

## HOW DOES MATERNAL WEANING WEIGHT (MILK) AFFECT BODY CONDITION SCORE AT WEANING IN ANGUS CATTLE

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### SUMMARY

This paper reports the heritability estimates for mature body composition traits in Australian Angus cattle and the interaction with the maternal component of weaning weight. These traits include mature body weight (MCW), mature cow fat score (MBC), mature cow height (MCH), weaning weight (WWT) and the maternal component of weaning weight (MILK) with industry data obtained from breeders registered with Angus Australia. Heritability for MCW, MBC, MCH, WWT and MILK was estimated to be 0.44, 0.49, 0.15 and 0.13, respectively. MCW had a moderate genetic correlation with MBC of 0.61 and 0.46 for MCH. MBC and MCH had a genetic correlation of -0.06 but had a large standard error due to low cross-over of cows with phenotypes for the two traits. MILK had a negative genetic correlation with MBC of -0.48 and small positive genetic correlations of 0.12 and 0.23 with MCW and MCH, respectively. These results indicate that selection for mature body composition traits is possible but care should be taken when considering interactions with the maternal trait MILK.

### INTRODUCTION

Mature body composition traits of mature beef cows have not been as well measured in seedstock populations as compared to corresponding traits at younger ages (Donoghue *et al.* 2018). However, a high percentage of female cattle in a self-replacing herd will spend up to significantly more time as a mature animal compared to their first two years. Australian seedstock beef breeders have made significant gains in production traits where traits can be easily measured in large and complete cohorts in the first two years of age (Walmsley *et al.* 2018). Given the challenges of measuring traits on mature cows, the estimation of breeding values in routine analysis for mature body composition traits has been challenging. Mature cow body composition traits are an important aspect for self-replacing herds to focus on in their breeding objective. Traits such as mature body condition score (MBC), mature weight (MCW), mature hip height (MCH) are associated with feed maintenance costs and reproduction rates (Walmsley *et al.*, 2018). Previous studies in Angus research populations in Australia and United States of America have estimated heritability from MBCS, MCW and MCH to be 0.11-0.21, 0.40-0.71, and 0.62-0.83, respectively (Choy *et al.* 2002; Decker *et al.* 2012; Donoghue *et al.* 2018). Genetic correlations of mature body composition traits has not been well investigated in beef but dairy cattle analysis suggest a negative genetic correlation of 0.50 between milk yield and MBC (Berry *et al.* 2003).

The aim of this paper is to estimate genetic and residual variation and correlations of the three body composition traits above and the maternal component of weaning weight using industry data from the Angus Australia database.

### METHODS

**Animals.** Industry data from animals in the Angus Australia database born in 2003 and after were included in the analysis. All males were excluded for MCW, MBC and MCH. For individuals to be included for these traits, there needed to be at least 10 females in a contemporary group. Records for WWT to be included were the corresponding progeny measured at the same point of MCW or MBC

measurement. Contemporary grouping for all traits were created based on Graser *et al.* (2005) where the concatenation of herd, day of measurement and breeder-defined management group was used. Females were excluded if the first measurement for any trait was older than 5 years of age. Table 1 displays the number of records for traits and pairs of traits. The number of contemporary groups for each trait is found in Table 1.

**Measurements.** Weaning weight was measured between 60 and 300 days of age. Both MBC and MCW were measured within two weeks of weaning. The minimum age for MBC and MCW was 830 days of age while MCH was 730 days of age. All traits were measured following Angus Australia measuring protocols.

**Statistical analysis.** Single measurements were used for all traits. Records more than 4 standard deviations from the database mean were identified as outliers and removed from the analysis. Contemporary group was fitted as described above and age at measurement was fitted for all traits. Age of calf was fitted for MCW and MBC, while age of dam was fitted for WWT. The maternal component for weaning weight was fitted to estimate the maternal affect (MILK). Genetic parameters and predicted means were estimated using an animal model in WOMBAT (Meyer 2007). Genetic covariance was not estimated between WWT direct and maternal component of WWT (MILK). A numerator relationship matrix based on a four generation pedigree was used. Genetic and phenotypic parameters were estimated from a multivariate analyses.

**Table 1. Means, standard deviations, minimums, maximums and number of contemporary groups for each trait**

	Records	Mean	SD	Min.	Max.	Cont. Groups
WWT	56409	237.5	52.0	56	445	2892
MCW	31455	538.2	86.8	316	966	1044
MBC	4915	3.1	0.75	1	6	188
MCH	2952	133.1	5.16	117	155	116

## RESULTS AND DISCUSSION

Table 2 contains summary statistics for mature body composition traits. All traits were heritable with low standard errors which suggests that selection for genetic progress can be made. Heritabilities from the multivariate analysis matched univariate analysis with small and insignificant differences between standard errors.

