GENETIC EVALUATION OF COAT TYPE FOR AUSTRALIAN ANGUS

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SUMMARY

Animals with sleeker coats are commonly considered to have better heat tolerance, tick resistance, and a lower incidence of dags in feedlot environments. The objective of this study was to estimate genetic parameters for coat type traits and to estimate genetic correlations between coat type and scan and carcass weight traits using single-step methods. Two coat type traits were defined based on the month of scoring where scores recorded in April to October were considered as coat type 1 (CT1) and those recorded in November to March were categorized as coat type 2 (CT2). The coat type traits were moderately heritable, and the heritability of CT1 (0.36 ± 0.04) was higher than CT2 (0.32 ± 0.03). Genetic correlations between coat type traits and steer and heifer ultrasound scan traits (eye muscle area, intramuscular fat) were either low to moderate in strength, but favourable in direction. The outcomes of this study suggest selection for sleeker coat type is possible without any associated detrimental effect on scan and carcase traits.

INTRODUCTION

It is common for domestic livestock to shed their hairy coats for a sleeker coat at the onset of summer in preparation for warmer months. A lower core body temperature and greater perspiration have been previously observed among sleeker coat-typed cattle showing superior heat tolerance ability (Yeates 1955; Dikmen *et al*. 2008). Sleeker and shorter coats are also associated with tick resistance since hairy and thicker coats support tick attachment and prevent the removal of ticks via the animal's self-grooming (Hansen 2004). Therefore, *Bos taurus* cattle with a predominantly sleeker coat are advantaged over hairy coat cattle during summer or in tropical or sub-tropical conditions where the heat and tick infestations are the highest. In addition, beef cattle with sleeker hair types have a lower incidence of dags in a feedlot environment, with less associated challenges of dag removal prior to slaughter, particularly in colder and wetter climates.

Since 2019 Angus Australia has published a research breeding value (RBV/RBVs (plural)) for the coat type through the TransTasman Angus Cattle Evaluation (TACE). This has enabled the selection of a desirable coat type to match with the beef cattle production systems. Preliminary data analyses for coat type in Australian Angus cattle showed that the coat type is moderately heritable, however, the association between coat type and other economically important traits are yet to be explored. Therefore, the objective of this study was to estimate the genetic parameters and genetic correlations between coat type and live-animal ultrasound assessed traits and carcass weight using single-step methods.

MATERIALS AND METHODS

Data and traits. Coat scores were collected assessing the animal's hair length, fibre diameter, and handle based on a one to seven numbered scoring guide according to Turner and Schleger (1960). Scores range from; score one, animals with extremely short sleek hair similar to the hair found in *Bos indicus* to score seven being a very hairy coat.

Coat scores of 6188 animals were extracted from the Angus Australia database for progeny from the Angus Sire Benchmarking Program (Parnell *et al*. 2019). Data was collected year-round, and scores were available from animals born from 2008 to 2021. Since coat type may vary as the animal

ages (Durbin *et al*. 2020), coat scores collected after 720 days were excluded from the analyses. Only purebred Angus animals were used in the analyses by selecting animals with an Angus breed percentage of 87.5 or above. Multiple records per animal were excluded by keeping only the earliest record. The contemporary groups were constructed by concatenating the year-month of measurement, herd, and the breeder-defined management group. The contemporary groups with at least ten individuals were selected for the analyses. The data cleaning process resulted in 6177 records for analysis. Individuals scored for coat type were the progeny of 401 sires and included 2115 females and 4062 males. Coat score measures were broadly classified into two traits based on the phenotypic averages and variation in each month of scoring. Accordingly, coat scores recorded from April to October were identified as coat type 1 (CT1) and the scores collected during the rest of the year as coat type 2 (CT2).

Live-animal ultrasound scan traits and carcass weight were also extracted for animals with a coat type record from the Angus Australia database to estimate the genetic correlations with coat type traits. The live-animal ultrasound scan traits extracted were eye muscle area (EMA, measured in cm^2), intramuscular fat (IMF, measured in %), and P8 fat (P8, measured in mm). The data cleaning process was similar to that described for coat type traits. The contemporary groups for the scan and carcass weight traits were formulated as described by Graser *et al*. (2005). The live-animal ultrasound scan traits were separated as steer (S) and heifer (H) traits. Genomic information for animals with a phenotypic record of which were imputed for 45364 markers per genotype (Aliloo and Clark, 2021) was also extracted.

Statistical analyses. The genetic parameters for different traits were estimated using single-step univariate and bivariate animal models. The contemporary group and sex were fitted as the fixed effects, linear and quadratic effects of age were fitted as the covariates, and the animal effect was fitted as the random effect in animal models for coat type traits. Sire by herd interaction was not significant for CT1 and CT2, therefore, was not included in the final models. The model parameters used for scan traits and carcass weight were as described by Graser *et al*. (2005). The variance components were estimated using the single-step method implemented in airemlf90 (Misztal, *et al*. 2018).

