final report

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Prepared by:	Linda Cafe
	NSW Department of Primary Industries
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Retail Beef Yield Lead-In Project – Year 1 Data Collection

Executive summary

Dressing percentage and saleable meat yield are key economic drivers for the Australian beef industry. The estimate breeding value (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 (EMA) and fat depths due to limited recording of abattoir carcase data and actual RBY% phenotypes. Since the original correlations were calculated in 2001, 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.

The Angus Australia and MLA co-funded Angus Sire Benchmarking Project (ASBP) provides a unique opportunity to collect quality RBY% data. The animals in this project have Angus Australia registered sires with close genetic links to current industry populations, have extensive phenotypic records collected from birth to slaughter, and are genotyped as part of that project. This project was conducted as a lead-in to a larger project, and to ensure the opportunity was not lost to collect retail beef yield and related data on available animals from the Angus Sire Benchmarking Project.

Retail bone out data was collected on 154 ASBP Cohort 5 (2015 born) steers from the NSW DPI Glen Innes and Trangie research cow herds in April 2017 at John Dee, Warwick abattoir. Following commercial AUS-MEAT carcase preparation, carcases were weighed and hot P8 fat depth recorded. Carcases were tagged and chilled overnight, and Meat Standards Australia (MSA) carcase grading data collected by registered MSA graders on the right hand sides the following morning prior to bone out. A standard set of AUS-MEAT boneless primals and standard trim of 10mm fat were selected for bone out of the right sides.

This small group of steers displayed substantial variation in weight, fatness and RBY%. Correlations between fat measures and RBY% were negative, and correlations between EMA and muscle score were positive. Correlations between RBY% and IMF% scan data were negative but low, and the correlations between RBY% and carcase measures of marbling or IMF% measured in the lab were very low. The correlation between RBY% and MSA Index was also very low. Regressions using animal liveweight, live ultrasound scan data and live assessment of muscle score accounted for 19.9% to 30.4% 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 25.2% of the variation in RBY%.

Overall, ultrasound scan measures of fatness in the live steers and carcase measures of fatness had negative relationships with RBY%, while live and carcase measures of EMA and muscle score had positive relationships. These relationships are logical and in keeping with previously reported results and the RBY% correlations used in BREEPLAN.

While the dataset is too small to use to assess genetic parameters, this is likely to be feasible once the number of records increases towards 1,000 in the large project. This small data set will be a valuable addition to BREEDPLAN, and will be included in the mid-December Angus BREEDPLAN analysis.

Collecting RBY% data on these steers provided a useful preparatory step in the planning towards conducting RBY% data collection on 1000 animals.

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1   Background

1.1   Introduction

This project was conducted as a lead-in to a larger Retail Beef Yield Project which has been approved for funding through the National Livestock Genetics Consortium (NLGC), however this was not finalised before the first cohort of steers produced for the project reached slaughter specifications. This small project was conducted to ensure the opportunity was not lost to collect retail beef yield and related data on available animals from the Angus Sire Benchmarking Project.

1.2   Background and purpose of research

Dressing percentage and saleable meat yield are key economic drivers for the Australian beef industry. Consequently, these traits are given consistently high weighting in 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 carcase 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 will impact the RBY% EBVs estimated via the correlation 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 the 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 in 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 (currently1,414).These cattle also provide a useful opportunity to validate other RBY predictive technologies available at the time (eg DEXA/MEXA, RGBD cameras) in collaboration with other projects. This dataset will 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 2014, McPhee et al. 2014).

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 carcase yield to the genetic evaluation for the trait.

2   Project objectives

2.1 Collect RBY and MSA data on 157 2015-born steers from NSW DPI ASBP herds at slaughter.
2.2 Collect RGBD camera data on the 157 steers.
2.3 Analyse the RBY data in Angus BREEDPLAN.
2.4 Inform the development of the larger RBY project (which has been developed as part of the NLGC) aiming to collect and analyse 1,000 RBY records.
2.5 Build industry capacity in the effective collection of RBY data with involvement of at least 2 Angus Australia technical staff.

