PHENOTYPIC VARIATION IN RETAIL BEEF YIELD IN ANGUS CATTLE

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SUMMARY

This paper reports preliminary estimates of phenotypic variation and relationships for carcase traits using records from 386 Angus steers. Carcase traits recorded included carcase weight (CWT), retail beef yield (RBY), carcase intramuscular fat (CIMF), carcase P8 fat (CP8), carcase rib fat (CRIB) and carcase eye muscle area (CEMA). Carcase trait averages for animals used in this study were higher than for those used for the previous estimation of RBY parameters, and the differences evident between summary statistics for historic and contemporary carcase traits records highlights the value of continually recording carcase traits, as well as the value of re-examining relationships between carcase traits. Phenotypic correlations between carcase traits indicated that animals with higher RBY also had, phenotypically, heavier CWT ($r_p = 0.12$), larger CEMA ($r_p = 0.31$), lower CRIB and CP8 ($r_p = -0.28$ and -0.10 respectively) and lower CIMF ($r_p = -0.16$). For every 1-kg increase in RBY EBV, recorded CWT, RBY and CEMA were greater by 2.08kg, 0.24% and 2.77cm^2, respectively. In contrast, for every 1-kg increase in RBY EBV, recorded CIMF, CRIB and CP8 were lower by 0.39%, 1.31mm and 1.81mm, respectively. These preliminary results highlight the importance of continually recording carcase traits as well as the value of periodically re-examining relationships between carcase traits.

INTRODUCTION

Retail Beef Yield (RBY) is a key driver of profitability in the Australian beef industry, and the RBY EBV underpins BreedObject $Indices which allow selection for profitability in the major beef breeds. However, in current genetic evaluations, the trait of RBY is estimated almost exclusively from correlations with live weight, live animal scanned eye muscle area and fat depths. This is due to very limited recording of abattoir carcase data and specifically, RBY phenotypes. RBY phenotypes are not generated routinely because accurate data is time-consuming and expensive to collect. Previous estimates of phenotypic and genetic parameters for RBY were undertaken on a relatively small number of animals (n=1,930) born between 1994 and 2000 (Reverter *et al*. 2000; Reverter *et al*. 2003). Genetic improvement in carcase traits in the 20 years since the last RBY records were collected has led to significant improvements in carcase traits (Johnston 2007).

The purpose of this project is to generate RBY phenotypes on 1,000 fully pedigreed, genotyped and genetically described Angus steers. These will be used to re-estimate BREEDPLAN RBY parameters for incorporation into BREEDPLAN analyses to provide RBY EBVs. Animals in the project will be measured for a comprehensive suite of traits from birth until slaughter, including live weight and scan data taken from weaning until feedlot exit, and these traits will be assessed for their relationship with RBY. This will provide information to determine the effectiveness of exploiting early in life measurements as genetic indicators for RBY which may reduce the need to record actual RBY. The collection of RBY data will provide a reference population on which genomic information will be applied to provide RBY EBVs. Data used in this study comprises animals from the first two cohorts (of four) of the RBY project and provides preliminary estimates of phenotypic relationships between RBY and other carcase traits.

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MATERIALS AND METHODS

The animals used in this project were steers from the NSW DPI Trangie and Glen Innes research herds born in 2015 (n=150) and 2016 (n=236). All steers were fully pedigreed and, in collaboration with the Angus Sire Benchmarking Program had a comprehensive suite of traits measured from birth, based on BREEDPLAN collection protocols, and genomic testing (GGP-LD or Angus GS profile) conducted. There were 109 sires represented in the dataset, with the number of progeny for each sire ranging from 1 to 7. Fifty three of the 109 sires had progeny represented in both herds (Trangie and Glen Innes), and these 53 sires accounted for 58% (224/386) of the data.

Following weaning on the birth property, all steers were backgrounded on irrigated ryegrass /oats pasture and other pastures at Grafton Primary Industries Institute and were grain finished at UNE Tullimba Research Feedlot for 150 days to fit the John Dee, Warwick Angus Gold Grid. The steers were slaughtered in lots of approximately 50 animals at John Dee, Warwick, to suit the number of sides which can be boned for out for RBY at the facility in one shift. The cohorts were split into kill groups to ensure the integrity of the contemporary groups and based on balance for sire and live weight.

