Proc. Assoc. Advmt. Breed. Genet. 21: 253-256

IMPACT OF SCANNING LEAN CATTLE ON THE GENETIC CORRELATION BETWEEN SCAN AND CARCASE INTRAMUSCULAR FAT IN ANGUS AND HEREFORD CATTLE

S.F.Walkom, M.G.Jeyaruban and D.J.Johnston

Animal Genetics and Breeding Unit[1], University of New England, Armidale, NSW 2351, Australia

SUMMARY

BREEDPLAN, the Australian beef cattle genetic evaluation system, uses ultrasound scan intramuscular fat as a correlated trait for predicting carcase intramuscular fat. More recently, it has been observed that seedstock herds are being scanned at younger ages and lower levels of fatness and this research was undertaken to examine the effect on heritability and the genetic correlation estimates when scan records are removed using fat depth thresholds. Using BREEDPLAN data to estimate these genetic relationships, this study yielded genetic correlation estimates of 0.37 and 0.36 in Angus and 0.69 and 0.54 in Hereford for bull and heifer scan intramuscular fat, respectively. The results showed a useful improvement in the genetic correlation between bull intramuscular fat and carcase intramuscular fat in Angus cattle to 0.48. However, for Angus heifers and Hereford bulls and heifers there was no significant improvement, suggesting that strategies to reduce lean scanning will not improve the genetic correlation estimates in those cases.

INTRODUCTION

Current genetic correlation estimates used in BREEDPLAN, the Australian beef cattle genetic evaluation system, (Johnston *et al.* 1999) between scan intramuscular fat (IMF) and abattoir carcase intramuscular fat (CIMF) are based on a pooled temperate breeds analysis from the Beef Cooperative Research Center I (Reverter *et al.* 2000). Subsequent re-analysis of the genetic correlations between scan intramuscular fat and CIMF of industry data have produced estimates for Angus (Reverter and Johnston 2001; Bòrner *et al.* 2013) and Hereford (Reverter and Johnston 2001; Meyer *et al.* 2004) lower than the pooled breed analysis.

Compared to 2010 the scanning of Angus bulls in 2014 occurred on average 40 days younger due to a trend towards producers scanning bulls at 400-days. Bòrner *et al.* (2013) estimated that scanning younger bulls (mean age 426 days) compared to older bulls (590 days) reduced the genetic correlation for scan intramuscular fat and CIMF from 0.43 to 0.34. It was hypothesised that the genetic variation in intramuscular fat was not being expressed at the younger age, or could not be detected by the ultrasound machines in the leaner cattle.

Preliminary analysis (pers. comm. M.G. Jeyaruban) showed that the lower genetic correlations were, in part, a consequence of scanning a large number of contemporary groups (CG) with a mean rib fat below 3mm and a mean P8 fat below 5mm. However, BREEDPLAN users were cautious of implementing rib and P8 fat restrictions to scan IMF records as restrictions would lead to a large proportion of records, up to 50% in Angus bulls, being excluded from evaluations, unfairly disadvantaging herds with genetically lower fat levels.

The objective of this study was to determine the merit of using rib and P8 fat depth thresholds as criteria to improve the genetic correlation between scan IMF and CIMF in Angus and Hereford breeds. The study also explored the impact of retaining lean CG that had large variation in scan IMF on genetic correlation estimates.

[1]AGBU is a joint venture of the NSW Department of Primary Industries and University of New England

MATERIALS AND METHODS

The study analysed data submitted to the Angus Society of Australia and Herefords Australia databases for BREEDPLAN evaluations prior to November 2014. The majority of CIMF records in the Angus and Hereford data sets were from the Beef CRC (Reverter *et al.* 2000) with only a few breeders progeny testing and recording CIMF. 7,833 Angus CIMF and 1,836 Hereford CIMF records were used in this study (Table 1 and 2). The Angus ultrasound scanning data set contained 226,687 BIMF and 245,840 HIMF records (Table 1) and there were 86,603 BIMF and 70,020 HIMF records for Hereford (Table 2).

