Final report

Genetics R&D: Phenotypic and genetic relationships between retail beef yield, live animal and carcase traits

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Abstract

Saleable meat yield is a key economic driver of the beef industry, improvement of which is underpinned by the retail beef yield (RBY) estimated breeding value (EBV) in BREEDPLAN. This EBV is estimated almost exclusively from correlations with animal liveweight and ultrasound scan data due to the small number of carcase and RBY phenotypes collected. This project aimed to generate RBY phenotypes on at least 1000 fully pedigreed and genetically described Angus cattle for use in re-estimating BREEDPLAN RBY parameters to provide more accurate carcase RBY EBVs aligned to modern beef cattle. Phenotypes for RBY and other production and carcase traits were collected on 1036 cattle, and have been submitted to Angus BREEDPLAN. Live and carcase trait relationships with retail beef yield were assessed. Generally, fatness traits had stronger relationships with retail beef yield when measured close to slaughter than when measured earlier in life, whereas muscling traits showed strong relationships at all times. Eye muscle area and muscle score both explain significant variation in retail beef yield, but do not provide the same information when predicting retail beef yield. This highlights the value of including muscle score when selecting for improved retail beef yield and that development of technologies, such as 3D cameras, would provide a more objective assessment of muscle score to improve the ability of industry to effectively utilise this trait.

Executive summary

Background

Saleable meat yield is a key economic driver of the beef industry, improvement of which is underpinned by the retail beef yield (RBY) estimated breeding value (EBV) in BREEDPLAN. This EBV is estimated almost exclusively from correlations with animal liveweight and ultrasound scan data due to the small number of carcase, and in particular, RBY phenotypes being collected. A small number of RBY records collected mostly between 1994 and 1997 drive the correlations currently. Since this data was collected, selection has led to large genetic increases in liveweight and eye muscle area (EMA), and smaller changes in fat traits, while RBY has remained relatively unchanged. This project was conducted to determine whether these genetic changes have impacted the correlations between these traits, and to provide phenotypes to update the correlations used in BREEDPLAN if necessary. The data will be used to re-estimate BREEDPLAN RBY parameters that will provide more accurate carcase RBY EBVs aligned to the modern beef cattle population.

Objectives

The aim of this project was to generate retail beef yield (RBY) phenotypes on at least 1000 fully pedigreed and genetically described Angus cattle suitable for use in re-estimating BREEDPLAN RBY parameters to provide more accurate carcase RBY EBVs align with the modern beef cattle population. Phenotypes for RBY and various production and carcase traits were collected on 1036 cattle, and have been submitted to BREEDPLAN to allow re-estimation of these parameters.

A further aim was to assess the role visual muscle score (MS) has in the prediction of RBY, and to examine the effects of the 821del11 myostatin mutation in cattle with a broader genetic base than the NSW Department of Primary Industries (DPI) muscling selection line herd.

Methodology

Data was collected on pedigreed and performance recorded cattle bred from NSW DPI Angus research cow herds. These herds were involved in the Angus Sire Benchmarking Program, resulting in strong genetic links to the modern Angus cattle population. A comprehensive suite of BREEDPLAN and additional traits were measured on the cattle from birth. This included liveweights from birth through to the end of feedlot finishing; low density genotyping; individual feed intake; ultrasound scanning for rib and rump fat, EMA and intramuscular fat percentage at feedlot entry and after 100d on feed; visual MS assessment at feedlot entry and after 100d on feed; AUS-MEAT and MSA carcase data; and a full side boneout to measure retail beef yield on each carcase. Raw data was analysed to examine the relationships between the measured traits and RBY, and BREEDPLAN adjusted data was used for the genetic analyses of all traits.

Results/key findings

- EMA and MS provide important information for predicting RBY but they provide different information to assist that prediction.
- The value of using fat measurements for predicting RBY varies with time from slaughter with the most useful being provided by carcass fat traits, and little value provided by fat traits measured at feedlot entry.
- Little relationship was observed between RBY and other carcase and productions traits, indicating that selection for improved RBY can be undertaken with little impact on other traits influencing profitability.

- Weak relationships between RBY and IMF, marble scores and MSA Index suggest that increases in RBY can be achieved while also improving meat quality.
- This research has been conducted outside the NSW DPI muscling herd using industry relevant animals and the findings suggest that previous findings from the muscling herd appear to be transferable to the commercial industry.

Benefits to industry

- Data will be available to re-estimate genetic parameters for RBY in the Angus BREEDPLAN genetic evaluation.
- Once this data has been analysed for BREEDPLAN parameter estimation, RBY EBV accuracy and associated selection index accuracy for the ASBP sires and related animals is expected to increase resulting in opportunities for increased rates of genetic gain for commercially relevant traits.
- As the progeny and sires have genomic profiles and phenotypes available, this will seed BREEDPLANs genetic evaluation with quality RBY phenotypes collected on animals which are well linked to the current Angus population.

Future research and recommendations

The findings from this research support the need to collect high quality RBY phenotypes into the future including the development of technologies to reduce the cost and increase the efficiency of collecting such data in the abattoir. The findings from this research also support the need to further develop, and integrate into the beef industry, objective live animal assessment tools for recording both EMA (developments in ultrasound scanning) and MS (development of 3D camera technology) to aid both genetic evaluation and on-farm management decisions to produce future improvements in carcass yield in association with meat quality and other on-farm profit drivers (calving ease, growth, fertility, temperament, etc).

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1. Background and purpose of research

Dressing percentage and saleable meat yield are key economic drivers for the Australian beef industry. Consequently, these traits are consistently given high weightings by the BreedObject selection indexes for all breeds. For example, the current Angus Breeding selection indexes place 22% emphasis on these two traits combined compared to the 15% emphasis that is placed on sale weight. The EBV for retail beef yield (RBY) is the selection criteria that underpins these profit drivers. The RBY EBV is estimated almost exclusively from correlations with liveweight and live animal scanned eye muscle area and fat depths due to limited recording of abattoir carcase data and actual RBY phenotypes (there were 1,414 RBY phenotypes vs 501,252 600-day weight phenotypes analysed in the mid-July 2017 Angus BREEDPLAN analysis). The data that underpin the current Angus BREEDPLAN RBY genetic parameters were collected by the Beef Quality CRC between 1994 and 1997. When reporting genetic parameters estimated from this data, Reverter *et al*. (2000) noted that the dataset was small (for RBY 1043 Angus and 386 Hereford) to generate reliable heritabilities and genetic correlations, and that more data was needed before confidence could be placed in these parameters. The genetic correlations between RBY and other traits that form the basis for the parameters currently used in Angus BREEDPLAN are re-estimated periodically but only using the RBY data described in Reverter *et al.* (2000). Since 1997, no RBY data has been entered into Angus BREEDPLAN by industry or research sources, other than approximately 470 records from the NSW DPI Angus muscling herd.

The genetic parameters published on the Angus Australia website for RBY (heritability of 0.6, genetic correlations with EMA (+0.55), P8 (-0.50), Rib fat (-0.50) and IMF% (-0.40)), and used in the Angus BREEDPLAN analysis, drive the selection of cattle towards lower fatness and higher EMA when selecting for increased RBY. This is based on an understanding that improvement in retail beef yield can be achieved by decreasing fatness and/or increasing muscling. However, the negative correlated response in fatness associated with selection to improve RBY is increasingly being perceived negatively by breeders and is not considered sustainable.

Additionally, there is a trend for ultrasound measurements submitted to BREEDPLAN to be collected at younger ages, to ensure EBVs for carcass traits are available on yearling bulls for early selection and publication at annual sales. This has seen a decrease in the level of variation in scanned fat traits, which impacts the RBY EBVs estimated via the correlations with these traits. Apart from the need to increase the number and quality of phenotypes for RBY in the analysis, the change in animals evaluated for the correlated traits which form the basis of the RBY EBV provide additional motivation to test and re-estimate the genetic correlations which underpin the RBY EBV and its accuracy. Since these correlations were calculated, selection has led to large genetic increases in liveweight and EMA, and smaller changes in fat traits, while RBY has remained relatively stagnant. It is possible that these genetic changes have impacted the correlations between these traits.

Retail beef yield phenotypes are not collected routinely because accurate data is time-consuming and expensive to collect. It requires a team with expertise to measure it, and a strong relationship with a commercial abattoir to allow effective data collection, within the constraints of commercial processing.

The Angus Australia and MLA co-funded Angus Sire Benchmarking Project (ASBP, Angus Australia Progeny Test and Information Nucleus - PSH.0528), provides a unique opportunity to collect quality RBY data. The animals in this project, by design, have Angus Australia registered sires with close genetic links to current industry populations, and are genotyped as part of that project. Extensive phenotypic records are being collected from birth to slaughter on these animals, including growth, ultrasound scanning (400d and 600d), fertility, feed efficiency and abattoir carcase traits. These animals will also have half-sib bulls and heifers that will have liveweights and ultrasound scan records recorded in seedstock herds. The NSW DPI Glen Innes (Muscling) and Trangie herds are the only herds contained in the ASBP for which the cows are Angus Australia registered with full pedigree and performance history recorded, meaning that their progeny have known information on both the paternal and maternal sides of the pedigree. RBY is not recorded as part of the ASBP. Collecting RBY on these animals will provide the following benefits:

1. Data will be available to re-estimate the genetic parameters for RBY in the Angus BREEDPLAN evaluation.
2. Once BREEDPLAN analysed, RBY EBV accuracy and associated selection index accuracy for the ASBP sires and related animals will significantly increase resulting in opportunities for high rates of genetic gain for commercially relevant traits.
3. As the progeny and sires will have genomic profiles and phenotypes available, this will seed BREEDPLANs genetic evaluation with quality RBY phenotypes collected on animals which are well linked to the current population.

