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GENETIC CORRELATIONS BETWEEN MATURE BODY CONDITION, WEIGHT, AND HIP HEIGHT AND EARLY FAT DEPTH TRAITS IN AUSTRALIAN ANGUS CATTLE

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SUMMARY

The objective of this study was to estimate genetic correlations between mature cow traits: body condition (MBC), weight (MCW), hip height (MCH), and live animal ultrasound scan and carcass fat depth traits: P8 fat (P8) and rib fat (RIB) in Australian Angus cattle. Genetic parameters were estimated using univariate animal models, and up to four records per cow were used in the analyses for MBC, MCW, and MCH. The heritability estimates for MBC, MCW, and MCH were 0.21 ± 0.01, 0.43 ± 0.01, and 0.55 ± 0.03, respectively. The strongest genetic correlation was observed between the MBC and MCW (0.87 ± 0.01), followed by MCW and MCH (0.83 ± 0.01). Moderate genetic correlations were observed between MBC and ultrasound scan P8 fat (0.35 ± 0.03) and rib fat (0.31 ± 0.03) traits measured on heifers and steers. Genetic correlations between MBC and carcass P8 fat (0.19 ± 0.08) and rib fat (0.30 ± 0.15) were low to moderate. Progress from selection for MBC based on live animal ultrasound scan and carcass fat depth traits measured on young cattle would be slow due to low genetic correlations. Since MBC is adequately heritable, this trait could be used as a direct measure to improve cow condition through selection.

INTRODUCTION

Mature cow body condition and size (height and weight) are important traits influencing the productivity and reproductive efficiency of mature cows. However, mature cow traits are generally recorded less frequently than early life traits due to practical challenges. Therefore, selection decisions for mature cow body composition traits, such as body condition, are often based on similar traits, like fat depth measurements taken at early ages.

Angus Australia has been publishing an estimated breeding value (EBV) for cow weight, body condition and height through the TransTasman Angus Cattle Evaluation (TACE). Understanding the genetic correlations between traits measured in young animals, such as those obtained via ultrasound scans and direct carcass measurements, and mature cow body condition and mature cow size is important for genetic improvement in cow herd productivity. The objective of this study was to estimate the genetic correlations between mature cow traits, body condition, hip height, and body weight, and live animal ultrasound scan and carcass fat depth traits and carcass weight using data from Australian Angus.

MATERIALS AND METHODS

Data. All data including phenotypes and pedigrees used for this study were extracted from the Angus Australia database. Mature cow body condition (MBC, recorded as a score), mature cow weight (MCW, measured in kg), and mature cow hip height (MCH, measured in cm) were measurements taken at the time of weaning of its calf. Mature body condition scores were collected using a zero to five scoring guide where score 0 represents emaciated body condition, and score 5 represents extremely fat body condition (Angus Australia 2024). For analysis, body condition scores were renumbered from 1 to 6. Data cleaning criteria for MCW, as outlined by Graser *et al.* (2005), were applied to define MBC and MCH. Data cleaning for MBC, MCH, and MCW resulted in 37,329, 13,640, and 177,931, records, respectively.

The ultrasound scan traits used for this study were P8 fat (P8, measured in mm) and rib fat (RIB, measured in mm). All ultrasound scan traits were separately analysed as bull (B) or heifer and steer (H) traits. Records of carcass fat depth at p8 rump site (CP8, measured in mm), carcass rib fat (CRIB, measured in mm), and carcass weight (CWT, measured in kg) were used in the analyses.

Statistical analyses. A repeatability animal model including an animal permanent environmental effect was used for all three mature cow traits. The model was also fitted with quadratic effects of the animal age (for MBC, MCH, and MCW) and quadratic effects of calf age (for MBC) as covariates. Contemporary group and other fixed effects fitted in the univariate animal models for scan and carcass traits were as described by Graser *et al.* (2005). Sire by herd was fitted as an additional random effect for scan traits. The genetic correlations between traits were estimated by bivariate animal models. The variance components were estimated using pedigree-based models implemented in airemlf90 (Misztal *et al.* 2018).

RESULTS

Most of the animals had a favourable body condition score, with an average score of 3.3 ± 0.77 (Table 1). On average, mature cows were 134 cm in height and weighed 572 kg (Table 1). All mature cow traits were measured on average at an age of 1,422 days with an average calf age at weaning of 195 days. There was a substantially higher number of records available for scan traits compared to carcass traits (Table 2).