Following commercial AUS-MEAT carcase preparation (Anon. 2007), carcasses were weighed and hot P8 fat depth recorded. Fat trim following hot standard carcase weight measurement was restricted over the 12/13 rib to allow meaningful MSA rib fat data collection, and standard excess fat trim was conducted on the remainder of the carcase. Carcasses were tagged and chilled overnight, and Meat Standards Australia (MSA) carcase grading data (Anon. 2008) was collected by registered MSA graders on the right hand sides the following morning prior to boneout. A sample of the cube roll was collected for lab analysis to determine IMF% by the Meat Science Department at the University of New England following the near infrared spectrophotometry (NIR) method described by Perry *et al.* (2001).

For boneout a standard set of AUS-MEAT boneless primals, standard trim of 10mm fat, and estimated chemical lean of trim of 65% was conducted. The primal cuts included in the measure of RBY were: cube roll, chuck, chuck tender, blade, brisket, intercostals, FQ shin/shank, rib end meat, inside skirt, FQ trim, topside/inside, thick flank, rump, striploin, tenderloin, thin flank, silverside, HQ shin/shank, HQ trim. Carcase components of FQ fat trim, FQ bone, HQ fat trim and HQ bone did not contribute to RBY. Boning room pre-trim was weighed for completeness, though this was usually only 50 to 200g of fat and added to the weight of fat trim. The cold weight of the sides was measured prior to quartering and entering the boning room. This cold weight was used as a measure of reliability of the RBY data, as the recovery of this weight should be close to 100% and should be consistent across sides.

Data available for the analyses included carcase weight (CWT), eye muscle area (CEMA), retail beef yield percentage (RBY), intramuscular fat percentage (CIMF), subcutaneous fat depths at the P8 rump (CP8) and the 12th and 13th rib (CRIB) sites.

Model of analysis. Contemporary group for carcase records included effects of herd of origin and kill date. Variance and covariance components were estimated with an animal model using ASReml (Gilmour *et al*. 2015). A fixed effect of contemporary group, random direct genetic effects, and residual effects were included in the standard model. Univariate analyses were undertaken to obtain phenotypic variances for each trait, while pairwise bivariate analyses were undertaken to obtain phenotypic correlations. Regression of recorded carcase traits on the corresponding BREEDPLAN carcase EBVs were undertaken using PROC REG (SAS). Carcase traits were adjusted as per standard BREEDPLAN analyses (CWT adjusted to 750 days and all other traits adjusted to 400 kg carcase weight) for the regression analyses. BREEDPLAN carcase EBVs on animals were obtained prior to the inclusion of carcase data from the project in the genetic evaluation.

RESULTS AND DISCUSSION

Summary statistics for the carcase traits are shown in Table 1. Most carcase trait averages for animals used in the previous estimation of RBY parameters were markedly lower than those presented in Table 1 (From Reverter *et al*. 2003: Slaughter age = 630±128 days; CWT= 269±55 kg; RBY=67.03±3.69%; CIMF=4.64±2.23%; CP8=10.19±4.57 mm; CRIB=8.21±4.45 mm; CEMA=81.59±15.9 cm^2). The differences evident between summary statistics for historic and contemporary carcase trait records highlight the value of recording carcase traits in modern cattle populations, as well as the value of re-examining relationships between carcase traits in this population.

