APPROPRIATENESS OF COMBINING CARCASS DATA FROM ANGUS SIRE BENCHMARKING PROGRAM AND BREEDER HERDS IN A SINGLE GENETIC EVALUATION

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SUMMARY

The objective of this study was to investigate whether the two different sources of abattoir carcass phenotypes that are currently submitted for inclusion in the TransTasman Angus Cattle Evaluation are genetically the same trait, being abattoir carcass phenotypes measured on cattle in the Angus Sire Benchmarking Program (ASBP), and abattoir carcass phenotypes measured on Angus animals in breeder herds. The abattoir carcass traits used were carcass MSA marble score (CMMS), carcass fat depth at p8 rump site (CP8, measured in mm), and dressed carcass weight (CWT, measured in kg). Additive genetic correlations between the same traits across the two sources were estimated with bivariate animal models. The additive genetic correlations for CP8, CMMS, and CWT were 0.99 ± 0.17, 0.84 ± 0.24, and 0.73 ± 0.23, respectively. Therefore, the two different sources of abattoir carcass phenotypes can be considered genetically to be the same trait and can be included in a unified genetic evaluation as the same trait.

INTRODUCTION

Variations in breeding goals and data collection processes can yield different heritability estimates for the same trait even though the same phenotype is collected. Further, the genetic correlations between the same trait from two different data sources can be low raising concerns regarding the genetic similarity of the traits and the validity of combining data from various sources in a single genetic evaluation. Currently, phenotypes from two different sources are submitted for inclusion in the TransTasman Angus Cattle Evaluation (TACE), i.e., phenotypes from the Angus Sire Benchmarking Program (ASBP) (Parnell *et al*. 2019), and phenotypes measured on Angus animals in breeder herds. This study was formulated to investigate whether the carcass phenotypes collected on the two different data sources are genetically the same trait. Therefore, the objective of this study was to estimate the heritability and additive genetic correlations among the same traits between ASBP and breeder herds to determine the suitability of combining abattoir data from both sources in the TACE.

MATERIALS AND METHODS

Data. Phenotypic records of carcass traits and pedigree were extracted from the Angus Australia database. Among the different carcass traits, carcass MSA marble score (CMMS), carcass fat depth at p8 rump site (CP8, measured in mm), and dressed carcass weight (CWT, measured in kg) were selected based on the availability of an adequate number of records in both ASBP and breeder herds (Table 1).

Extracted carcass records were used in the analyses if, they were pure Angus i.e., Angus percentage is higher than or equal to 87.5 %; the animals were born after 2010; the age at slaughter is available for carcass weight, and a carcass weight record is available for other carcass records; the sire is known, and if the observations are within three standard deviations from each trait mean which is calculated within each data source. Furthermore, contemporary groups with less than five animals and single-sire contemporary groups were discarded from the analyses. Contemporary groups were formed as described by Graser *et al*. (2005). The number of contemporary groups formed in CWT for ASBP and breeder data were 75 and 271, respectively. The average number of

individuals within a contemporary group was greater in ASBP data than breeder data (39 vs. 16 for CWT). The data cleaning process excluded ASBP data by 16% and breeder herd data by 29%, respectively. After data cleaning, a total of 3,041 animals from ASBP herds originating from 329 sires and 2,502 dams, and 4621 animals from breeder herds originating from 352 sires and 3,796 dams were used in the study.

Estimation of genetic parameters. Genetic parameters for each trait were estimated with univariate animal model, and the model fitted was as follows.

$$y = Xb + Za + e$$

Where y is the vector of observations for CMMS, CP8, and CWT, b is the vector of fixed effects of contemporary group and linear and quadratic effects of the slaughter age (for CWT) or linear and quadratic effects of CWT (for CMMS and CP8) as covariates, a is the vector of random animal effects, e is the vector of random residual effects, and X and Z are design matrices which relate records to fixed effects and random animal effects, respectively. The covariates fitted in the model, slaughter age and CWT were adjusted for 750 days of slaughter age or 400 kg of CWT as specified in TACE (Angus Australia 2023). The variance components for the random effects were denoted as $Var(a) = A\sigma_a^2$ and $Var(e) = I\sigma_e^2$, where A is the numerator relationship matrix, σ_a^2 is the additive genetic effects variance of the animal, I is the identity matrix, and σ_e^2 is the residual variance. The pedigree consisted of only the animals with records for analysis plus the previous four generations. Additive genetic correlations between the same trait across the two data sources were estimated with bivariate animal models. Variance components for univariate and bivariate models were estimated using the WOMBAT software (Meyer 2007).

RESULTS

The descriptive statistics of the carcass traits are shown in Table 1. On average, animals in breeder herds were slaughtered 26 days later, and they were 7 kg heavier than ASBP animals. Marbling trait mean (CMMS) was also higher for animals in breeder herds by comparison to ASBP animals but not for CP8.

