenotypic variance was significantly lower, and there was negligible additive variance, leading to a heritability estimate of 0.05. In comparison to MQ and HQ datasets the Black Baldy results had much higher heritability for MSA marble, ossification and MSA-Index but similar heritabilities for rib fat, EMA and HSCW.

The lower additive variance for the same traits between dataset with similar phenotypic variance provides insights on the loss of precision in evaluation when using commercial data. For example, irrespective of data set (data quality) rib fat depth had similar heritability estimates and broadly similar phenotypic variance. In contrast, MSA marble had much lower phenotypic variance for both HQ and MQ compared with Black Baldy; this is especially so for the MQ data (representing the data with more poorly described lifetime management groups). Moreover, MQ had the highest mean MSA marble (366.5) and a similar observed standard deviation to Black Baldy (56.03 vs. 49.61. Therefore, it is unlikely the low variance is a function of low mean MSA-marbling. Importantly for the HQ dataset heritability remained moderate.

CONCLUSIONS

The results for HQ compared with MQ demonstrate the importance of using only data of the best possible quality within the constraints of commercial beef production systems. Based on this project, where poorer (e.g. MQ) quality data was accepted, the genetic variance in key traits like MSA-Marble was too low for the carcass record to be of substantial value. Therefore, any further efforts must focus solely on records with very high confidence that animals to be processed have fixed effects that can be described well for factors including calving period, dam age (heifer, cow). This does not mean they have to have all this data recorded exactly, but that they meet our understanding of "born and raised together".

Table 1. Estimated phenotypic variance (V_P), additive variance (V_A) for MSA traits by dataset

	Phenotypic variance (V_P).	Additive variance (V_A)	Heritability (h^2)
	HQ		
HSCW	468.50	182.29	0.39
EMA	38.18	15.71	0.41
Rib	8.52	2.70	0.32
MSA Marble	4983.21	1470.23	0.30
Ossification	218.16	45.10	0.21
MSA Index	2.10	0.68	0.33
	MQ		
HSCW	483.85	166.25	0.34
EMA	43.75	6.00	0.14
Rib	7.10	2.17	0.31
MSA Marble	2025.66	102.84	0.05
Ossification	225.95	77.54	0.34
MSA Index	1.98	0.50	0.25
	Black Baldy		
HSCW	901.37	422.83	0.47
EMA	52.64	10.89	0.21
Rib	5.93	1.93	0.32
MSA Marble	2834.42	2089.98	0.74
Ossification	124.75	49.41	0.40
MSA Index	1.44	0.64	0.45

ACKNOWLEDGEMENTS

This project was funded by Meat and Livestock Australia (P.PSH.0989), Herefords Australia and University of Adelaide. The authors thank all collaborating breeders & supply chains for support.

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