3   Methodology

3.1   Live animal data

Data was collected on 154 ASBP Cohort 5 (2015 born) steers from the NSW DPI Glen Innes and Trangie research cow herds. Three of the initial 157 steers were lost between weaning and slaughter, two were euthanased after sustaining physical injuries, and one was culled at feedlot entry due to being an outlier in liveweight (small).

As part of the ASBP the steers had a comprehensive suite of BREEDPLAN traits measured from birth, low density genotyping (average of 25842 SNPs) conducted, and were grain finished at Tullimba Research Feedlot for 150 days to the fit the John Dee Angus Gold Grid. Feed intake, growth rate and ultrasound scan data (at feedlot entry and after 100d on feed) were collected during the feedlot period. Muscle score was also assessed by trained assessors at feedlot entry and after 100d on feed.

RGBD camera images were captured in collaboration with University of Technology Sydney (UTS) as part of project B.GBP.0014 (Prototype on-farm 3D camera system to assess traits in Angus cattle) at feedlot entry and approximately two weeks prior to slaughter.

3.2   Slaughter data

The 154 steers were slaughtered in 3 lots on the 4th, 10th and 12th April 2017 at John Dee, Warwick. Previous experience at conducting RBY data collection in the training boning room at John Dee indicated that approximately 50 sides could be boned out and measured in one day shift. Accordingly, the steers were divided into lots of 50, 53 and 51. The cohort of 101 steers originating from Trangie Research Station was split into two kill days balanced for sire, liveweight and ultrasound scan fat measures. The 53 steers originating from Glen Innes Research Station were killed in one lot.

Following commercial AUS-MEAT carcase preparation (Anon. 2007), carcases 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. Carcases 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 bone out. A team from Murdoch University collected Japanese digital camera images on the right sides immediately following grading, results will be included in the Advanced Livestock Measurement Technologies R&D for profit project (ALMTech).

It was not possible to collect RGBD carcase camera data on this group of animals, but there are opportunities to pursue collecting it in the larger project.

A standard set of AUS-MEAT boneless primals and standard trim of 10mm fat were selected for bone out. 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, even if different plants became involved.
3. Were compatible with samples required by MSA for sensory testing for further MSA model development on a subset of the Glen Innes cohort.

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 (60% 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 (60% chemical lean), FQ fat trim, FQ bone

Boning room pretrim 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 them being quartered and entering the boning room. This cold weight is 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.

A sample of the striploin was collected for later 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)

A number of primals from 18 carcases were sampled for use in two MSA projects. The projects are L.EQT.1620 - Product Collection for Future MSA Eating Quality Research and L.EQT.1720 - Enhancing MSA beef model accuracy and testing novel cut by cook combinations. These primals will be utilised to test new and existing cuts/muscles for further MSA development. The new and existing cuts will be tested for both new cook methods and existing cook methods in the model which may not have been tested for a few years.

3.3   Statistical analysis

Data from 150 steers was used in the analysis. Data from three steers was omitted due to excess trim/damage of the carcases during processing casting uncertainty on their overall RBY% result, and data from one steer omitted as it was an outlier (mean ± 3 standard deviations) for bone and meat yield.

Pearsons correlations of RBY% with live and carcase traits associated with it were conducted using PROC CORR in SAS. Regressions modelling the prediction of RBY% were conducted using Generalized Linear Models in Genstat V18.

There were 51 sires represented in the data, with the number of progeny for each sire ranging from 1 to 7. Twenty six of the 51 sires had progeny represented in both herds (Glen Innes and Trangie), and these 26 sires accounted for 69% (103/150) of the data.

4   Results

4.1   Project objectives achieved

The objectives for this project have been achieved.

2.1 Collect RBY and MSA data on 157 2015-born steers from NSW DPI ASBP herds at slaughter.
Data was collected on the 154 steers which remained alive at the end of the feedlot period.