The aim to collect 1000 new RBY phenotypes in Angus cattle would significantly increase the number of records available to the Angus BREEDPLAN analysis for this trait (currently 1,414). These cattle would also provide a useful opportunity to validate other RBY predictive technologies that become available during the life of the project (eg DEXA/MEXA, RGBD cameras) in collaboration with other research projects. This dataset could be exploited to provide information on the genetic correlations of lean and fat yield estimated by these methods, with current BREEDPLAN traits, and could be the first opportunity to assess how the RBY EBV might incorporate these new measurements. The possibility exists to further value-add to this project by incorporating validation of other live measurements, such as the RGBD camera objective muscle score, hip height and rump fat (McPhee *et al.* 2017).

Analysis of data from the NSW DPI Glen Innes Angus muscling herd, selected for divergent visual muscle score over 24 years, has demonstrated that including a phenotypic measure of muscling (muscle score) in the phenotypic prediction of RBY improves the accuracy of the estimation by up to 50%. The inclusion of the NSW DPI muscling herd in the ASBP, and the collection of muscle scores on all ASBP progeny, also allows the relationships between muscle score, EMA, P8 and Rib fat, as well as RBY, to be validated outside the muscling herd. If the trait can be confirmed to have significant genetic relationships with RBY in contemporary industry animals and is heritable under industry recording of young seedstock bulls and heifers, it represents a relatively simple and economical opportunity to add information about carcass yield to the genetic evaluation.

2. Objectives

The purpose of this project is to generate retail beef yield (RBY) phenotypes on 1000 fully pedigreed and genetically described steers. These will be used to re-estimate BREEDPLAN RBY parameters and to provide more accurate carcase RBY EBVs to suit the modern beef cattle population. RBY

phenotypes are not generated routinely because accurate data is time-consuming and expensive to collect. The RBY EBV is the selection criteria that underpins the BreedObject selection index profit drivers, but is estimated almost exclusively from correlations with liveweight, live animal scanned eye muscle area and fat depths. This is due to very limited recording of abattoir carcase data and actual RBY phenotypes.

This project will lead to higher accuracy RBY EBVs being calculated for Angus cattle and will value-add to industry Beef Information Nucleus (BIN) projects by collecting RBY phenotypes. Each commercially prepared carcase will have a full boneout of one side, resulting in 100% recovery of the cold side weight. All primals trimmed to market specifications, bones, trim and fat waste must be weighed. The core animals will be those produced from NSW DPI research herds as part of the Angus Sire Benchmarking Project (ASBP). The ASBP progeny will have detailed phenotypic records collected for growth, ultrasound scans, fertility, feed efficiency, abattoir carcase traits and genetic information (pedigree and genomic) which presents a unique opportunity to evaluate and leverage the phenotypic and genetic relationships of RBY with other live and carcase parameters in the current population.

Key objectives of the NLGC which this project addresses include:

- Maximising the effectiveness and value of genetic improvement tools;
- Stimulating demand for genetic improvement across the value chain;
- Developing world leading genetic improvement technologies and resources;
- Fast tracking genetic gain.

Project outputs and their achievement:

1. The RBY parameters in BREEDPLAN will be re-estimated using measurements from beef cattle in the current populations to provide more accurate parameter estimates, which will improve confidence in and uptake of EBVs;

Met successfully: Data included in the current re-parameterisation exercise for Angus cattle by Animal Genetics and Breeding Unit (AGBU). Discussed in Section 4.3

2. The $Indices, which allow selection for profitability in the major breeds in Australia will be underpinned by more accurate assessment of carcase yield which is a key driver of profitability in the Australian beef industry;

Met successfully: This outcome will flow from the successful delivery of Outcome 1.

3. Once RBY has been measured, the value of using an assessment of whole body muscling (muscle score by competent assessor or RGBD cameras) as a RBY predictor will be validated outside the NSW DPI muscling herd;

Met successfully. Results discussed in Section 4.2

4. Provide data to validate the predictive capacity of any future novel RBY technologies and estimate their relationships with BREEDPLAN traits at the genetic level;

No novel RBY technologies were sufficiently developed to allow validation on the cattle in this project at the time of slaughter. Collaboration with project teams developing various live and carcase assessment technologies occurred where possible.

5. The liveweight and scan data taken from weaning until feedlot exit will be assessed for their relationships 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;

Met successfully. Results discussed in Sections 4.2 and 4.3

6. The collection of RBY data will provide a larger and more contemporary reference population on which genomic information can be applied to provide RBY EBVs.

Met successfully. Genomics were conducted and DNA samples stored for all animals in this project.

3. Methodology

3.1 Animals and their management

The use of animals and the procedures performed in this study were approved by NSW DPI Orange Animal Ethics Committee, under animal research authority numbers ORA14/17/010, ORA14/17/011, ORA17/20/010 and ORA18/21/013. In addition, the use and procedures performed during feed intake testing at UNE's Tullimba feedlot were approved by the UNE Animal Ethics Committee, under animal research authority number AEC 18-091.

Data was collected on pedigreed and performance recorded cattle bred from NSW DPI Angus research cow herds at Glen Innes Agricultural Research and Advisory Station, Glen Innes; Trangie Agricultural Research Centre, Trangie; and Elizabeth Macarthur Agricultural Institute (EMAI), Menangle. It was collected across four cohorts of cattle from four consecutive birth years of 2015 to 2018, with resulting slaughters conducted from 2017 to 2020. The Glen Innes and Trangie herds were enrolled as co-operator herds in the ASBP for joining from 2014 to 2017. The EMAI cow herd was comprised of the heifer progeny born in 2015 through this program from both the Glen Innes and Trangie herds. Cohorts 1 to 3 of this project were comprised of the steer progeny from the Glen Innes and Trangie ASBP programs born in 2015, 2016 and 2017. Cohort 4 was comprised of steer and heifer progeny born in 2018 from the Glen Innes ASBP program, steer and heifer progeny from the EMAI herd, and a small group of 2017-born heifers from the Trangie ASBP program which were not suitable for joining.

Historically, the Glen Innes herd was developed to study the effects of selection for divergent muscling on carcase and maternal productivity traits. Part of this research included a line of highly muscled cows carrying one copy of the 821del11 myostatin mutation (Grobet *et al.* 1997). The herd remained comprised of the divergent muscling lines when the progeny in this project were bred. Care was taken at AI to join each sire to a mix of carrier and normal cows, and the genotype of all progeny from carrier cows was assessed in addition to standard genomic testing. The number of animals with data included in the dataset is presented in Table 1, including the number of animals which were 821del11 carriers.

Similarly, the Trangie herd has a long selection history for several traits, including selection for divergent growth (1974-1992), divergent residual feed intake (1993-2008) and divergent methane yield (2009-2014). Upon joining the ASBP in 2015, the Trangie herd was comprised of females from the divergent methane yield lines.

Calves were raised on their dams at pasture until weaning at approximately 8 months of age. The exception to this was the Glen Innes Cohort 4 calves, as severe drought conditions led to hand feeding a complete ration to the cow herd throughout lactation, and the calves were weaned two months earlier than usual. Soon after weaning all were transported for backgrounding on pasture until target feedlot weights were attained. Cohort 1 steers were backgrounded at Bundarra and at UNE's Tullimba property. Cohorts 2 and 3 steers were backgrounded at Grafton Primary Industries Institute, Grafton. Cohort 4 cattle from the Glen Innes herd were backgrounded on the DPI North Coast properties of Wollongbar Primary Industries Institute and Duck Creek Field Station. Cohort 4 cattle from the EMAI herd were backgrounded on site at EMAI. NSW was under varying levels of drought conditions for most of the project, particularly 2018 and 2019, and supplementation was used to maintain a reasonable growth rate in the cattle during backgrounding as required. Management was conducted with consideration of the contemporary groupings within each cohort throughout backgrounding.

Table 1. Number of data points through feedlot finishing to slaughter by cohort, sex and genotype for the 821del11 myostatin mutation in the complete data set.

		Feedlot entry scan	100 d scan	Feedlot exit weight	Carcase data	RBY data
Cohort 1 Steers	Total	154	154	154	154	154
	821del11 normal	147	147	147	147	147
	821del11 carrier	7	7	7	7	7
Cohort 2 Steers	Total	236	236	236	236	236
	821del11 normal	214	214	214	214	214
	821del11 carrier	22	22	22	22	22
Cohort 3 Steers	Total	340	340	340	340	340
	821del11 normal	314	314	314	314	314
	821del11 carrier	26	26	26	26	26
Cohort 4 Steers	Total	187	181	178	177	163
	821del11 normal	170	164	161	160	146
	821del11 carrier	17	17	17	17	17
Cohort 4 Heifers	Total	147	144	144	143	143
	821del11 normal	125	122	122	121	121
	821del11 carrier	22	22	22	22	22
Total Steers		917	911	908	907	893
Total Heifers		147	144	144	143	143
Grand total		1064	1055	1052	1050	1036

Following backgrounding, all cattle were transported to UNE's Tullimba Research Feedlot for feed intake testing and grain finishing. Cohorts 1 and 2 were grain fed for just over 150 days, and Cohorts 3 and 4 for just over 100 days. The cattle were allocated to feed pens at Tullimba and slaughter groups concurrently to take account of both pen size limits at Tullimba (maximum of 40 or 80) and maximum boneout limits of 50 animals per day at the abattoir. The allocations were based on maintaining effective BREEDPLAN contemporary groups at slaughter while sires and age at slaughter were balanced when yearling contemporary groups needed to be split. Average weight at feedlot entry and feedlot exit (for kill group) was also considered where possible during allocations after sire

and age were balanced. Groups were fed in pens of up to 40 or 80 individuals to suit pen size and availability as well as Growsafe feeder capacity. At the completion of grain finishing the cattle were transported to John Dee Warwick abattoir in Warwick, Qld for slaughter.

