Final report

Corriedale eating quality genomics

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Abstract

The project has a very committed and active team from New South Wales, Victoria, South Australia and Tasmania. The project was undertaken to collect data on as many traits as possible, but especially shear force and intramuscular fat content in Corriedale sheep. Four joinings (3 AI) have been conducted and 764 carcasses have been slaughtered and processed. Data from the first cohort was supplied to Sheep Genetics in September 2018, for second cohort has been supplied in August 2019 and subsequent cohorts in 2021. The final phenotyping of meat samples was delayed due to COVID-19, but has now been completed. Genotyping was been delayed while platforms were being established by the genotyping companies. Genotyping of progeny and sires (high density) has also been completed by Neogen. It is tremendous to have had Honours students Hannah Gordon in 2018 and Sarah Welsh in 2019 involved in the project. Genetic parameters estimated herein lack accuracy and the data should be analysed in combination with other data from the Sheep Genetics database. The final phenotype and genotype data will be supplied to Sheep Genetics. The project has provided focus for the Performance Corriedale Group, will hopefully attract new members into Sheep Genetics and will significantly increase accuracy of ASBVs as well as providing data on traits not currently recorded.

Executive summary

Background

The Performance Corriedale Group are a group of breeders committed to working together to maximise genetic improvement and marketing of higher performance sheep. They initiated the trial following a desire to utilise genomics and have the tools available to maximise genetic improvement in lamb eating quality. The data from the project will contribute to the Sheep Genetics database. Genetic improvements are cumulative and flow throughout the industry. The project also provides a model for engagement of breeds which are lower in number but still significant in impact.

Objectives

The aim was to collect performance and genomic data on as many progeny and sires as possible with the following specific objectives.

A. Conduct a sire evaluation program on leading young Corriedale sires with strong genetic links to Merino and other maternal breeds.
B. Conduct extensive phenotyping on lambs including intramuscular fat, shear force and fat melting point measurements.
C. 50K SNP Genotype Corriedale lambs to enable genomic selection to be utilised.
D. Provide a model for engagement for smaller breeds.

Methodology

The aim was to inseminate 375 ewes per year from 15 sires to result in 300 lambs for 3 years for a total of 900 lambs.

Results/key findings

The model of engagement with the Performance Corriedale Group worked well as the working relationship between researchers and breeders is strong. In addition, two Honours students have been trained in the project. The project achieved 764 lambs from 44 sires, 37 of which were genotyped. The data will be supplied to Sheep Genetics for reporting of ASBVs although reporting to breeders who are not part of Sheep Genetics still needs to be resolved.

Benefits to industry

Increasingly Corriedale sires are being used to increase wool value in maternal composite flocks. The data collected adds confidence to stud breeders to maximise genetic progress and their clients to select more profitable rams.

Future research and recommendations

The current resource flock strategy of subsidising meat sample and processing by breeders and especially groups with well-designed contemporary groups should continue as the benefits of the data are substantial and the less tangible benefits of working together are significant.

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1. Background and Objectives

1.1 Project description

Through the Sheep CRC's Information Nucleus there have been many sires tested for eating quality of their progeny in additional to multiple other traits. This has led to the development of genomic tests for the two traits having the largest effect on eating quality (shear force and intramuscular fat) as well as traits such as lean meat yield and other production traits recorded. While 14 Corriedale rams have been included (just 220 of 420 progeny genotyped to date) and there is ongoing recording through the MLA Resource Flock, there are insufficient records for the genomic tests to be valuable to Corriedale breeders. As a breed the aim should be to have 2000 progeny genotyped from a wide range of sires (up to 200).

The project was initiated by the Performance Corriedale Group who only account for 11% of registered Corriedales, but in 2018 accounted for 40% of ram sales, and this is growing. The vision is to breed sheep that have higher wool value and superior eating quality to other maternal breeds with maximum weight of lambs weaned from ewes of moderate size and adapted to high rainfall regions. The purpose of this project is to address the deficit in genotyped Corriedales by genotyping 900 progeny from a range of Corriedale sire lines. By using purebred Corriedale ewes, the project has more Corriedale haplotypes represented than if the sires were crossed to another breed.