Table 1. Descriptive statistics for carcase traits

Trait	No. records	Average (SD)	Minimum	Maximum	σ^2_p (SE)
Age at slaughter (days)	386	596.4 (21.8)	536.0	635.0	-
CWT (kg)	386	344.7 (30.1)	269.0	428.5	889.10 (72.96)
RBY (%)	386	73.84 (2.02)	68.69	78.92	1.59 (0.12)
CIMF (%)	386	6.29 (2.04)	2.01	13.99	2.91 (0.22)
CP8 (mm)	386	16.24 (4.18)	10.00	30.00	13.73 (1.04)
CRIB (mm)	386	12.58 (4.45)	4.00	28.00	11.09 (0.81)
CEMA (cm^2)	386	81.48 (8.44)	57.00	108.0	37.27 (2.89)

Phenotypic correlations (r_p) between carcase traits were similar to those reported in the literature for the same traits in temperate breeds (Reverter *et al*. 2003) for the majority of traits (Table 2). Of those that were different to previous estimates, the majority of r_p were in the same direction but of a different magnitude; r_p between RBY and CIMF (-0.16 vs -0.31 in literature); r_p between and RBY and CP8 (-0.10 vs -0.40 in literature); r_p between RBY and CEMA (0.31 vs 0.14 in literature). The remaining estimates that indicated relationships in a different direction to previous estimates are most likely a reflection of the relatively low numbers analysed so far in this project; r_p between CWT and CIMF (0.12 vs -0.19 in literature); r_p between CWT and CP8 (0.15 vs -0.19 in literature); r_p between CWT and CRIB (0.19 vs -0.19 in literature).

Table 2. Phenotypic correlations (SE) between carcase traits

Trait	RBY	CIMF	CP8	CRIB	CEMA
CWT	0.12 (0.05)	0.12 (0.06)	0.15 (0.05)	0.19 (0.05)	0.38 (0.05)
RBY		-0.16 (0.05)	-0.10 (0.05)	-0.28 (0.05)	0.31 (0.05)
CIMF			0.07 (0.05)	0.06 (0.05)	-0.14 (0.05)
CP8				0.25 (0.05)	-0.09 (0.05)
CRIB					-0.17 (0.05)

Phenotypic correlations between carcase traits would indicate that animals with higher RBY also had, phenotypically, heavier CWT (r_p = 0.12), larger CEMA (r_p = 0.31), lower CRIB and CP8 (r_p = -0.28 and -0.10 respectively) and lower CIMF (r_p = -0.16). In summary, results so far would indicate that phenotypic relationships between recorded carcase traits follow the pattern expected, given previous estimates, and make sense biologically. This confirms the quality of the data that is being collected and highlights the value of the data to estimate updated genetic parameters for these traits once more records have been obtained.

Regression coefficients from regression of recorded carcase traits on corresponding BREEDPLAN carcase EBVs are presented in Table 3. These results indicate that, on average, for every 1-kg increase in RBY EBV, recorded CWT, RBY and CEMA were greater by 2.08kg, 0.24% and 2.77cm^2, respectively. In contrast, for every 1-kg increase in RBY EBV, recorded CIMF, CRIB and CP8 were lower by 0.39%, 1.31mm and 1.81mm, respectively.

Table 3. Regression coefficients from regression of recorded carcase traits on corresponding BREEDPLAN carcase EBVs

Trait	CWT EBV	RBY EBV	CIMF EBV	CP8 EBV	CRIB EBV	CEMA EBV
CWT	2.11**	2.08	7.22	-5.26**	-5.44**	-0.25
RBY	-0.01*	0.24**	-0.08	-0.05	-0.07	0.13**
CIMF	0.006	-0.39**	1.31**	0.08	0.10	-0.07
CP8	-0.05**	-1.81**	-0.22	1.17**	1.27**	-0.26**
CRIB	-0.03	-1.31**	-0.10	0.70**	1.00**	-0.33**
CEMA	-0.04	2.77**	-1.67**	-0.52**	-0.71**	1.31**

* Significance at $P<0.05$; ** Significance at $P<0.001$

CONCLUSIONS

In the majority of cases, phenotypic correlations and regression coefficients were such that relationships between carcase traits were in the expected direction and similar in magnitude to literature estimates. As the number of carcase records increase as this project continues it is anticipated that genetic parameters for carcase traits will be estimated. This will allow more detailed investigations into the appropriateness of the current BREEPLAN carcase genetic parameters for contemporary Angus cattle.

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