3.2 Live data collection

A comprehensive suite of BREEDPLAN and additional traits were measured on the cattle from birth in collaboration with the ASBP. This included liveweight at birth, weaning and yearling ages, and throughout backgrounding and feedlot finishing. Low density genotyping was conducted on all animals and DNA stored. Individual feed intake was measured during grain finishing using the GrowSafe intake system (GrowSafe System Ltd., Airdrie, AB, Canada) at Tullimba. Ultrasound scanning for rib and rump fat, eye muscle area and intramuscular fat percentage was conducted by a BREEDPLAN accredited assessor at feedlot entry and after 100d on feed. Muscle score was assessed by trained assessors at feedlot entry and after 100d on feed. Muscle score (MS) is a visual assessment of the thickness and convexity of the live animal, relative to skeletal size and adjusted for fatness (McKiernan 2007). For research purposes the 5-point MS scale can be expanded to 15 points by adding + and – to each category, so that E–, or 1, is the least muscled and A+, or 15, is the heaviest muscled.

Collaborative efforts with other research projects resulted in additional data collection on the live cattle where appropriate through the project. The team from the objective real-time assessment of *Bos taurus* cattle to improve profitability and productivity of the beef value chain (MLA project B.GBP.0051) assessed over 300 cattle with 3D camera technology. In addition, Murdoch University/ALMTech researchers tested a portable microwave system for use in assessing live rib and rump fat depths on 150 steers at Tullimba in 2019

3.3 Carcase data collection

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) collected by registered MSA graders on the right hand sides the following morning prior to boneout.

A standard set of AUS-MEAT boneless primals with standard trim of 10mm fat were applied at boneout. The aim was to select a set of primals which:

1. Represented realistic commercial product
2. Was standard enough that it could be repeated on 1000 sides over several years, even if different plants became involved.

The primals (plus Ham number) collected were:

HINDQUARTER: Topside/inside (2000), silverside (2020), thick flank (2060), striploin (2140), tenderloin (2160), rump (2090), thin flank (2200), HQ shin/shank (2360), HQ trim (65% chemical lean), HQ fat trim, HQ bone

FOREQUARTER: Cube roll (2240), rib end meat, brisket (2320), chuck (2260), blade (2300), chuck tender (2310), intercostals (2430), FQ shin/shank (2360), inside skirt (2205), FQ trim (65% chemical lean), FQ fat trim, FQ bone

Boning room hygiene pre-trim was weighed for completeness and included in the weight of trim for each side. The amount of pre-trim was minor, averaging around 100g of fat per side.

The cold weight of the sides was measured prior to quartering and entry to the boning room. This cold weight was used as a measure of reliability of the RBY data, as the recovery should be close to 100% and should be consistent across sides. All primals plus the FQ and HQ trim were included in the calculation of the weight of retail beef product in each side. The RBY was calculated as the weight of retail beef product/total recovered side weight.

A sample of the M. *longissimus lumborum* (LLM) was collected for later laboratory analysis to determine the percentage of intramuscular fat (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). A steak was sliced from the anterior end of each cube roll to coincide with the MSA grading site. The muscle was cut into cubes and sampled avoiding any subcutaneous or intramuscular fat seams. Approximately 50g samples were placed in centrifuge tubes and refrigerated.

A number of carcase assessment technologies under development were conducted on the carcases throughout the project in collaboration with Murdoch University/ALMTech researchers. These included hyperspectral and MIJ cameras on the cold carcases, and a portable microwave system on hot and cold carcases.

3.4 Statistical methods

The formation of contemporary groups for analysis was conducted following standard BREEDPLAN processes (Graser *et al.* 2005). Briefly, this included using BREEDPLAN contemporary groups for 400-day weight as the basis of allocating animals to feedlot pens and kill groups (described in Section 3.1 above). The BREEDPLAN contemporary groups included on-farm assigned management groups, twin status and age-sliced groups. Contemporary groups for feedlot exit, abattoir and bone-out traits were formed from the 400-day contemporary group along with pen, kill and boneout dates.

Regression analyses. The regression analyses were conducted using the lm function in the R statistical package (R Core Team 2020). Analysis of RBY included 821del11 myostatin genotype, boneout contemporary group and sire as fixed effects with live animal traits recorded at feedlot entry or after 100 days in Tullimba, or carcass traits fitted as covariates. All non-significant terms were removed from the models. In all analyses sire and contemporary group were significant. Least-squares means using the emmeans package in R was used to provide the trait means for myostatin genotype. Pairwise comparisons are reported using the Tukey statistical test. Tests at $P < 0.05$ were adopted as the critical level of probability for a type-I error. Pairwise comparisons presented were averaged across sires and contemporary groups.

Genetic analyses. Adjusted carcase trait records were obtained from Angus Australia for analyses, with traits adjusted as per standard BREEDPLAN (CWT adjusted to 750 days and all other traits adjusted to 400 kg carcase weight). Carcase traits analysed 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/13th rib site (CRIB). In addition to the carcase traits, the full set of adjusted BREEDPLAN records were obtained for all animals, including growth (birth, 200-day, 400-day and 600-day weights) and body composition (ultrasound scan rib and rump fat, intramuscular fat % and eye muscle area) traits, as well as gestation length. These traits were adjusted using the standard BREEDPLAN adjustments, as described by Graser *et al.* (2005). Contemporary groups for these traits were the BREEDPLAN contemporary groups obtained from the file provided by Angus Australia. Variance and covariance components were estimated with a sire model using ASReml (Gilmour *et al*. 2015). The fixed effect of contemporary group was included in the model for all traits, along with random direct genetic and residual effects. The fixed effects of mating type (AI or back-up) and myostatin genotype (carrier or normal) were included in the model when significant. Maternal and maternal permanent environment effects were included in the model for analyses of gestation length and birth, weaning and yearling weight. Univariate analyses were undertaken to obtain phenotypic and genetic variances for each trait, while pairwise bivariate analyses were undertaken to obtain phenotypic and genetic correlations. Pedigree depth of 10 generations was used for all genetic analyses.

4. Results and Discussion

4.1 Description of the data set

A total of 1064 cattle reached feedlot entry across the four cohorts. Small losses of animals for various reasons led to 1054 cattle remaining on grain for 100d, and 1050 animals being slaughtered at John Dee for carcase data collection. Of the 1050, RBY was collected successfully on 1036 carcases. Descriptive statistics for the live traits collected at feedlot entry and after 100d on grain are presented in Table 2, and for the carcase traits in Table 3.

Table 2. Descriptive statistics for raw liveweight, ultrasound scan measurements and visual muscle score assessment at feedlot entry and after approximately 100 d on feed for complete data set (EMA, eye muscle area; IMF, intramuscular fat).

	Number	Mean	SD	Min	Max
		Feedlot entry			
Liveweight (kg)	1064	404	40.9	260	538
P8 fat (mm)	1064	6.1	2.60	1	18
Rib fat (mm)	1064	4.4	1.80	1	13
EMA (cm^2)	1063	57.5	6.45	34	82
IMF (%)	1064	5.0	1.14	1.7	7.8
Hip height (cm)	674	125	4.60	111.5	141
Muscle score (1-15)	1064	7.5	1.54	1	13
		100 d on feed			
Liveweight (kg)	1055	565	51.1	396	732
P8 fat (mm)	1055	14.8	3.34	3	31
Rib fat (mm)	1055	10.0	1.85	3	17
EMA (cm^2)	1055	75.1	6.33	50	100
IMF (%)	1055	7.5	0.57	4.4	8.3
Hip height (cm)	565	128	5.3	110	143
Muscle score (1-15)	1054	7.5	1.52	3	13

Table 3. Descriptive statistics for raw carcase traits for complete data set (HSCW, hot standard carcase weight; MSA, Meat Standards Australia; AUS, AUS-MEAT; EMA, eye muscle area; MB, marbling; LD*, longissimus dorsi;* IMF, intramuscular fat; RBY, retail beef yield).

	Number	Mean	SD	Min	Max
Final Liveweight (kg)	1052	600	56.7	410	770
Slaughter age (d)	1050	602	68.2	504	1037
HSCW (kg)	1050	323	33.7	211.3	428.5
Ossification (100-590)	1050	135	20.6	100	230
Hot P8 fat (mm)	1050	15.2	4.28	5	33
MSA Rib fat (mm)	1050	10.5	3.83	3	28
MSA MB (110-1190)	1050	380	70.1	200	790
AUS MB (0-9)	1050	1.4	0.72	0	5
MSA EMA (cm^2)	1050	80.6	8.82	53	112
MSA Index (30-80)	1037	62.6	2.02	55.6	68.7
LLM chemical IMF (%)	1049	5.8	1.95	1.96	17.29
RBY (%)	1036	74.2	1.74	68.7	79.0

4.2 Assessing predictors of RBY

A number of traits and factors were assessed for their effectiveness in predicting RBY through regression analyses. There is value in assessing the ability of traits measured earlier in life to predict RBY to provide support to industry in animal management and targeting specific markets. Models using live data collected at feedlot entry (Table 4), after 100d on grain (Table 5) and using carcase data (Table 6) are presented below.