Heritability for MCW was 0.43. This is similar to Johnston *et al.* (1996) and Choy *et al.* (2002) but lower than Decker *et al.* (2012) and Donoghue *et al.* (2018). Heritability for MCH was 0.44 which was lower compared to most other Angus genetic parameter studies in Australia (Donoghue *et al.* 2018) and the USA (Choy *et al.* 2002; Decker *et al.* 2012) which estimated heritabilities ranging from (0.58-0.82). Heritability for MBC was 0.16 and was similar to other Angus genetic parameter studies (Choy *et al.* 2002; Donoghue *et al.* 2018). Results from this study are in agreement with past published studies that there is the potential to select for mature body composition traits. Weaning weight and its maternal component was 0.18 and 0.13, respectively. This is in agreement with Meyer's (1992) study where covariance between direct and maternal effect is not estimated.

**Table 2. Phenotypic variance and heritabilities (with standard errors) for multivariate analysis**

	$\sigma_p$	$h^2$ ■
WWT	90.5	0.18 (0.01)
MILK	72.8	0.13 (0.01)
MCW	901	0.43 (0.02)
MBC	0.043	0.16 (0.03)
MCH	6.15	0.44 (0.05)

**Table 3. Genetic correlation above diagonal and phenotypic below diagonal from multivariate analysis with (standard errors)**

	WWT	MILK	MCW	MBC	MCH
WWT	-	-	0.49 (0.03)	-0.09 (0.11)	0.46 (0.09)
MILK	-	-	0.12 (0.03)	-0.48 (0.09)	0.23 (0.08)
MCW	0.44 (0.01)	0.41 (0.01)	-	0.62 (0.07)	0.47 (0.08)
MBC	0.15 (0.02)	0.10 (0.02)	0.44 (0.01)	-	-0.01 (0.16)
MCH	0.31 (0.03)	0.31 (0.00)	0.45 (0.01)	0.07 (0.03)	-

Phenotypic and genetic correlations and their associated standard errors between mature body composition traits and weaning weight are reported in Table 3. MCW was moderately genetically correlated with MBC (0.62), MCH (0.47) and WWT (0.49). These genetic correlations are lower when compared to previous literature. Lower heritabilities and genetic correlations in this study could be caused by using industry data where culling takes place. The other cause may be due to using single measurement only where permanent environment effect is not accounted for (Kaps *et al.* 1999). Furthermore we did not fit sire-by-herd. Repeated measures to account for permanent environment effects as well as fitting sire-by-herd should give better genetic estimates. The genetic correlation between MBC and MCW was close to zero which corresponds to previous studies (Donoghue *et al.* 2018). Moving forward, Angus Australia members will need to make sure they are measuring both MBC and MCH on the same animals to provide more accurate genetic correlations between the two traits.

The genetic correlation between the maternal component of WWT (MILK) and MBC (which was measured at weaning) suggest that high milking cows will genetically lower body condition score animals with a genetic correlation of -0.48 (Table 3). However, this correlation could be broken with body condition score measured at weaning and selection for higher MILK and higher MBC possible. This genetic correlation is in agreement to Berry *et al.*'s (2003) study in milking cattle where they estimated a genetic correlation of -0.50 between milk yield and body condition score. The phenotypic correlation between these two traits is 0.10. This suggests Angus breeders are managing body condition score to make their performance recorded animals are in good body condition when raising a calf.

We did not estimate genetic covariance of WWT and MILK because our model did not use repeated records and we could not fit permanent environment effects as well as sire-by-herd effects. Bijma (2006) and Meyer (1992) explain the difficulties of estimating covariance of direct and maternal components of traits and is the next step for research with this study.

Mature body condition and MCW were measured at the weaning of their calves or within two weeks of weaning. The measuring of weight helps with the maternal 200 day weight EBVs of their calves. However, studies suggest that MBC are different traits at different stages of lactation. Dono-

ghue *et al.* (2018) suggested that weaning MBC and pre-calving MBC in Australian Angus cattle while Wolcott *et al.* 2013 demonstrated that joining and weaning MBC were also two different traits in *Bos Indicus* cattle.

Investigation of mature body composition traits at joining and the genetic relationships with maternal productivity traits such as MILK and fertility would be a logical next step.

## CONCLUSION

Genetic variation in mature composition traits is present in the Angus Australia database, confirming there is potential to select for more efficient females in a self-replacing herd. More cows in the database need phenotypes for both body condition (fat) score and mature hip height to be able to calculate genetic correlations with confidence. Including some early in life measurements will give these mature body composition breeding values some context.

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