The following approaches were taken to remove lean CG prior to estimation of the genetic correlations between scan and carcase intramuscular fat.

- All data: all scan intramuscular fat records were retained
- Subset 1: Scan CG with a mean rib fat depth below 3mm and a mean P8 fat depth below 5mm are removed except for CG with a mean P8 > 4mm and where the sum of the CG's mean and standard deviation for P8 fat was greater than 5
- Subset 2: sub set 1 + CG with high phenotypic variation for scan IMF (sd. of IMF in top 25%)

For both the Angus and Hereford heifers the analysis was repeated with a more stringent cut off based on a rib fat depth of 5mm and P8 fat depth of 7mm.

Statistical Analysis. Genetic variances, correlations and variance ratios were estimated by applying restricted maximum likelihood (REML) in a series of bivariate animal model evaluations with three generations of pedigree in WOMBAT (Meyer 2007). For Angus ≈ 52% of the CIMF records had a corresponding HIMF record. However, no Angus bulls or Herefords with a scan IMF record had a corresponding CIMF record.

The model fitted for CIMF had fixed effects of CG, linear and quadratic effects of carcase weight as covariates and a random additive genetic effect of animal. CG were defined as per Graser *et al.* (2005). Models fitted for BIMF and HIMF included the random additive genetic effect of animal and sire x herd as a random effect. The model also included the fixed effects season of birth (2 levels, summer and winter), sex (fitted to HIMF, 2 levels), dam age (scaled to 5yrs old) x season, dam age squared x season, heifer factor deviation x season (if the dam was a heifer age was deviated from 2yrs old), and age (centred at 500 days) x sex

RESULTS AND DISCUSSION

Means and Variation. In Angus the mean CIMF was 8.32% compared to means of 3.28% and 4.86% for BIMF and HIMF, respectively (Table 1). The standard deviation for the scan IMF traits was also lower than observed for CIMF. Removing the lean CG from the scan records increased the mean to 3.84% and 5.18% for BIMF and HIMF, respectively without noticeably reducing standard deviation.

Hereford CIMF had a mean of 4.29% which was higher to the mean for BIMF (3.20%) and HIMF (3.83%; Table 2). However, the variation in CIMF (sd. of 2.16%) was noticeably greater than observed for BIMF (1.35%) and HIMF (1.65%; Table 2). As observed for Angus scan IMF traits, removing the lean CG increased the mean without significantly reducing the standard deviation (Table 2) for scanned traits.

Genetic Variation and Heritability. The heritability of CIMF in Angus was moderate (0.32) (Table 2) and similar to earlier estimates from Angus BREEDPLAN data (Reverter and Johnston 2001; Bǒrner *et al.* 2013). The heritability of CIMF in Herefords (0.37; Table 2) aligns with the observation in Angus and earlier estimates from the Hereford BREEDPLAN data (Reverter and Johnston 2001, Meyer *et al.* 2004).

Additive genetic variation for BIMF and HIMF in Angus was lower than observed for CIMF (Table 1). The all data BIMF and HIMF records for Angus had heritability estimates of 0.17 and 0.27, respectively and were similar to previous estimates of Reverter and Johnston (2001) and

Börner *et al.* (2013). Removing the leaner CG from the Angus BIMF records led to a slight increase in the additive genetic variance and heritability (0.21; Table 1). The heritability of HIMF was not improved by removing CG for a rib fat of 3mm and P8 fat of 5mm (Table 1). However, if fat depth thresholds were set at a rib fat of 5mm and P8 fat of 7mm the heritability of HIMF increased to 0.33 (Table 1).