Table 1. Descriptive statistics of four carcass traits in Angus Sire Benchmarking Program (ASBP) and breeder herds

Traits[1]	No of animals	Mean	SD	CV	Min	Max	Mean age	Mean weight
ASBP								
CMMS	3026	523.98	120.82	0.23	160	890	757	453
CP8	3017	22.94	6.42	0.28	4	42	758	453
CWT	2940	457.73	36.91	0.08	315	571.5	762	458
Breeder								
CMMS	2011	568.57	101.31	0.18	230	900	774	449
CP8	4454	21.43	6.07	0.28	6	40	785	464
CWT	4520	464.96	45.21	0.10	279.4	580.5	788	465

[1]CMMS, carcass MSA marble score; CP8, carcass p8 fat (measured in mm); CWT, dressed carcass weight (measured in kg).

The additive genetic variances and heritability estimates for all carcass traits were higher in ASBP herds than breeder herds (Table 2). The additive genetic correlations between the same trait across ASBP and breeder herds were highest for CP8 (0.99 ± 0.17), followed by CMMS (0.84 ± 0.24) while the additive genetic correlations for CWT was the lowest (0.73 ± 0.23, Table 3). The

additive genetic correlations between the two data sources increased with an increasing number of common sires between the two herds.

Table 2. Additive genetic (σ_a^2) and residual (σ_e^2) variances, and heritability ± standard errors ($h^2 \pm SE$), from univariate analyses of carcass traits for Angus Sire Benchmarking Program (ASBP) and breeder herds

Traits[1]	ASBP			Breeder		
	σ_a^2	σ_e^2	$h^2 \pm SE$	σ_a^2	σ_e^2	$h^2 \pm SE$
CMMS	5218	6388	0.45 ± 0.06	2234	4730	0.32 ± 0.08
CP8	14.85	15.24	0.49 ± 0.06	12.28	14.68	0.46 ± 0.06
CWT	676	374	0.64 ± 0.07	297	624	0.32 ± 0.05

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

Table 3. Additive genetic correlations ± standard errors (SE), number of common sires, and number of offspring per sire between ASBP and breeder herds

Traits[1]	Genetic correlations ± SE	No. of common sires	No. of offspring per sire	
			ASBP	Breeder
CMMS	0.84 ± 0.24	8	98	59
CP8	0.99 ± 0.17	11	133	152
CWT	0.73 ± 0.23	10	124	156

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

DISCUSSION

This study aimed to evaluate whether the phenotypes collected for carcass traits in ASBP and breeder herds are genetically the same trait by estimating additive genetic correlations among the same traits between ASBP and breeder herds. If the additive genetic correlations are closer to one, then the traits from two herds can be declared as being sufficiently similar for analysis as the same trait in the TACE. In this study, the proportion of additive genetic variance shared between the same trait across two data sources were high and significantly different from zero indicating that the genetic influences on the same trait across two herds are almost identical. Therefore, CWT, CP8, and CMMS are genetically the same trait across ASBP and breeder herds.

The variance components and heritability estimates are higher than 0.32 for all carcass traits across the two herds and consistent with past studies on carcass traits (Duff *et al.* 2021; Samaraweera *et al.* 2021; Torres-Vázquez *et al.* 2018; Börner *et al.* 2013; Reverter *et al.* 2000). Accordingly, the heritability for CWT varies from 0.41 ± 0.04 (Börner *et al.* 2013) to 0.75 ± 0.06 (Duff *et al.* 2021); for CP8 ranges from 0.36 ± 0.04 (Börner *et al.* 2013) to 0.56 ± 0.06 (Duff *et al.* 2021) for Australian Angus.

In this study, the additive genetic variances and the heritability estimates were higher in ASBP herds than breeder herds particularly for CWT and CMMS. Similar to this study, higher values have been reported for ASBP collected data, for example, an additive genetic variance of 709 and a heritability of 0.75 ± 0.06 were reported for CWT by Duff *et al.* (2021). This may be a result of the project design of minimal harvesting prior to slaughter (i.e. whole contemporary group) and the general focus on phenotype quality. Conversely, the lower additive genetic variance in the carcass data from breeder herds may be explained by general pre-slaughter harvesting or the commercial nature of the phenotype collection.

The TACE utilizes the variances estimated across all herds, and the herd origin is accounted for in the contemporary group formation, hence in the genetic model as described by Graser *et al.*

(2005). The genetic similarity of the carcass traits between ASBP and breeder herds used in this study further confirms the ability to use them as the same trait in TACE.

CONCLUSION

Phenotypically collected abattoir carcass traits are genetically consistent across ASBP and breeder herds based on the genetic correlations between the same trait across the two herds. Therefore, the abattoir carcass traits used for this study can be treated as identical traits in the TACE.

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