Table 4. Regression model to predict carcase RBY using live traits measured at feedlot entry. Full model included liveweight; ultrasound scan rib and rump fat, eye muscle area (EMA) and intramuscular fat; muscle score, contemporary group as pertaining to bone-out date and sire. Non-significant terms were removed from the model. Myostatin genotype, carcase contemporary group and sire were significant but regression coefficients for these effects are not presented.

r^2		0.64	
se		1.02	
Trait	**Coefficient**	**se**	**p-value**
Intercept	72.2	0.77	<0.001
Liveweight	-0.006	0.002	<0.001
EMA	0.067	0.011	<0.001
Muscle Score	0.154	0.032	<0.001

Fatness at feedlot entry was not significant, while there was a small negative effect of liveweight. Both scan EMA and muscle score were highly significant and both had positive regression coefficients with RBY.

Table 5. Regression models to predict carcase RBY using live traits measured after 100 d on grain; and muscle score assessed at either feedlot entry (FE) or after 100 d on grain. Full model included liveweight; ultrasound scan rib and rump fat, eye muscle area and intramuscular fat; muscle score, contemporary group as pertaining to bone-out date and sire. Non-significant terms were removed from the model. Myostatin genotype, carcase contemporary group and sire were significant but regression coefficients for these effects are not presented.

	FE muscle score			100 d muscle score		
r^2	0.65			0.65		
se	1.01			1.01		
Trait	**Coefficient**	**se**	**p-value**	**Coefficient**	**se**	**p-value**
Intercept	71.9	0.95	<0.001	71.65	0.97	<0.001
P8 fat (mm)	-0.044	0.014	0.002	-0.032	0.015	0.027
EMA (cm^2)	0.055	0.008	<0.001	0.054	0.008	<0.001
IMF (%)	-0.215	0.078	<0.001	-0.184	0.078	0.019
Muscle Score (1-15)	0.184	0.031	<0.001	0.168	0.032	<0.001

After 100d on grain, ultrasound scan rib fat and IMF% were negatively related to RBY, while scan EMA and muscle score were strongly positively related to RBY. Muscle score assessed at feedlot entry or after 100d on grain had similar regression coefficients with RBY. A similar result was found for EMA recorded at feedlot entry or 100d on grain.

Table 6. Regression models to predict carcase RBY using carcase traits; and muscle score assessed at either feedlot entry (FE) or after 100 d on grain. Full model included hot standard carcase weight, hot P8 fat, MSA cold rib fat, MSA eye muscle area and AUS marble score; live muscle score contemporary group as pertaining to bone-out date and sire. Non-significant terms were removed from the model. Myostatin genotype, carcase contemporary group and sire were significant but regression coefficients for these effects are not presented. The model was also run using MSA Mb or Lab IMF% as the marbling descriptor, but neither were significant.

	FE muscle score			100 d muscle score		
r^2	0.66			0.66		
se	0.99			0.99		
Trait	**Coefficient**	**se**	**p-value**	**Coefficient**	**se**	**p-value**
Intercept	70.83	0.69	<0.001	70.58	0.67	<0.001
P8 fat (mm)	-0.02	0.01	0.043	-	-	-
MSA EMA (cm^2)	0.046	0.006	<0.001	0.045	0.006	<0.001
AUS Marble (0-9)	-0.194	0.061	0.002	-0.191	0.061	0.001
Muscle Score (1-15)	0.158	0.031	<0.001	0.157	0.031	<0.001

The regression analyses of RBY with carcase traits were similar to those conducted using the 100d live data, with P8 fat, EMA, AUS marbling and muscle score having significant regression coefficients. Using muscle score assessed at feedlot entry or after 100d on grain again resulted in similar

regression coefficients, indicating that muscle score was a repeatable live animal measure that is related to RBY of the carcase.

Muscle score and EMA showed highly significant regression coefficients regardless of time from slaughter. This suggests that both traits provide information that explains realised RBY but it may not be the same information. This is shown below in Table 7 containing the r^2 for different effects and combinations of effects as the final model is built for the feedlot entry muscle score and other live animal traits from Table 4 above. When feedlot entry muscle score or EMA are added to a model containing myostatin genotype, contemporary group and sire the r^2 increases by differing amounts. When EMA or muscle score are added to models containing feedlot entry liveweight the r^2 are lower than the model that contains both muscle score and EMA but not liveweight at feedlot entry. The Pearsons correlations between feedlot entry muscle score and feedlot entry EMA, 100 day fed EMA and carcass EMA were 0.25, 0.169 and 0.266 suggesting that although related these are not the same trait, which supports the conclusion that muscle score and EMA contribute different information to predicting RBY.

Table 7. Variation in RBY explained (r^2) as different effects are added to build the final regression model using live traits (LW, liveweight; EMA, ultrasound scan eye muscle area; MS, muscle score) measured at feedlot entry (FE), cold carcass weight contemporary group (CCWCG), myostatin genotype (MYO) and sire.

Model	r^2
CCWCG	0.456
Sire	0.418
CCWCG + Sire	0.526
MYO + CCWCG + Sire	0.606
MYO + FEMS + CCWCG + Sire	0.624
MYO + FEEMA + CCWCG + Sire	0.622
MYO + FEWT + CCWCG + Sire	0.605
MYO + FEEMA + FEMS + CCWCG + Sire	0.634
MYO + FEWT + FEEMA + CCWCG + Sire	0.630
MYO + FEWT + FEMS + CCWCG + Sire	0.624
MYO + FEWT + FEEMA + FEMS + CCWCG + Sire	0.640

As the interval between trait recording and slaughter reduced (feedlot entry vs 100 days on grain) the relationships subcutaneous (P8) and intramuscular (IMF or marble score) had with RBY became significant. This result supports that of previous research in that carcase fat traits have significant relationships with RBY but their utility decreases with increasing time between measurement and slaughter (Wolcott 2001). This is in contrast to both muscle score and EMA which always had significant and consistent relationships with RBY regardless of the time interval between measurement and slaughter. This is consistent with findings published from the NSW DPI muscling selection herd research, which indicated that increased muscle score led to increased RBY (Cafe *et al.* 2014), and that weaning and yearling muscle scores where strongly genetically correlated (Robinson *et al.* 2014).

The effect of 821del11 myostatin genotype on RBY was found to be significant in all models presented above in Tables 4, 5 and 6, reflecting the change in r^2 value in Table 7 when myostatin

genotype is included in the model. For the model in Table 7, the least-square means estimates of RBY for myostatin carrier and normal animals were 75.03% and 73.95%, respectively. The 1.08% difference between carriers and non-carriers was significant (P < 0.001) when averaged across sires and contemporary groups and liveweight, entry EMA and entry muscle score were the same. These results support the impacts myostatin genotpye has on traits found in the genetic analysis presented below. In lieu of presenting further myostatin results here please refer to the findings from the genetic analysis in Table 10.

4.3 Genetic relationships

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. Genetic improvement in carcase traits in the 20 years since the last RBY records were collected has led to significant improvements in carcase traits in modern animals. Summary statistics for adjusted carcase, growth and body composition traits recorded in this project are presented in Table 9, and a key to the trait abbreviations used throughout this section is presented in Table 8. Carcase trait averages for animals used in the previous estimation of RBY parameters were markedly lower than those presented in Table 9 here (From Reverter *et al.*, 2003: Carcase WT= 269 kg; Carcase P8=10.2 mm; Carcase RIB=8.2 mm; Carcase EMA=81.6 cm^2; Carcase IMF=4.6%; RBY=67.03%). The differences in summary statistics evident between historic and contemporary carcase trait records highlights 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. The majority of animals were slaughtered at approximately 600 days of age, however a small number (n=19) of Trangie heifers in Cohort 4 were slaughtered at approximately 1,030 days of age. Genetic analyses were undertaken with and without these animals included, with negligible impact on the resulting genetic parameters. Therefore, these animals were retained in the dataset for all genetic analyses.

Table 8. BREEDPLAN adjusted trait abbreviations used in genetic analyses, and the associated raw measures described and used in the remainder of the report.

BREEDPLAN Trait Name	Abbreviation	Unit	Raw data equivalent
Carcase weight	CWT	kg	HSCW (kg)
Carcase eye muscle area	CEMA	cm^2	MSA EMA (cm^2)
Carcase rib fat	CRIB	mm	MSA Rib fat (mm)
Carcase P8 fat	CP8	mm	Hot P8 fat (mm)
Carcase IMF	CIMF	%	LD chemical IMF (%)
Retail Beef Yield	RBY	%	RBY (%)
Birth weight	BWT	kg	
Gestation length	GL	days	
200-day weight	WWT	kg	
400-day weight	YWT	kg	
600-day weight	FWT	kg	
Scan rib fat thickness	SRIB	mm	Rib fat (mm)
Scan P8 rump fat thickness	SP8	mm	P8 fat (mm)
Scan eye muscle area	SEMA	cm^2	EMA (cm^2)
Scan intramuscular fat	SIMF	%	IMF (%)

Table 9. Descriptive statistics for adjusted carcase, growth and body composition traits

Trait[a]	No. records	Average (SD)	Minimum	Maximum
Slaughter age (d)	1,050	602 (68)	504	1,037
CWT (kg)	1,050	359.3 (38.5)	224.1	473.4
CEMA (cm^2)	1,050	88.2 (8.6)	63.1	123.9
CRIB (mm)	1,050	12.5 (4.3)	3.4	35.5
CP8 (mm)	1,049	18.1 (5.0)	7.1	42.9
CIMF (%)	1,049	6.2 (2.1)	2.2	19.3
RBY (%)	1,032	73.0 (1.8)	67.8	78.8
BWT (kg)	1,044	38.9 (5.0)	19.7	57.6
GL (days)	541	278.8 (4.3)	266.1	294.9
WWT (kg)	1,050	244.2 (31.6)	135.8	341.7
YWT (kg)	987	376.1 (54.4)	183.6	532.4
FWT (kg)	1,034	571.5 (104.9)	246.8	784.4
SRIB (mm)	1,042	5.5 (3.0)	-2.5	16.2
SP8 (mm)	1,039	7.4 (4.3)	-4.7	23.5
SEMA (cm^2)	1,046	61.1 (9.9)	21.9	91.3
SIMF (%)	1,050	5.6 (1.6)	-1.2	8.8
FEMS (score)	1,050	7.5 (1.5)	1.0	13.0
100day MS	1,049	7.5 (1.5)	3.0	13.0

[a] Refer to Table 8 for full trait description

Least-square means were estimated using the PROC MIXED procedure in SAS for the 821del11 myostatin mutation in order to determine whether the difference between myostatin mutation carrier (821del11) and non-carrier animals was statistically significant (Table 10).