The heritability of BIMF in Herefords was estimated at 0.20 (Table 2) which was slightly lower than previous estimates using Hereford BREEDPLAN data (Reverter and Johnston 2001, Meyer *et al.* 2004). Removing the lean CG increased the heritability of BIMF and HIMF to 0.23 and 0.30, respectively (Table 2). As observed for Angus heifers, using the more stringent fat depth cut offs resulted in a larger increase in the heritability estimate for HIMF (Table 2).

Table 1: Estimates of additive genetic variance (σ^2_a), heritability (h^2) of scan IMF traits and genetic correlation (r_g) between scan and carcase intramuscular fat (CIMF) for Angus

Subset	Records	% of data	Mean (%)	SD	σ^2_a	h^2	r_g CIMF
Carcase IMF							
All data	7,833	100	8.32	3.90	1.324 ± 0.202	0.32 ± 0.05	
Bull IMF (fat cut offs BRF=3,BP8F=5)							
All data	226,687	100	3.28	1.49	0.163 ± 0.007	0.17 ± 0.01	0.37 ± 0.11
Subset 1	120,636	53	3.84	1.38	0.190 ± 0.010	0.21 ± 0.01	0.48 ± 0.13
Subset 2	149,122	66	3.61	1.50	0.198 ± 0.010	0.19 ± 0.01	0.47 ± 0.12
Heifers and steer IMF (fat cut offs HRF=3,HP8F=5)							
All data	245,840	100	4.86	1.85	0.395 ± 0.009	0.27 ± 0.01	0.36 ± 0.07
Subset 1	204,551	83	5.18	1.74	0.427 ± 0.010	0.29 ± 0.01	0.37 ± 0.07
Subset 2	235,580	96	4.93	1.84	0.408 ± 0.010	0.27 ± 0.01	0.36 ± 0.07
Heifers and steer IMF (fat cut offs HRF=5,HP8F=7)							
Subset 1	137,850	56	5.60	1.62	0.444 ± 0.013	0.33 ± 0.01	0.39 ± 0.08
Subset 2	162,373	66	5.31	1.80	0.440 ± 0.012	0.28 ± 0.01	0.37 ± 0.08

Genetic Correlations. If all BIMF records were incorporated in the bivariate analysis of BIMF and CIMF for Angus, the genetic correlation estimate was 0.37 (Table 1). This estimate was higher than correlations reported by Reverter and Johnston (0.13; 2001) but similar to the estimates by Börner *et al.* (2013) in young (0.34) and older bulls (0.43). By removing lean CG, the genetic correlation estimate between BIMF and CIMF in Angus increased to 0.48 (Table 1). Reintroducing some of the lean CG that had IMF variation in the top 25% lead to only a small reduction in the genetic correlation compared to when all lean CG are removed (0.47) and remained noticeably higher than when all data was included (Table 1). Increasing the variation threshold to include CG in the top 50% resulted in a genetic correlation of 0.39 (not presented). The results suggest that applying a threshold based on minimum fat depth to scan IMF data resulted in higher estimates of the genetic associations between scan and carcase IMF.

Removing lean CG from the Angus HIMF records did not improve the genetic correlation with CIMF (Table 1). While using more stringent fat cut offs (rib fat < 5mm P8 fat < 7mm) leads to increases in the additive variance and heritability of HIMF the increase in the genetic correlation with CIMF was minimal (Table 1). The correlation between HIMF and CIMF in the Angus industry data was previously reported at 0.45 (Reverter and Johnston 2001) and 0.39 (mean age 443 days) and 0.42 (583 days; Börner *et al.* 2013).

In Herefords, removing data selectively did not result in increases in either heritability estimates for BIMF or HIMF, or in the genetic correlations between BIMF and CIMF, or HIMF and CIMF (Table 2). The genetic correlation between BIMF and CIMF in Hereford was 0.69 (all data) which was slightly stronger than the previous estimate of 0.59 presented by Meyer *et al.*

(2004). This may, in part, be due to Hereford bulls being scanned on average 30 days older and 0.5mm fatter over the rib then the Angus Bulls. The genetic correlation between HIMF and CIMF in Herefords was considerably lower than the previous estimate presented by Meyer *et al.* (2004) of 0.97.

