It’s easier to use commercial beef carcass data than we think

W.S. Pitchford

Davies Research Centre, School of Animal and Veterinary Sciences, University of Adelaide, Roseworthy Campus, SA 5371 Australia
Wayne.Pitchford@adelaide.edu.au (Corresponding Author)

Summary

Despite there being large numbers of commercial beef carcasses graded each year, there are almost none that are being used for genetic evaluation. Seven cattle sire breeds were crossed with mature Hereford cows to produce 1201 carcasses. The traits analysed included carcass weight, loin eye muscle area, P8 rump fat depth and intramuscular fat content. The correlation between EBVs for HSCW between a reduced and full model of fixed effects had a correlation of 0.93 but all other traits were much more highly correlated (>0.96) indicating little re-ranking due to fitting reduced fixed effects. 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.

Keywords: carcass quality, genetic evaluation, commercial data

Introduction

The Australian beef grading system to ensure eating quality is Meat Standards Australia (MSA). There are currently 3.2M carcasses that are MSA graded annually but 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. Bertrand (2009) reviewed other studies and concluded that they average approximately 0.70 for both traits. These values 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 meat yield and 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 large numbers of single nucleotide polymorphism (SNP) markers can be tested on animals. Thus, SNP chips can be used to effectively reconstruct pedigree on commercial animals. 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, commercial performance can 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. Pitchford (2016) demonstrated that as genetic evaluation of carcass quality traits such as loin eye muscle area and intramuscular fat are adjusted for carcass weight, the effect of drafting on genetic evaluation of these traits is minimal.

The aim of this paper is to quantify the loss of precision of commercial cattle when less information (fixed effects) is collected than commonly recorded in seedstock herd recording programs.

Methods

The "Southern Crossbreeding Project" was conducted at Struan Research Centre, Naracoorte SA and various feedlots in southern Australia (Pitchford *et al.* 2006). Mature Hereford cows (637, no maidens) were mated to 97 sires from 7 breeds: Jersey, Wagyu, Angus, Hereford, South Devon, Limousin and Belgian Blue. There were 1201 carcasses from heifer and steer calves born 1994-97. Cattle were slaughtered when the majority of heifer carcasses were >200 kg (average 16 months) and steer carcasses >300 kg (average 23 months) at various commercial abattoirs. With 4 years and 2 sexes, there were 8 slaughter groups. They were assessed for hot standard carcass weight (HSCW, kg), and carcass traits of eye muscle area (EMA, cm^2) and P8 rump fat depth (mm). Chemical extraction of intramuscular fat (IMF, %) was conducted subsequently in the University laboratory.

The data was analysed with an animal model including fixed effects of management group and sire breed in all models using ASReml-R (Butler *et al.* 2009). A full (model 1) and two reduced fixed effects models (models 2 and 3) were fit to the data. The focus of this study is on genetic variation within a sex (heifer or steer) and sire breed group (7 combinations) so all models included those effects first. For model 1, the next effects were year (1994-97) and birth location (Struan or Wandilo). A series of two and three-way interactions were then included, e.g. Location x Year x Sex (LYS). Age effects were included as birth month (BM, March or April) and birth date (BD). Interactions that allowed for different age effects within management groups (combinations of location, year and sex) were fitted next. The number of carcasses in each of the 32 combinations of Location x Year x Sex x Birth month was fairly evenly spread with a mean of 37.5 and range 23-63. Lastly, post-weaning management group (P) and age of dam (AOD) were included. The carcass quality traits (P8, EMA and IMF) were analysed both without and with carcass weight included as a covariate for models 1-3. A reduced model 2 was then fitted based on the assumption that commercial producers would know location, year, sex, breed and birth month. The location x year x sex interaction had 16 combinations and birth month was fitted within these so there were 32 combinations. Lastly, model 3 included only year, sex and breed. The year x sex interaction had 8 combinations.

Results

Sex, breed and year main effects and the interaction between year and sex were, as expected, extremely large for all traits and so was the carcass weight (HSCW) covariate when fitted to P8, EMA and IMF (Table 1). Pre-weaning property (Location) had a big effect on all traits except IMF and EMA when carcass weight was included as a covariate. The interaction between location, year and sex (LYS) was only significant for P8 fat depth. Birth month was significant for HSCW and unadjusted EMA, but not for P8 or IMF. Day of birth (BD) was also generally not significant. Post-weaning management group and age of dam had no effect.