Table 10. Least-square means for adjusted carcase traits for myostatin genotype (n=1,050)

Trait[a]	normal (n=956)	carrier (n=94)	Significance[b]
CWT	353.3	354.1	*ns*
CP8	18.8	16.8	**
CRIB	12.3	10.1	**
CEMA	87.6	99.6	**
CIMF	6.3	5.0	**
RBY	72.8	74.8	**
MS	7.3 (C-)	9.1 (C+)	**
BWT	37.1	37.4	*ns*
GL	285.5	285.5	*ns*
WWT	235.5	228.8	*ns*
YWT	366.2	357.8	*ns*
FWT	552.3	540.0	*ns*
SP8	6.8	5.7	**
SRIB	5.1	4.2	**
SEMA	58.0	62.6	**
SIMF	5.4	4.8	**

[a] Refer to Table 8 for full trait description

[b] ** Significance at P≤0.0001; *ns* non-significance at P>0.05

On average, animals with the 821del11 myostatin mutation had significantly higher muscle score, carcase EMA and RBY than normal animals. Animals with the 821del11 myostatin mutation also had on average, significantly lower fat (P8, RIB and IMF), but there was no statistical difference between the average carcase WT in the two groups. Least-square means for scan body composition traits

followed the same pattern as the corresponding carcase traits, and there was no statistical difference between average growth traits for 821del11 myostatin mutation carrier and non-carrier animals. Thus, myostatin genotype was included as a fixed effect in further analyses of carcase traits where statistically significant.

Genetic parameters for the carcase traits are presented in Table 11, including direct (σ^2_d), maternal (σ^2_m), maternal permanent environment (σ^2_c) and phenotypic (σ^2_p) variances; direct (h^2_d) and maternal (h^2_m) heritabilities and maternal permanent environmental variance as a proportion of phenotypic variance (c^2). Heritabilities of carcase traits in this data set were moderate to high (0.19 for CRIB to 0.89 for CIMF). Heritabilities for CRIB, CP8 and RBY were within the range of published estimates for Australian Angus (Reverter *et al.*, 2003; Borner *et al.*, 2013; Jeyaruban *et al.*, 2017). Heritabilities for the remaining carcase traits, however, were higher than previous published estimates for this breed; CWT h^2_d=0.76 vs 0.39-0.66 in literature (Reverter *et al.*, 2003; Borner *et al.*, 2013; Jeyaruban *et al.*, 2017); CEMA h^2_d=0.60 vs 0.30-0.54 in literature (Crews and Kemp 2001; Reverter *et al.*, 2003; Borner *et al.*, 2013); CIMF h^2_d=0.89 vs 0.33-0.62 in literature (Reverter *et al.*, 2003; Borner *et al.*, 2013; Duff *et al.*, 2019). These results highlight that, in this dataset, genetic variation exists for carcase traits such that genetic improvement of these traits via selection is possible. It is imperative that further work is undertaken to ensure that the genetic parameters for carcase traits presented in this study truly reflects the genetic variation present in the wider Australian Angus population.

Table 11. Genetic parameters (SE) for carcase, growth and body composition traits

Trait[a]	σ^2_d	σ^2_m	σ^2_c	σ^2_p	h^2_d	h^2_m	c^2
CWT	579.6 (131)	-	-	758.6 (39.8)	0.76 (0.15)	-	-
CEMA	29.3 (7.5)	-	-	48.5 (2.4)	0.60 (0.14)	-	-
CRIB	2.37 (1.33)	-	-	12.4 (0.6)	0.19 (0.11)	-	-
CP8	9.11 (2.79)	-	-	20.5 (1.0)	0.44 (0.13)	-	-
CIMF	2.97 (0.62)	-	-	3.34 (0.18)	0.89 (0.15)	-	-
RBY	0.51 (0.18)	-	-	1.40 (0.07)	0.36 (0.12)	-	-
BWT	9.98 (2.78)	3.61 (1.24)	2.16 (1.34)	19.30 (0.98)	0.52 (0.13)	0.19 (0.06)	0.11 (0.07)
GL	9.78 (3.07)	5.96 (1.26)	0	16.29 (1.13)	0.60 (0.17)	0.37 (0.07)	0
WWT	212.6 (73)	142.2 (46)	118.3 (47)	632.0 (31.5)	0.34 (0.11)	0.23 (0.07)	0.19 (0.07)
YWT	465.8 (115)	164.3 (56)	33.7 (59)	793.7 (41.6)	0.59 (0.13)	0.21 (0.07)	0.04 (0.07)
FWT	1,340 (285)	-	-	1,612 (85)	0.83 (0.15)	-	-
SRIB	1.08 (0.27)	-	-	1.51 (0.08)	0.72 (0.15)	-	-
SP8	2.00 (0.53)	-	-	3.14 (0.16)	0.64 (0.15)	-	-
SEMA	10.1 (2.5)	-	-	18.0 (0.88)	0.56 (0.13)	-	-
SIMF	0.33 (0.08)	-	-	0.59 (0.03)	0.56 (0.13)	-	-
MS	1.43 (0.20)	-	-	1.68 (0.09)	0.85 (0.08)	-	-

[a] Refer to Table 8 for full trait description

Heritability estimates for growth and body composition traits (Table 11) were moderate to large. With the exception of WWT, SIMF and GL, all estimates of direct heritability (h^2_d) were higher than previous estimates for Australian Angus. This was particularly evident for the body composition traits; SRIB h^2_d=0.76 vs 0.23-0.43 in literature (Borner *et al.*, 2013; Donoghue *et al.*, 2016); SP8 h^2_d=0.64 vs 0.27-0.44 in literature (Borner *et al.*, 2013; Jeyaruban *et al.*, 2013; Donoghue *et al.*, 2016); SEMA h^2_d=0.56 vs 0.21-0.30 in literature (Borner *et al.*, 2013; Jeyaruban *et al.*, 2013; Donoghue *et al.*, 2016); and MS h^2_d=0.85 vs 0.56-0.63 in literature (Robinson *et al.*, 2014).

Table 12. Genetic (above diagonal) and phenotypic (below diagonal) correlations (SE) for carcase traits

Trait[a]	CWT	CEMA	CRIB	CP8	CIMF	RBY
CWT	1	0.31 (0.16)	-0.05 (0.25)	-0.13 (0.18)	0.08 (0.15)	0.32 (0.18)
CEMA	0.19 (0.07)	1	-0.64 (0.22)	-0.31 (0.19)	-0.29 (0.15)	0.66 (0.16)
CRIB	-0.006 (0.07)	-0.22 (0.06)	1	0.68 (0.24)	0.18 (0.24)	-0.66 (0.27)
CP8	-0.07 (0.07)	-0.18 (0.07)	0.33 (0.06)	1	-0.01 (0.18)	-0.16 (0.23)
CIMF	0.05 (0.08)	-0.19 (0.07)	0.10 (0.07)	0.04 (0.07)	1	-0.009 (0.19)
RBY	0.34 (0.06)	0.41 (0.06)	-0.23 (0.06)	-0.13 (0.07)	-0.06 (0.07)	1

[a] Refer to Table 8 for full trait description

Phenotypic correlations between carcase traits (Table 12) ranged from -0.23 (CRIB:RBY) to 0.41 (CEMA:CRBY). It is expected that phenotypic correlations between CWT and the other carcase traits should not be significantly different to zero, as, by definition, these traits are adjusted to a 400-kg carcase weight. While phenotypic correlations between CWT and fatness traits in this dataset were as expected, moderate positive phenotypic correlations were observed between CWT and CEMA (0.19) and CWT and RBY (0.34). Reverter *et al.* (2003) observed similar moderate positive phenotypic relationships between CWT and CEMA/RBY using the same trait definitions as this project. Phenotypically, animals with higher RBY had higher CWT and CEMA and lower subcutaneous fat (CP8 and CRIB), with little phenotypic relationship between RBY and CIMF.