Table 1. Descriptive statistics of mature body condition (MBC), mature cow height (MCH), and mature cow weight (MCW)

Trait	Unit	No. of records	No. of animals with records	Mean	SD	Min	Max
MBC	Score	37,329	23,047	3.3	0.77	1	6
MCH	cm	13,640	9,871	134	5	117	155
MCW	kg	177,931	97,797	572	97	176	1004

Table 2. Summary statistics of scan and carcass traits used in the study

Trait[1]	Unit	No. of records	Mean	SD	Min	Max
P8_B	mm	194,104	5.0	2.5	1	15
P8_H	mm	184,428	7.5	3.5	1	21
RIB_B	mm	194,571	4.0	1.9	1	11
RIB_H	mm	184,249	5.8	2.6	1	16
CP8	mm	11,862	21.1	6.6	3	46
CRIB	mm	4,279	16.4	6.2	3	41
CWT	kg	12,086	443	64	214	611

[1]Scan traits: B and H refers to bull and heifer scanned traits, P8: live-scan P8 fat, RIB: live-scan rib fat; Carcass traits: CP8: carcass fat depth at p8 rump site, CRIB: carcass rib fat, CWT: dressed carcass weight.

Mature cow traits have moderate to high heritability, with the highest heritability observed for MCH (0.55 ± 0.03), followed by MCW (0.43 ± 0.01), and MBC (0.21 ± 0.01) (Table 3). Both MCH (0.73) and MCW (0.74) were more repeatable than MBC (0.37). The heritability estimates of heifer scan traits were higher than those for bull scan trats (Table 3). The heritability estimates for scan fat depth traits ranged from 0.23 ± 0.01 for RIB_B to 0.40 ± 0.01 for P8_H. The heritability for CWT (0.49 ± 0.03) was greater than those for carcass fat depth traits, with the lowest for CRIB (0.35 ± 0.05).

Mature cow height is strongly associated with MCW (r_G = 0.83 ± 0.01). The genetic correlation between MBC and MCW in this study was also strongly positive (0.87 ± 0.01). The genetic correlation between MBC and MCH was low (0.26 ± 0.03).

Table 3. Heritability estimates with standard deviations ($h^2 \pm SD$), additive genetic (σ_a^2), animal permanent environmental (σ_{pe}^2), sire by herd (σ_{sxh}^2), phenotypic (σ_p^2) variances for mature cow and scan traits based on univariate analyses

Trait[1]	σ_a^2	σ_{pe}^2	σ_{sxh}^2	σ_p^2	$h^2 \pm SD$
MBC	0.057	0.044		0.272	0.21 ± 0.01
MCH	7.360	2.517		13.450	0.55 ± 0.03
MCW	1067	755		2469	0.43 ± 0.01
P8_B	0.484		0.048	1.778	0.27 ± 0.01
P8_H	1.530		0.117	3.840	0.40 ± 0.01
RIB_B	0.199		0.021	0.852	0.23 ± 0.01
RIB_H	0.733		0.072	1.987	0.37± 0.01
CP8	12.98			26.94	0.48 ± 0.03
CRIB	6.82			19.48	0.35 ± 0.05
CWT	491			1001	0.49 ± 0.03

[1]Traits and units are as given in Table 1 and Table 2.

The genetic correlations between mature cow traits and scan and carcass fat depth traits and CWT are given in Table 4. Accordingly, MBC and heifer and steers scan (P8_H, RIB_H) or the carcass fat depth traits (CP8 and CRIB) were lowly to moderately genetically correlated. The genetic correlation between MBC and RIB_B (0.11 ± 0.05) is lower than that between MBC and RIB_H (0.31 ± 0.03). As expected, CWT and MCW (0.39 ± 0.05) and MCH (0.21 ± 0.09) were positively genetically correlated.

Table 4. Genetic correlations between mature cow traits and carcass and scan traits from bivariate analyses

Traits[1]	MBC	MCH	MCW
P8_B	0.08 ± 0.04	-0.19 ± 0.05	-0.22 ± 0.02
P8_H	0.35 ± 0.03	-0.28 ± 0.03	-0.11 ± 0.01
RIB_B	0.11 ± 0.05	-0.20 ± 0.05	-0.23 ± 0.02
RIB_H	0.31 ± 0.03	-0.23 ± 0.03	-0.10 ± 0.01
CP8	0.19 ± 0.08	-0.16 ± 0.09	-0.30 ± 0.05
CRIB	0.30 ± 0.15	0.01 ± 0.15	-0.13 ± 0.10
CWT	0.05 ± 0.09	0.21 ± 0.09	0.39 ± 0.05

[1]Traits and units are as given in Table 1 and Table 2.