Table 1. Tests of significance (Wald F statistics) of fixed effects in the animal model

	DF	HSCW	P8	P8[A]	EMA	EMA[A]	IMF	IMF[A]
HSCW	1			780.60		764.80		374.30
Sex	1	6108.00	41.96	46.54	50.20	47.95	40.46	50.14
Breed	6	50.29	420.20	19.96	269.40	29.92	249.30	4.71
Year	3	113.30	48.46	4.23	36.27	34.05	61.57	65.36
Location	1	26.92	28.08	12.44	6.03	0.29	2.19	0.08
Year:Sex	3	226.60	43.82	19.91	32.72	21.53	145.60	76.40
Year:Loc	3	5.87	5.53	2.83	2.12	1.46	2.03	1.90
LYS	4	0.98	6.81	6.31	2.33	2.62	0.24	0.26
Bmonth	1	6.49	1.06	0.08	5.91	2.98	0.05	0.14
LYS:Bmonth	15	2.09	1.29	1.02	1.36	2.14	0.45	0.41
LYS:BM:BD	32	5.88	2.70	1.67	1.35	1.76	0.85	0.81
LYSP	12	2.47	1.18	0.59	1.68	1.21	0.50	0.46
AOD	1	0.48	0.00	0.01	1.72	1.38	0.11	0.15

[A] Includes carcass weight as a covariate

For all traits except IMF, the full model had a lower phenotypic variance than the reduced or minimal model. The correlation between EBVs for HSCW between the reduced and full model had a correlation of 0.93 but all other traits were much more highly correlated (>0.96) indicating little re-ranking. The minimal model which made no account of age or pre-weaning location had lower correlations between EBVs although was still surprisingly high for the carcass quality traits (>0.93 for P8 with HSCW covariate and EMA and 0.98 for IMF). The heritabilities were highest for carcass weight and were relatively stable across the different models.

Table 2. Variance components and correlations between models

	HSCW	P8	P8[A]	EMA	EMA[A]	IMF	IMF[A]
Model 1							
Phenotypic variance	612	16.1	15.1	74.6	60.8	2.33	2.33
Heritability	0.51	0.16	0.20	0.32	0.23	0.10	0.12
Model 2							
Phenotypic variance	708	17.0	15.4	76.0	62.5	2.31	2.31
Heritability	0.54	0.21	0.23	0.31	0.27	0.13	0.15
EBV correlation [B]	0.93	0.96	0.98	0.98	0.97	0.99	0.99
Model 3							
Phenotypic variance	737	17.9	15.8	77.6	64.0	2.30	2.29
Heritability	0.54	0.23	0.23	0.32	0.28	0.14	0.17
EBV correlation [B]	0.91	0.93	0.96	0.96	0.95	0.98	0.98

[A] Includes carcass weight as a covariate; [B] Correlation with Model 1.

Discussion

The aim of this paper was to test how few fixed effects can be recorded in commercial data. The premise is that there is a sensible middle ground that can be exploited between the detailed data currently required by BREEDPLAN (Graser *et al.* 2005) and the full 3.2 million MSA graded carcasses each year. As expected, the variances estimated herein are similar to those estimated for Hereford cattle by Reverter *et al.* (2000).

In well managed properties in southern Australia it is common for calves to be born in a tight calving pattern (2 month spread) into large management groups (>100) that remain until slaughter for grass-fed or feedlot entry for grain-fed. In some cases, even in the feedlot these contemporary groups remain intact. Thus, what defines a management group can easily be herd, year, sex, location and birth month. There were no maiden cows in this trial and it is expected that if there were then adjustment would also be required for that. The fact that the specific day of birth effects within birth month were not significant and the correlations between EBVs were so high demonstrates that recording birth day is unnecessary for P8 fat, EMA and IMF. This is especially the case when the traits were adjusted for carcass weight which is part of BREEDPLAN protocol (Graser *et al.*, 2005).

It was surprising that in this data set not adjusting for month of birth and location also had minimal effects as demonstrated by their lack of significance (Table 1) and still high correlations between EBVs (>0.95, Table 2). However, in this experiment there were only two birth months (March, April) of calves by AI and the birth locations were very similar in climate. Thus, it seems fool hardy to make a recommendation that genetic evaluation of carcass traits should not require knowledge of month of birth and property for inclusion in the analysis.

This paper demonstrates that contemporary groups of cattle that are born in the same herd, year and month, are from mature cows and of the same sex, are raised together and slaughtered on the same day can provide extremely useful data for genomic selection of carcass quality traits. With the introduction of objective measures of lean meat yield and predictors of eating quality (primarily IMF), even greater accuracy of EBVs should be available to seedstock breeders to make faster rates of genetic gain.

List of References

Bertrand, JK, 2009, Using actual and ultrasound carcass information in beef genetic evaluation programs. Revista Brasileira de Zootecnia, 38:58-63.

Butler, DG, Cullis, BR, Gilmour, AR and Gogel, BJ, 2009 ASReml-R reference manual, https://www.vsni.co.uk/resources/documentation/

Graser, H-U, Tier, B, Johnston, DJ, Barwick, SA, 2005 Genetic evaluation for the beef industry in Australia. Aust. J. Exp. Agric. 45:913-921.

Meuwissen, THE, Hayes, BJ, Goddard, ME, 2001, Prediction of total genetic value using genome-wide dense marker maps, Genetics 157:1819-1829.

Pitchford, WS, Mirzaei, HM, Deland, MPB, Afolayan, RA, Rutley, DL and Verbyla, AP, 2006, Variance componentsfor birth and carcass traits of crossbred cattle, Aust. J. Exp. Agric. 46:225-231.

Reverter, A, Johnston, DJ, Graser, H-U, Wolcott, ML and Upton, WH, 2000, Genetic analysis of live-animal ultrasound and abattoir carcass traits in Australian Angus and Hereford cattle, Journal of Animal Science 78:1786-1795.