Genetic correlations between carcase traits (Table 12) ranged from -0.66 (CRIB:RBY) to 0.68 (CRIB:CP8). As expected, the two measures of subcutaneous fat (CP8 and CRIB) were well correlated genetically (0.68), meaning that selection for one of these traits will also lead to genetic improvement in the other trait. CWT had moderate positive relationships with CEMA (0.31) and RBY (0.32), but no significant relationship with the fatness traits and CIMF. Both fatness traits (CP8 and CRIB) had negative genetic relationships with CEMA and RBY, however the magnitude of the genetic correlation between CRIB and CEMA/RBY was much higher (-0.64 to -0.66) than for CP8 with the same traits (-0.16 to -0.31). This result was surprising given the large positive genetic correlation observed between CRIB and CP8. Reverter *et al.* (2003) also observed a stronger genetic correlation between CRIB and RBY (-0.65) compared to the correlation between CP8 and RBY (-0.48), but the difference between the two estimates was not of the same magnitude as observed in this dataset.

Greater error associated with measurement of CP8 in the abattoir could be a contributing factor to the differences in relationships between CP8 and CRIB observed in this study. CP8 is measured on the chain by abattoir staff, while CRIB is measured by trained MSA graders during carcass grading prior to carcass boneout. The genetic correlation observed between CRIB and RBY (-0.66) in this dataset is much closer to that expected than the genetic correlation observed between CP8 and RBY (-0.16), lending weight to greater confidence in the accuracy of the CRIB data.

All genetic correlations between CIMF and other carcase traits were not significantly different to zero, except for with CEMA, where a moderate negative genetic correlation was observed (-0.29). It is expected that these estimates would be close to zero, with the exception of correlations with CEMA and RBY, which would be expected to be moderately negative. While the estimate in this study for CIMF-CEMA was similar to expected, the estimate for CIMF-RBY was quite different to expectation, as well as previous literature estimates (-0.38 to -0.53) (Reverter *et al.*, 2003; Borner *et al.*, 2013). Further investigation using CIMF data from all animals in the Angus Australia database may be required to understand the cause of this difference. The selection of sires for the ASBP, particularly the genetic diversity for CIMF in this subset of animals, could also be introducing some level of bias for this trait. CEMA was moderately positively correlated with RBY (0.66), and similar to published estimates (0.44 to 0.76; Reverter *et al.*, 2003; Borner *et al.*, 2013). Genetically, higher yielding animals also had higher CWT, larger CEMA, and lower carcase fat at both the rib and rump sites. Thus, based on the result in this study, selection for animals with higher RBY genetically, would also result in animals with higher CWT, larger CEMA, lower CP8 and CRIB, with minimal impact on CIMF.

Table 13. Phenotypic correlations (SE) between carcase and production traits

Trait[a]	CWT	CEMA	CRIB	CP8	CIMF	RBY
BWT	0.28 (0.07)	0.14 (0.07)	-0.23 (0.06)	-0.21 (0.07)	-0.16 (0.07)	0.008 (0.07)
GL	-0.01 (0.09)	-0.02 (0.09)	-0.10 (0.09)	-0.24 (0.08)	0.09 (0.09)	0.10 (0.09)
WWT_d	0.53 (0.05)	0.16 (0.07)	-0.08 (0.06)	-0.15 (0.06)	0.02 (0.07)	0.10 (0.07)
YWT	0.83 (0.02)	0.10 (0.07)	-0.08 (0.07)	-0.10 (0.07)	0.06 (0.07)	0.21 (0.07)
FWT	0.92 (0.01)	0.04 (0.07)	-0.02 (0.07)	-0.06 (0.07)	0.04 (0.08)	0.18 (0.07)
SRIB	0.18 (0.08)	-0.10 (0.07)	0.41 (0.06)	0.42 (0.06)	0.23 (0.07)	-0.01 (0.07)
SP8	0.28 (0.07)	-0.05 (0.08)	0.27 (0.07)	0.52 (0.05)	0.22 (0.07)	0.05 (0.07)
SEMA	0.48 (0.06)	0.46 (0.05)	-0.12 (0.06)	-0.10 (0.07)	0.03 (0.07)	0.39 (0.06)
SIMF	0.31 (0.07)	0.01 (0.07)	0.13 (0.06)	0.16 (0.07)	0.42 (0.06)	0.13 (0.07)
MS	0.34 (0.07)	0.31 (0.07)	-0.09 (0.07)	-0.15 (0.07)	-0.15 (0.08)	0.38 (0.06)

[a] Refer to Table 8 for full trait description

Phenotypic correlations between carcase and growth and production traits can be found in Table 13. CWT was moderately to strongly phenotypically correlated (0.18-0.92) with growth and body composition traits. CEMA, CRIB, CP8 and CIMF had moderate phenotypic correlations with their corresponding scan traits (0.27-0.52), but had little phenotypic relationship with other traits, with the exception of CEMA, which had a moderate positive relationship with MS (0.31). RBY had little phenotypic relationship with any production traits, except SEMA (0.39) and MS (0.38).

Phenotypically, animals with higher RBY had higher SEMA and MS, with little phenotypic relationship with growth traits or other body composition traits.

Table 14. Genetic correlations (SE) between carcase and production traits

Trait[a]	CWT	CEMA	CRIB	CP8	CIMF	RBY
BWT	0.16 (0.17)	0.37 (0.17)	-0.64 (0.23)	-0.34 (0.19)	-0.29 (0.16)	-0.04 (0.22)
GL	-0.09 (0.20)	-0.04 (0.23)	-0.33 (0.36)	-0.70 (0.24)	0.19 (0.19)	0.34 (0.27)
WWT_d	0.48 (0.15)	0.39 (0.19)	-0.58 (0.32)	-0.55 (0.22)	0.15 (0.19)	-0.03 (0.25)
YWT	0.88 (0.05)	0.21 (0.17)	-0.25 (0.27)	-0.21 (0.19)	0.17 (0.16)	0.25 (0.20)
FWT	0.96 (0.02)	0.10 (0.16)	-0.03 (0.24)	-0.06 (0.18)	0.07 (0.15)	0.14 (0.19)
SRIB	0.13 (0.16)	-0.19 (0.17)	0.63 (0.15)	0.57 (0.14)	0.36 (0.14)	-0.06 (0.21)
SP8	0.45 (0.15)	-0.11 (0.18)	0.41 (0.23)	0.68 (0.12)	0.36 (0.15)	0.11 (0.22)
SEMA	0.46 (0.13)	0.72 (0.12)	-0.49 (0.25)	-0.22 (0.19)	0.17 (0.16)	0.57 (0.17)
SIMF	0.45 (0.15)	0.10 (0.18)	0.12 (0.25)	0.20 (0.19)	0.66 (0.11)	0.31 (0.21)
MS	0.38 (0.13)	0.41 (0.14)	-0.14 (0.23)	-0.19 (0.16)	-0.20 (0.14)	0.58 (0.14)

[a] Refer to Table 8 for full trait description

Genetic correlations between carcase, growth and production traits can be found in Table 14. Moderate to high positive genetic correlations were observed between CEMA, CRIB, CP8 and CIMF and their corresponding scan traits (0.63-0.72), indicating that the same trait measured on the live animal and on the carcase are highly related, genetically. The estimates obtained in this study between the same trait on the live animal and carcase were very similar to recent published estimates in the Australian Angus population (Borner *et al.*, 2013; Duff *et al.*, 2019). Similar to the pattern observed in the phenotypic relationships, CWT was moderately to strongly genetically correlated (0.38-0.96) with growth and body composition traits except BWT (0.16), GL (-0.09) and SRIB (0.13). Other relationships of interest include a moderate positive genetic correlation (0.41), between CEMA and MS. RBY had moderate positive genetic relationships (0.57-0.58) with SEMA and MS, and the estimate between RBY and SEMA was similar in magnitude to that observed by Reverter *et al.* (2000) and Borner *et al.* (2013). There was, however, little evidence of significant genetic relationships between RBY and any other growth or body composition traits. The moderate positive genetic correlations between RBY and SEMA and MS highlight that both traits could assist in genetic selection for higher yielding animals. SEMA and MS are themselves only moderately positively genetically correlated (rg=0.25, not published), indicating that, genetically, they are not the same trait, and each trait would make a separate but useful contribution towards the genetic selection of higher yielding animals. Robinson *et al.* (2014) observed slightly higher estimates of the genetic correlation between MS and SEMA (0.53-0.56), but drew the same conclusion: that MS and SEMA are independent traits. Given both SEMA and MS can be measured on the live animal, and much earlier in life than RBY, they have potential to be used jointly as early-life measures to increase the accuracy of selection for RBY.

Selection history of the herds involved may play a role in the inflation of genetic variance for growth and body composition traits, along with CWT, CIMF and CEMA. In past analyses of data from the Trangie herd, analysis of data from the divergent residual feed intake lines required the addition of performance and pedigree information from the Angus Australia database to estimate genetic

parameters (Arthur et al, 2001). This allowed the authors to account for potential selection bias based on EBV that may have occurred in the sampling of sires used to generate progeny for feed intake measurements. Discussions have been ongoing throughout the analyses between project members and scientists at the Animal Genetics and Breeding Unit (AGBU) regarding potential causes of the inflated genetic variance, and several different solutions suggested have been tested by the project team. These include incorporating additional pedigree depth (10 generations were used in all genetic analyses instead of standard 3 generations); the analysis of unadjusted records instead of adjusted records, and conducting genetic analyses using a sire model rather than an animal model. In order to fully determine the underlying cause, further investigations regarding genetic parameters for all traits should include analyses using all available data in the Australian Angus population, rather than just limited to the herds involved in this study. It is expected that this will minimise any potential bias arising in the data from the history of the herds and design of the ASBP, and allow genetic parameters to be estimated that accurately reflect the genetic variation in the Angus population. AGBU has recently undertaken these analyses as part of their ongoing work program to support BREEDPLAN, and have successfully used carcase data from this project (in conjunction with all other carcase data in the Angus Australia database) to estimate updated genetic parameters for carcase traits.