2.2 Collect RGBD camera data on the 157 steers.
RGBD camera data was collected on 155 steers at feedlot entry, and on 53 steers 2 weeks prior to slaughter. The latter data was collected to compare to RGBD camera carcase data, as collection of this data was planned, but was not possible to conduct.

2.3 Analyse the RBY data in Angus BREEDPLAN.
Data has been submitted to Angus BREEDPLAN and it is planned that it will be analysed in the mid-December run when the carcase data for the complete cohort of ASBP steers is analysed.

2.4 Inform the development of the larger RBY project (which has been developed as part of the NLGC) aiming to collect and analyse 1,000 RBY records.
This lead-in data collection was very useful for informing the larger RBY project. It allowed NSW DPI to re-establish a good working relationship with management and staff of John Dee abattoir, and to train new NSW DPI staff in collection of the data. Importantly it has also confirmed that we can obtain good RBY data from John Dee, and that the staffing levels and time required is in keeping with previous experience.

2.5 Build industry capacity in the effective collection of RBY data with involvement of at least 2 Angus Australia technical staff.
Two Angus Australia staff assisted in manning the bone out sessions. A third staff member observed the bone out for one day. These staff developed a realistic appreciation of what is required to collect effective RBY data.

4.2   RBY% and relationships with other live and carcase measurements

This small group of steers displayed substantial variation in weight, fatness and RBY%. Descriptive statistics for live animal measures taken at feedlot entry and after 100 d on feed are presented in Table 1. At feedlot entry they had a liveweight spread of 192kg, P8 fat of 13mm, and muscle scores

from E+ to B. After 100 d on feed the liveweight spread was 218kg, P8 fat spread of 15mm and muscle score range from D- to B.

Table 1. Descriptive statistics for liveweight, ultrasound scan measurements and visual muscle score assessment at feedlot entry and after 100 d on feed.

	Number	Mean	SD	Min	Max
Feedlot entry					
Liveweight (kg)	150	420	33.9	338	530
P8 fat (mm)	150	6.8	3.03	1	14
Rib fat (mm)	150	4.7	1.97	1	9
IMF%	150	5.0	1.32	2	7.2
EMA (cm^2)	150	58.3	4.56	48	73
MSc (1-15)	150	7.5	1.36	3	11
100 d on feed					
Liveweight (kg)	150	588	42.8	488	706
P8 fat (mm)	150	14.7	2.77	8	23
Rib fat (mm)	150	10.5	1.82	6	16
IMF%	150	7.5	0.55	5.3	8.2
EMA (cm^2)	150	73.3	4.32	62	90
MSc (1-15)	150	7.6	1.44	4	11

Descriptive statistics for the carcase and RBY% data are presented in Table 2. The steers were tight in age at slaughter with a spread of only 54 d. The range in HSCW was 129kg, Hot P8 fat 20mm, MSA EMA 48 cm^2. The RBY% range was 6.65% units.

Table 2. Descriptive statistics for carcase traits

Trait	Number	Mean	SD	Min	Max
Slaughter age (days)	150	581	16.5	558	612
HSCW (kg)	150	340	24.7	287.5	416.5
Hot P8 fat (mm)	150	16.8	4.18	10	30
MSA Rib fat (mm)	150	15.2	4.23	7	28
MSA EMA (cm^2)	150	78.3	6.70	57	105
MSA MB (110-1190)	150	371	54.9	300	580
MSA Index (30-80)	150	62.7	1.50	59.58	67.21
Lab IMF (%)	150	6.0	2.18	2.01	12.97
RBY (%)	150	72.0	1.43	68.69	75.34

The correlations between RBY% and a number of live and carcase traits were assessed. These are presented in Table 3. Correlations between fat measures and RBY% were negative, and correlations between EMA and muscle score were positive. Correlations between RBY% and IMF% scan data were negative but low, and the correlations between RBY% and carcase measures of marbling or IMF% measured in the lab were very low. The correlation between RBY% and MSA Index was also very low.