RESULTS

Descriptive statistics of different traits used in the analyses are given in Table 1. The mean CT1 was higher than CT2 (2.8 vs. 2.0), and scores for CT1 and CT2 ranged from 1 to 5 and 1 to 4.5, resp-

Table 1. Descriptive summaries of coat type traits, 1 and 2

Trait[a]	No. of records	% Genotyped	Mean	SD	Minimum	Maximum
CT1	2221	98	2.8	0.6	1	5
CT2	3956	98	2.0	0.5	1	4.5
SEMA	3861	99	70.6	11.2	38	100
SIMF	3824	99	6.7	1.2	3	8.3
SP8	3838	99	10.5	4.4	1	22
HEMA	1912	97	61.5	7.3	41	82
HIMF	1901	97	6.2	1.3	2.5	8.3
HP8	1899	97	8.7	3.4	1	19
CWT	4084	99	422.7	68.9	238	607

[a]CT1: coat type scored for 04-10 months; CT2: coat type scored for 11-03 months; SEMA: Scan steer eye muscle area (cm^2); SIMF: Scan steer intramuscular fat (measured in %); SP8: Scan steer P8 fat (mm); HEMA: Scan heifer eye muscle area (cm^2); HIMF: Scan heifer intramuscular fat (ether extract %); HP8: Scan heifer P8 fat (mm); CWT: Carcass weight (kg).

-ectively. There were at least three scores in each coat type trait with more than 18% animals recorded. Therefore, there was an adequate coat score variation and an adequate number of records in each score to fit linear models for each coat type trait. More than 97% of animals recorded for all traits were also genotyped.

The heritability for CT1 (0.36 ± 0.04) was similar to CT2 (0.32 ± 0.03) (Table 2). Across all traits used in this study, the highest heritability was observed for CWT (0.45 ± 0.03) and the lowest was for HEMA (0.25 ± 0.05). The heritabilities of S-scan traits were higher than H-scan traits, and the heritability of scan traits was highest for P8 fat.

The correlation between CT1 and CT2 was 0.76 ± 0.08. The genetic correlation estimates between coat type traits and other traits were negative (*i.e.* favourable) except for CT1 in SP8 and CT1 and CT2 in HP8 where a very small positive correlation was obtained (Table 3). The genetic correlation coefficients between coat type and scan and carcass weight traits ranged from -0.26 to 0.03 in CT1 and -0.27 to 0.06 in CT2. The genetic correlations between scan and carcass traits and coat type traits were slightly lower for CT2.

Table 2. Additive genetic (V_a), sire by herd (V_{sxh}), and residual variances (V_e), and heritability ± standard deviations ($h^2 \pm SD$) from univariate single-step analyses

Trait[a]	V_a	V_{sxh}	V_e	$h^2 \pm SD$
CT1	0.10	-	0.17	0.36 ± 0.04
CT2	0.06	-	0.13	0.32 ± 0.03
SEMA	6.89	0.81	13.44	0.33 ± 0.03
SIMF	0.13	0.00	0.27	0.32 ± 0.01
SP8	2.20	0.09	2.62	0.45 ± 0.03
HEMA	4.47	0.92	12.62	0.25 ± 0.05
HIMF	0.22	0.00	0.53	0.29 ± 0.01
HP8	1.64	0.11	3.11	0.34 ± 0.05
CWT	449.14	35.48	505.57	0.45 ± 0.03

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

Table 3. Genetic correlations (± standard deviations) for CT1 and CT2 with steer and heifer live-animal ultrasound scan traits and carcass weight from bivariate single-step analyses

Traits[a]	No. of animals		Genetic correlations	
	CT1	CT2	CT1	CT2
SEMA	4819	5219	-0.22 ± 0.09	-0.26 ± 0.07
SIMF	4793	5208	-0.26 ± 0.01	-0.27 ± 0.01
SP8	4808	5207	0.03 ± 0.08	-0.12 ± 0.07
HEMA	4133	5868	-0.11 ± 0.10	-0.22 ± 0.09
HIMF	4122	5857	-0.06 ± 0.01	-0.13 ± 0.01
HP8	4120	5855	0.06 ± 0.10	0.06 ± 0.08
CWT	4928	5333	-0.25 ± 0.07	-0.25 ± 0.06

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

DISCUSSION

Coat type traits were moderately heritable in this study, therefore, genetic improvement towards a desired coat type can be achieved in breeding programmes. Angus Australia reports the RBVs for CT2 that are based on the coat scores recorded during the Australian summer. Studies based on a coat scoring system that records the extent of hair shedding at the onset of summer in the United States yielded similar heritability estimates to our study. For example, heritability estimates for

American Angus and Limousin cattle in the United States were 0.34 to 0.40 (Durbin *et al*. 2020) and 0.33 (Williams *et al*. 2006), respectively.

Genetic correlation estimates between coat type traits and scan and carcass traits were favourable in this study. Selecting animals with a sleeker coat using either CT1 and CT2 could result in improvements in CWT, EMA, and IMF in subsequent generations. These results are aligning with the anecdotal feedback from breeders suggesting that sleeker coats are associated with superior performance.The favourable genetic correlations are slightly stronger in CT2 than CT1 for most scan traits other than for heifer P8 fat. Therefore, CT2, which is used to produce an RBV, would be an agreeable trait to select for sleeker coat type while also improving the meat quality and carcass weight. However, this needs further investigations including more animals and estimation of genetic correlations for other production traits including weight and fertility traits.

CONCLUSIONS

Coat type traits were moderately heritable. Selecting animals for a sleeker coat type can lead to simultaneous improvements in both carcass weight and meat quality.

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