5. Conclusion

The major purpose of this project was to generate retail beef yield phenotypes on at least 1000 fully pedigreed and genetically described modern Angus cattle. This was achieved, with 1036 RBY phenotypes being added to the Angus BREEDPLAN database. These will be used to re-estimate BREEDPLAN RBY parameters and to provide more accurate carcase RBY EBVs aligned to the modern beef cattle population.

Relationships between retail beef yield and a number of live and carcase traits were assessed. Generally, fatness traits had stronger relationships with retail beef yield when measured close to slaughter than earlier in life, whereas the muscling traits eye muscle area and muscle score) had strong relationships with retail beef yield when recorded at feedlot entry, after 100 days on feed and at slaughter. Analyses indicated that eye muscle area and muscle score both explain significant variation in retail beef yield, but do not provide the same information when predicting retail beef yield. This highlights the value of continuing to utilise eye muscle area as a selection trait, but also including muscle score when selecting for improved retail beef yield. The development of technologies, such as 3D cameras, to provide a more objective assessment of muscle score will improve the ability of industry to utilise this trait effectively and make improvements in retail beef yield.

5.1 Key findings

- Eye muscle area and muscle score provide important information for predicting retail beef yield but the information they provide is different. This was apparent in both the regression and genetic analyses.
- The value of using fat measurements for predicting retail beef yield varies with time from slaughter with the most useful being provided by carcass fat traits and little value provided by feedlot entry fat traits. Again, this was apparent in both the regression and genetic analyses.
- Little relationship was observed between retail beef yield and other carcase and production traits, indicating that it is possible to select for improved retail beef yield with little impact on other traits influencing profitability.

- The weak relationships observed between retail beef yield and intramuscular fat, marble scores and MSA Index indicate that increases in retail beef yield may be achieved while also improving meat quality.
- This research has been conducted outside the NSW DPI muscling herd using industry relevant animals and the findings suggest that previous findings from the muscling herd appear to be transferable to the commercial industry.

5.2 Benefits to industry

The industry application of this project will be through BREEDPLAN, and the estimation of updated parameter estimates leading to retail beef yield estimated breeding values that are better align to the modern cattle population. Findings from the project also support the value of using muscle score along with eye muscle area and carcase fat traits to assist in the selection of increased retail beef yield. Muscle scoring is used by industry, but it's value could be highlighted to strengthen its use, particularly if objective measurement options become commercially available.

6. Future research and recommendations

The key adoption pathway for this research is through the use of the phenotypes collected by BREEEDPLAN to estimate updated genetic parameters that are better aligned to modern cattle. Given the strong relationship found between muscle score and retail beef yield, an objective assessment system for muscle score assessment would be valuable. This would allow muscle score to be used along with eye muscle area and carcase fat traits to assist in the estimation of retail beef yield estimated breeding values and their subsequent use as a major driver of BREEDPLAN or selection indexes.

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9. Appendix 1: Cohort four milestone report

9.1 Milestone description

Fourth cohort data collected.

9.2 Methods

Grain finishing at UNE's Tullimba Research feedlot was completed for 306 2018-born steers and heifers from the NSW DPI Glen Innes and Elizabeth Macarthur Agricultural Institute (EMAI) Angus cow herd plus 19 2017-born heifers from the Trangie Angus herd between April and June 2020. A further 13 cattle were culled from the trial or died during grain finishing for various health reasons, most commonly acidosis-related due to variable intakes caused by high rainfall events at the end of the drought.

The group from the Glen Innes herd was comprised of 82 steers and heifers sired by ASBP AI sires as part of ASBP Cohort 8, and 88 steers and heifers sired by industry bulls. Thirty two of these were heterozygous for the 821del11 myostatin mutation. The EMAI group was comprised of 133 steers and heifers sired by industry-sourced bulls, and out of Cohort 6 ASBP heifer dams from the DPI Glen Innes and Trangie herds, hence maintaining the valuable strong genetic links with the ASBP and the well described DPI herds. Seven of these were heterozygous for the 821del11 myostatin mutation.

Management practices implemented for Cohort 3 to improve the acclimation of the steers to the feedlot were repeated for Cohort 4. These included pre-conditioning with a grain-based supplement; ensuring all vaccination programs (including Bovilis® MH+IBR) were completed prior to trucking from the backgrounding property; and providing electrolytes in the drinking water several days prior to and following arrival at Tullimba.

COVID-19 restrictions at Tullimba from around the start of April 2020 caused some changes to visitors allowed on site, however all key data was collected within these restrictions. Collection of RGBD 3D data was conducted on later groups once restrictions had eased.

These cattle were slaughtered in April, May and June 2020, with the same carcase and yield data collected as described for the previous Cohorts, and in the body of the final report.

COVID-19 restrictions posed a significant challenge with John Dee abattoir located in Qld, and the NSW/Qld border closing just before the first slaughter. COVID safe practices at John Dee placed severe restrictions on visitor numbers, and social distancing resulted in a reduction in the number of staff in the training boning room utilised for yield data collection. Together this led to slower throughput and a reduction in the number of sides which could be processed through the training boning room in a shift. The slower pace resulted in very clean boneout data collection, but it also resulted in 13 sides from the first kill groups missing boneout data collection as the Government changes were implemented too close to slaughter to allow kill replicate size to be modified.

9.3 Results

The Cohort 4 steers and heifers displayed a similar variation in weight, fatness, muscle score and RBY% to the previous cohorts. Descriptive statistics for live animal measures taken at feedlot entry and after 100 days on feed are presented for the 2018-born steers, the 2018-born heifers, and the

2017-born heifers in Tables 1, 2 and 3 respectively. At feedlot entry there was a spread across the cohort in liveweight of 278kg, P8 fat of 17mm, and muscle scores from E+ to B+. After 100 d on feed the liveweight spread was 336kg, P8 fat spread was 28mm, and muscle score spread from E+ to B+. The 2017-born heifers were slightly heavier than the 2018-born steers and heifers at feedlot entry and after 100d on feed.

Table 1. Descriptive statistics for liveweight, ultrasound scan measurements and visual muscle score assessment at feedlot entry and after approximately 100 d on feed for Cohort 4 2018-born steers (EMA, eye muscle area; IMF, intramuscular fat).

	Number	Mean	SD	Min	Max
		Feedlot entry			
Liveweight (kg)	187	416	44.4	260	538
P8 fat (mm)	187	6.5	3.14	1	16
Rib fat (mm)	187	4.8	2.20	1	10
EMA (cm2)	187	60.2	8.04	34	82
IMF (%)	187	5.0	1.30	1.7	7.8
Muscle score (1-15)	187	7.4	1.38	3	12
Hip height (cm)	187	125	4.2	112	137
		100 d on feed			
Liveweight (kg)	181	560	46.6	396	688
P8 fat (mm)	181	15.0	3.44	3	26
Rib fat (mm)	181	9.8	1.85	3	14
EMA (cm2)	181	75.0	6.34	50	92
IMF (%)	181	7.4	0.64	4.4	8.3
Muscle score (1-15)	181	6.9	1.32	3	11
Hip height (cm)	181	125	4.8	110	137

Table 2. Descriptive statistics for liveweight, ultrasound scan measurements and visual muscle score assessment at feedlot entry and after approximately 100 d on feed for Cohort 4 2018-born heifers (EMA, eye muscle area; IMF, intramuscular fat).

	Number	Mean	SD	Min	Max
		Feedlot entry			
Liveweight (kg)	129	392	35.6	308	506
P8 fat (mm)	129	7.6	3.40	2	18
Rib fat (mm)	129	5.2	2.47	2	13
EMA (cm2)	129	59.5	5.50	46	75
IMF (%)	129	5.2	1.20	2.5	7.4
Muscle score (1-15)	129	6.9	1.65	2	11
Hip height (cm)	129	122	3.7	112	134
		100 d on feed			
Liveweight (kg)	129	542	47.6	430	698
P8 fat (mm)	129	17.9	3.75	10	31
Rib fat (mm)	129	10.8	1.84	7	17
EMA (cm2)	129	78.3	6.12	65	100
IMF (%)	129	7.7	0.56	4.6	8.3
Muscle score (1-15)	129	7.2	1.18	5	11
Hip height (cm)	129	128	5.5	116	143

Table 3. Descriptive statistics for liveweight, ultrasound scan measurements and visual muscle score assessment at feedlot entry and after approximately 100 d on feed for Cohort 4 2017-born heifers (EMA, eye muscle area; IMF, intramuscular fat).

	Number	Mean	SD	Min	Max
		Feedlot entry			
Liveweight (kg)	19	437	36.0	372	508
P8 fat (mm)	19	9.1	2.20	5	13
Rib fat (mm)	19	6.1	1.52	3	8
EMA (cm2)	19	62.1	4.75	53	72
IMF (%)	19	6.3	0.83	4.3	7.6
Muscle score (1-15)	19	6.6	1.54	3	8
Hip height (cm)	19	122	4.7	113	132
		100 d on feed			
Liveweight (kg)	19	596	60.5	502	732
P8 fat (mm)	19	19.6	3.82	14	30
Rib fat (mm)	19	11.6	2.43	6	15
EMA (cm2)	19	79.7	4.82	70	89
IMF (%)	19	8.0	0.25	7.5	8.3
Muscle score (1-15)	19	6.9	1.03	4	9
Hip height (cm)	19	131	4.9	122	140.5

Descriptive statistics for selected carcase traits and RBY% data are presented for the 2018-born steers, the 2018-born heifers, and the 2017-born heifers in Tables 4, 5 and 6 respectively. The 2017-born heifers were older at slaughter than the 2018-born cattle but had a smaller range in age at slaughter (35 d vs 163 d). Across the cohort the range in HSCW was 181kg, Hot P8 fat 26mm, and MSA EMA 59 cm^2. The RBY% range was 9.0% units.