Table 3. Correlations of RBY% with live ultrasound scan traits and carcase traits.

	Ultrasound scan traits		Carcase traits	
	Feedlot entry	100d on grain		
Weight	-0.11	-0.22	HSCW	-0.10
P8 fat	-0.10	-0.19	Hot P8	-0.20
Rib fat	-0.05	-0.33	MSA Rib fat	-0.37
EMA	0.21	0.23	MSA EMA	0.23
IMF%	-0.03	-0.11	MSA Marble	0.05
Muscle score	0.31	0.33	MSA Index	-0.03
			Lab IMF%	-0.04

The results from regressions modelling live and carcase traits to predict RBY% are presented in Table 4. The regressions using animal liveweight, live ultrasound scan data and live assessment of muscle score accounted for 19.9 to 30.4% 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 25.2% of the variation in RBY%. Overall, fat measures had a negative effect on RBY%, while EMA and muscle score had positive effects.

Table 4. Regression for models to predict RBY% using live and carcase traits.

	Feedlot entry[1]		100 d[1]			Carcase[2]	
Constant	70.22		71.01			71.31	
r^2	19.9		30.4			25.2	
se	1.29		1.2			1.24	
	b	se	b	se		b	se
Liveweight	-0.01001	0.00401	-0.00708	0.00251	HSCW	-0.00186	0.00463
P8 fat	-0.0917	0.0788	0.0843	0.0492	Hot P8	-0.045	0.026
Rib fat	0.062	0.122	-0.3134	0.0758	MSA Rib	-0.0804	0.026
EMA	0.0907	0.032	0.0875	0.0252	MSA EMA	0.0287	0.0183
MSc	0.2072	0.0868	0.1789	0.0731	MSc	0.2229	0.0859

[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.

5 Discussion

This small data set is useful to assess the success in achieving the collection of meaningful RBY% data. Although the aim of the larger RBY project is to study the genetic parameters around RBY%, this initial data set is not large enough to do so. The 51 sires represented in the data had good linkages across the two herds, and sires with progeny in both herds represented 69% of the data.

These linkages will ensure that the data is analysed effectively in BREEDPLAN and maximum value is gained from the data. Estimation of genetic parameters may be feasible once the number of records increases towards 1,000, and this data will be included in the analysis for the larger project.

The relationships of RBY% with live and carcase traits are consistent with those found previously and indicate that the data is sensible and reliable. Overall, ultrasound scan measures of fatness in the live steers and carcase measures of fatness had negative relationships with RBY%, while live and carcase measures of EMA and muscle score had positive relationships. These relationships are logical and in keeping with previously reported results and the RBY% correlations used in BREEPLAN. This data set is smaller and has a much tighter range in slaughter age, weight and fatness, and breed than the data set described by Wolcott *et al.* (2001) in reporting the relationships between ultrasound scan measurements and RBY%, hence the variation in RBY% accounted for by the regression using live scan traits is smaller than they reported.

In our dataset live muscle score generally shows around a 50% stronger relationship with RBY% than measures of EMA. This is consistent with results reported on steers from the DPI muscling selection line herd (Cafe *et al.* 2014). It is logical that an accurate assessment of whole body muscling would be more closely related to RBY% than the measurement of a single muscle, and reaffirms the value in following through on the development of a system to objectively measure whole body muscling, such as the RGBD cameras (McPhee *et al.* 2017).

6   Conclusions/recommendations

In conclusion, the objectives of this project have been met successfully. This group of ASBP steers displayed substantial variation in weight, fatness and RBY%, and the relationships between RBY% and live and carcase traits indicate that reliable data was collected. While the dataset is too small to use to assess genetic parameters, this is likely to be feasible once the number of records increases towards 1,000 in the large project. This data will be a valuable addition to BREEDPLAN. Collecting RBY% data on these steers proved a useful preparatory step to collecting RBY% data on 1000 animals.

7   Acknowledgements

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