DISCUSSION

There is sufficient additive genetic variation for effective selection of MBC, MCH, and MCW. Comparable heritability estimates have been reported in the literature. For example, heritability estimates from 0.16 ± 0.03 (Granleese and Clark 2019) to 0.21 (Johnston *et al.* 1996) for MBC, from 0.44 ± 0.05 (Granleese and Clark 2019) to 0.58 ± 0.06 (Donoghue *et al.* 2018) for MCH, and 0.43 (Granleese and Clark 2019; Johnston *et al.* 1996) for MCW in Australian Angus.

The high genetic correlations between MCW and MCH observed in our study (0.83 ± 0.01) indicates that selection for higher finishing weights and the associated correlated response for MCW could lead to an increase in MCH. A high genetic correlation between MBC and MCW in this study (0.87 ± 0.01) is expected given that MBC was not accounted for in the models for MCW. The genetic correlation between MBC and MCW in this study is greater than the previous studies by Granleese and Clark (2019) (0.62 ± 0.07), Donoghue *et al*. (2018) (0.74 ± 0.11 at weaning at parity two), and Johnston *et al*. (1996) (0.49). Placing selection emphasis on increasing CWT could lead to higher MBC due to positive genetic correlations between CWT and MCW (0.39 ± 0.05) as well as between MCW and MBC (0.87 ± 0.01).

Body condition, P8, and RIB measures reflect the fat cover thickness of an animal. However, low to moderate genetic correlations between MBC and heifer or steer scan (P8_H, RIB_H) or the carcass (CP8 and CRIB) fat depth traits measured on young animals in this study indicate that they are not genetically the same trait in young and mature animals. This also consistent with the biological differences in subcutaneous fatty tissue development in young and old animals (Robelin 1981). Low to moderate genetic correlations between MBC and scan fat depth similar to our study have been reported in the literature (Weik *et al*. 2022; Pitchford 2023). Results of our study suggest that optimising MBC based on scan and carcass fat depth traits measured on young cattle is possible, but a large change in the genetic merit of fat depth traits is required to achieve a small change in the genetic merit of MBC. Therefore, measuring MBC as a direct measure is easier and more cost effective than measuring scan fat depth in mature cows.

Targeting a higher rib fat or P8 fat at young and finishing cattle would decrease MCH and MCW as indicated by the negative genetic correlations obtained in this study. Similar negative genetic correlations between MCW and scan P8 (-0.28 ± 0.05), RIB (-0.32 ± 0.05), and CRIB (-0.40 ± 0.10) were reported by Weik *et al*. (2022). Similarly, the genetic correlations between MCH and scan P8 (-0.31 ± 0.05), and RIB (-0.32 ± 0.05), CRIB (-0.28 ± 0.10) were also negative (Weik *et al*. 2022). These negative genetic correlations are advantageous if the goal is to select for smaller mature cow size, thereby reducing feed requirement for maintenance and potentially allowing a higher stocking density on pasture. However, smaller cow weights lead to reduced returns for cull cows. Therefore, selection targets for MCW as well as MBC, and MCH should be aligned with the breeding objective.

CONCLUSION

There is sufficient genetic variation to directly select for mature cow traits. Fat depth traits measured in young animals have low genetic correlations with MBC, resulting in slow genetic progress for MBC if selection decisions for MBC are based on live animal ultrasound scan and carcass fat depth traits. Therefore, collecting MBC as a direct measure would be easy and cost effective rather than measuring scan fat depth in mature cows.

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REFERENCES

Angus Australia (2024) https://www.angusaustralia.com.au/education/breeding-and-genetics/collection-guidelines-for-angus-research/). (Accessed November 2024).
Donoghue K.A., Lee S.J., Parnell P.F. and Pitchford W.S. (2018) *Anim. Prod. Sci.* **58**: 145.
Granleese T. and Clark S.A. (2019) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **23**: 95.
Graser H.U., Tier B., Johnston D.J. and Barwick S.A. (2005) *Aust. J. Exp. Agric.* **45**: 913.
Johnston D.J., Chandler H. and Graser H.U. (1996) *Aust. J. Agric. Res.* **47**: 1251.
Misztal I., Tsuruta S., Lourenco D.A.L., Masuda Y., Aguilar I., Legarra A. and Vitezica Z. (2018) ‘Manual for BLUPF90 family of programs’, University of Georgia, Athens, USA.
Pitchford W.S. (2023) *Anim. Prod. Sci.* **63**: 957.
Robelin J. (1981) *J. Lipid Res.* **22**: 452.
Weik F., Hickson R.E., Morris S.T., Garrick D.J. and Archer J.A. (2021) *Animal* **12**: 25.