Table 4. Descriptive statistics for measured carcase traits for cohort 4 2018-born steers (HSCW, hot standard carcase weight; MSA, Meat Standards Australia; EMA, eye muscle area; MB, marbling; LD*, longissimus dorsi;* IMF, intramuscular fat; RBY, retail beef yield).

	Number	Mean	SD	Min	Max
Final Liveweight (kg)	178	589	47.0	410	736
Slaughter age (d)	177	596	45.1	521	658
HSCW (kg)	177	317	26.0	211.3	392.6
Hot P8 fat (mm)	177	13.4	3.83	7	25
MSA Rib fat (mm)	177	8.8	2.74	3	16
MSA EMA (cm2)	177	79.4	8.70	53	106
MSA MB (110-1190)	177	349	57.0	200	550
Ossification (100-590)	177	128	13.8	100	160
MSA Index (30-80)	177	61.4	2.36	55.6	66.1
LD chemical IMF%	176	5.5	1.83	2.34	12.06
RBY (%)	163	73.4	1.44	69.8	78.8

Table 5. Descriptive statistics for measured carcase traits for cohort 4 2018-born heifers (HSCW, hot standard carcase weight; MSA, meat standards Australia; EMA, eye muscle area, MB, marbling; LD*, longissimus dorsi;* IMF, intramuscular fat; RBY, retail beef yield).

	Number	Mean	SD	Min	Max
Final Liveweight (kg)	129	568	48.2	460	722
Slaughter age (d)	129	620	50.2	537	684
HSCW (kg)	129	300	25.6	241.7	375.3
Hot P8 fat (mm)	129	17.4	4.64	7	33
MSA Rib fat (mm)	129	8.9	2.82	4	17
MSA EMA (cm2)	129	81.3	10.51	62	112
MSA MB (110-1190)	129	353	68.3	220	790
Ossification (100-590)	129	165	15.2	120	200
MSA Index (30-80)	129	60.5	1.21	57.4	65.8
LD chemical IMF%	129	5.6	2.28	2.37	17.29
RBY (%)	129	74.4	1.56	71.4	78.0

Table 6. Descriptive statistics for measured carcase traits for cohort 4 2017-born heifers (HSCW, hot standard carcase weight; MSA, meat standards Australia; EMA, eye muscle area, MB, marbling; LD*, longissimus dorsi;* IMF, intramuscular fat; RBY, retail beef yield).

	Number	Mean	SD	Min	Max
Final Liveweight (kg)	19	614	59.7	512	740
Slaughter age (d)	19	1029	8.8	1001	1037
HSCW (kg)	19	326	34.1	271.4	389.8
Hot P8 fat (mm)	19	19.8	5.32	12	32
MSA Rib fat (mm)	19	11.8	3.69	5	18
MSA EMA (cm2)	19	84.1	9.35	67	105
MSA MB (110-1190)	19	378	53.0	320	540
Ossification (100-590)	19	193	25.4	140	230
MSA Index (30-80)	19	60.1	1.67	57	64.62
LD chemical IMF%	19	7.3	2.50	3.11	14.24
RBY (%)	19	74.6	1.10	73.0	77.3

The phenotypic correlations between RBY% and a number of live and carcase traits were assessed for 306 carcases (Table 7). Correlations between fat measures and RBY% were generally negative or not significant, and correlations between EMA and muscle score with RBY% were generally positive and highly significant. The correlations are also presented separately for steers and heifers in Tables 8 and 9 respectively.

The presence of 39 animals carrying one copy of the nt821del11 myostatin mutation is likely to be influencing the higher correlations between RBY% and the muscling traits than the fat traits. The correlation between RBY% and both MSA Marble and the Lab IMF% conducted on a sample of the *longissimus dorsi* from the boned side was generally significant and negative, however the correlation with MSA Index was not significant.

Table 7. Phenotypic correlations of RBY% with live ultrasound scan traits at feedlot entry and after 100d on grain, and carcase traits for all Cohort 4 steers and heifers (n=306). (HSCW, hot standard carcase weight; MSA, meat standards Australia; EMA, eye muscle area; MB, marbling; LD*, longissimus dorsi*).

	Ultrasound scan traits		Carcase traits	
	Feedlot entry	100d grain		
Liveweight (kg)	-0.25**	-0.02	HSCW (kg)	-0.00
P8 fat (mm)	-0.33**	-0.11+	Hot P8 fat (mm)	0.03
Rib fat (mm)	-0.39**	-0.13*	MSA Rib fat (mm)	-0.01
EMA (cm^2)	0.01	0.35**	MSA EMA (cm^2)	0.54**
Scan IMF%	-0.28**	-0.21**	MSA MB (110-1190)	-0.21**
Muscle score (1-15)	0.27**	0.43**	MSA Index (30-80)	-0.03
			LD IMF%	-0.36**

* Significance at P<0.05; ** Significance at P<0.001;+ Tendency at P<0.1

Table 8. Phenotypic correlations of RBY% with live ultrasound scan traits at feedlot entry and after 100d on grain, and carcase traits for Cohort 4 steers (n=163). (HSCW, hot standard carcase weight; MSA, meat standards Australia; EMA, eye muscle area; MB, marbling; LD*, longissimus dorsi*).

	Ultrasound scan traits		Carcase traits	
	Feedlot entry	100d grain		
Liveweight (kg)	-0.22*	-0.05	HSCW (kg)	0.08
P8 fat (mm)	-0.34**	-0.21*	Hot P8 fat (mm)	-0.11
Rib fat (mm)	-0.36**	-0.26**	MSA Rib fat (mm)	-0.08
EMA (cm^2)	-0.065	0.07	MSA EMA (cm^2)	0.39**
Scan IMF%	-0.25*	-0.27**	MSA MB (110-1190)	-0.29**
Muscle score (1-15)	0.45**	0.37**	MSA Index (30-80)	0.13
			LD IMF%	-0.33**

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

Table 9. Phenotypic correlations of RBY% with live ultrasound scan traits at feedlot entry and after 100d on grain, and carcase traits for Cohort 4 heifers (n=141). (HSCW, hot standard carcase weight; MSA, meat standards Australia; EMA, eye muscle area; MB, marbling; LD*, longissimus dorsi*).

	Ultrasound scan traits		Carcase traits	
	Feedlot entry	100d grain		
Liveweight (kg)	-0.18*	-0.10	HSCW (kg)	0.09
P8 fat (mm)	-0.56**	-0.36**	Hot P8 fat (mm)	-0.19*
Rib fat (mm)	-0.57**	-0.26*	MSA Rib fat (mm)	0.00
EMA (cm^2)	0.14	0.53**	MSA EMA (cm^2)	0.67**
Scan IMF%	-0.50**	-0.37**	MSA MB (110-1190)	-0.18*
Muscle score (1-15)	0.29**	0.50**	MSA Index (30-80)	-0.09
			LD IMF%	-0.51**

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

The results from regressions modelling live and carcase traits to predict RBY% are presented in Table 10. The regressions using animal liveweight, live ultrasound scan data and live assessment of muscle score accounted for 56 to 58% of the variation in actual RBY% at slaughter. The regression using carcase weight, carcase fat and EMA measurements, and the live muscle score at feedlot entry accounted for 59.9% of the variation in RBY%. Overall, fat measures had negative relationships with RBY%, while EMA and muscle score had positive relationships. This result is similar to previous Cohorts, and will be discussed in detail in the full analysis in the body of the final report.

Table 10. Regression for models to predict retail beef yield % using live and carcase traits of the 306 cohort 4 cattle. (HSCW, hot standard carcase weight; MSA, meat standards Australia; EMA, eye muscle area; MB, marbling; LD, *longissimus dorsi;* MSc, muscle score).

	Feedlot entry[1]		100 d[1]			Carcase[2]	
Constant	68.8		68.0			68.4	
r^2	58.0		56.0			59.9	
se	1.01		1.04			0.99	
	b	se	b	se		b	se
Liveweight	-0.009	0.0022	-0.004	0.0017	HSCW	-0.001	0.0025
P8 fat	-0.104	0.0502	-0.042	0.0244	Hot P8 fat	-0.046	0.0149
Rib fat	-0.104	0.0751	-0.080	0.0475	MSA Rib fat	-0.059	0.0227
EMA	0.119	0.0168	0.078	0.0147	MSA EMA	0.061	0.0080
MSc	0.238	0.0440	0.353	0.0531	MSc	0.251	0.0410

[1] Live model*: LW+P8+Rib+EMA+MSc+KILL DATE* for data collected at feedlot entry and after 100d on grain. Liveweight (LW, kg); ultrasound scanned P8 (P8 fat, mm) and rib fat (Rib fat, mm), and eye muscle area (EMA, cm2); visual muscle score (MSc, 1-15) assessed on scanning day; plus fixed effect of kill day.

[2] Carcase model: *HSCW+Hot P8+MSA Rib+MSA EMA+MSc+KILL DATE* for data collected on carcases. Hot standard carcase weight (HSCW, kg); Hot P8 fat (P8, mm), MSA Rib fat (MSA rib, mm), MSA Eye muscle area (MSA EMA, cm2); the live muscle score measured at feedlot entry (MSc, 1-15); plus fixed effect of kill day.