The estimates of the genetic correlation between scan IMF and CIMF by Bȍrner *et al.* (2013) and within this study suggest that scanning younger and leaner cattle will reduce the strength of the association. This may, in part, be due to a decline in the accuracy of the scan equipment when measuring lean cattle, but further research will be required to test this hypothesis.

Table 2: Estimates of additive genetic variance (σ^2_a), heritability (h^2) of scan IMF traits and genetic correlation (r_g) between scan and carcase intramuscular fat (CIMF) for Hereford

Cut off	Records	% of data	Mean (%)	SD	σ^2_a	h^2	r_g CIMF
Carcase IMF							
All data	1,836	100	4.29	2.16	0.46 ± 0.14	0.37 ± 0.10	
Bull IMF (fat cut offs BRF=3,BP8F=5)							
All data	86,603	100	2.93	1.35	0.12 ± 0.01	0.20 ± 0.01	0.69 ± 0.17
Subset 1	63,274	73	3.20	1.28	0.14 ± 0.01	0.23 ± 0.01	0.61 ± 0.18
Subset 2	69,931	81	3.10	1.33	0.14 ± 0.01	0.22 ± 0.01	0.62 ± 0.18
Heifers and steer IMF (fat cut offs HRF=3,HP8F=5)							
All data	70,020	100	3.83	1.65	0.30 ± 0.01	0.28 ± 0.01	0.54 ± 0.16
Subset 1	62,208	89	4.02	1.59	0.32 ± 0.01	0.30 ± 0.01	0.48 ± 0.15
Subset 2	64,250	92	3.97	1.62	0.32 ± 0.01	0.30 ± 0.01	0.47 ± 0.16
Heifers and steer IMF (fat cut offs HRF=5,HP8F=7)							
Subset 1	44,657	64	4.26	1.53	0.36 ± 0.02	0.33 ± 0.02	0.55 ± 0.18
Subset 2	51,049	73	4.06	1.64	0.36 ± 0.02	0.30 ± 0.01	0.46 ± 0.18

CONCLUSION

The continuing trend towards scanning Angus bulls at 400-days and at leaner subcutaneous fat depths is causing a decline in the genetic correlation between scan and carcase IMF. Removing contemporary groups based on fat depth thresholds resulted in a slight strengthening of the genetic correlation between scan and carcase IMF in Angus bulls. Producers should avoid scanning herds with fat levels below the cut offs presented, therefore allowing animals the opportunity to express their genetic merit for IMF. Increasing the number of CIMF records is desirable, yet difficulties in obtaining abattoir progeny test data mean there is also a need to improve the quality of scan IMF records. Alternatively the genetic correlations between scan and carcase IMF in BREEDPLAN evaluations should be adjusted, which will reduce the utility of scanning, but due to the large number of animals that can be scanned and the relative low cost of measuring scan IMF it still remains the most practical correlated trait for CIMF.

REFERENCES

Bȍrner, V., Johnston, D.J and Graser, H. U., (2013) *Ani. Prod. Sci.* **53**:1075

Graser, H-U., Tier, B., Johnston, D.J. and Barwick, S.A. (2005) *Aust. J. Exp. Agric.* **45**:916

Johnston, D. J., Tier, B., Graser, H. U., and Girard, C. (1999) *Proc. Assoc. Advmt. Anim. Genet.,* **13:**193

Meyer, K., Johnston, D.J and Graser, H. U., (2004) *Aus. J. Ag. Res.* **55**:195

Meyer, K. (2007). *J. Zhejiang Uni. Sci.B, **8***:815

Reverter A., Johnston, D. J., Graser, H-U., Wolcott, M.L. and Upton W.H. (2000) *Anim. Sci.* **78**:1786

Reverter A. and Johnston, D. J. (2001) *Proc. Assoc. Advmt. Anim. Genet.,* **14:**159