1.2 Background and plans

Performance Corriedale Group

The Performance Corriedale Group meets four times per year. The primary meeting is an annual workshop where breeders optimise breeding programs in collaboration with staff from Sheep Genetics. The Group has a number of link sires that are used across all member's flocks. These sires have been chosen to also provide links to New Zealand as the group have been a leader in promoting Trans-Tasman analysis. The group are making good progress and in 2016 it became obvious that the rams with the higher genetic merit for objectively measured traits were within members' flocks. The Group has developed an excellent culture combining a healthy mix of collaboration and competition which drives genetic progress. The Group provides a good model for strategies to make genetic improvement in breeds of significant, but not dominant number.

At the 2016 annual workshop there was significant discussion about marketing of rams in a way that clients can simply rank them. During the Olympics in August 2016, the new Gold, Silver and Bronze system was launched. Gold rams are top 10th percentile based on the Dual Purpose index (now MWP+ index), Silver 75-90th percentile and Bronze 40-75th percentile. The system was developed down to the 40th percentile to aid new members where it will take time for their Australian Sheep Breeding Values (ASBVs) and index values to get to Gold and Silver levels. Only Gold rams will be used as link sires in future. Already, premiums have been paid at ram sales for Gold rams, and breeding more of these will help focus Group members. The system was based on percentiles so that the performance threshold can constantly be increased as the breed makes genetic progress.

Within the group is a desire to use the latest genetic tools to maximise genetic progress. Genomics is an area of discussion at every annual workshop and there is a level of frustration that tools are not

sufficiently accurate for use by the Group. However, the recent focus of genomics for eating quality provides an opportunity that the Group are prepared to invest in. Most Corriedale breeders believe that Corriedale lamb is superior to other Maternal and Terminal breeds. This project was motivated by a desire to both benchmark current sires against other breeds and develop Genomic tools for ongoing genetic improvement. However, in developing the project it has become clear that it should focus on Corriedale genomics and the benchmarking will come through Sheep CRC and now industry Resource Flocks.

1.3 Contracted Objectives

A. Conduct a sire evaluation program on leading young Corriedale sires with strong genetic links to Merino and other maternal breeds.
B. Conduct extensive phenotyping on lambs including intramuscular fat, shear force and fat melting point measurements.
C. 50K SNP Genotype Corriedale lambs to enable genomic selection to be utilised.
D. Provide a model for engagement for smaller breeds.

2. Methodology

Corriedale progeny test

A progeny testing trial was proposed with the aim of benchmarking Corriedale sires and developing genomic tests for Corriedale breeders. The logic was to slaughter both ewe and wether progeny to maximise the information for carcass and eating quality traits. Reproduction and wool growth data is routinely collected in Group flocks and genomic tests could be developed subsequently without additional phenotyping costs required.

The progeny test is being run at Cressy Research and Demonstration Station in Tasmania. There is a flock of Corriedale ewes currently running on Cressy by one of the Performance Group members, Peter and Claire Blackwood. Most other Corriedale sires have been tested by mating Merino ewes. The advantage of using Corriedale ewes in this trial is that there will be more Corriedale haplotypes segregating for traits of interest. It is proposed that 45 sires will be tested over 3 years resulting in 900 lambs genotyped. While the project is referred to as a “progeny test”, this is really to aid promotion as breeders are used to this terminology. Really it is all about describing relationships between genetic variation and phenotypes and the number of sires is really aimed to sample genes across the breed.

A stated objective of the project was to have strong genetic links with Merino and other maternal breeds. However, early on in the project in collaboration with Julius van der Werf and Daniel Brown, it was decided that the genetic links should already be present through the Information Nucleus Flock and Resource Flock programs. Thus, the focus of this trial is to describe genetic variation within the Corriedale breed.

Corriedale rams are proposed by breeders but are accepted based on their relationships to sires that have been widely used to ensure a wide range of bloodlines are represented. Breeders who supply rams will gain valuable information on a range of performance traits. This is opened up to breeders not currently in the Performance Group as it is a great way to start performance recording.

Traits measured

The plan was that in each of the three years there would be 15 Corriedale rams tested. Ewes were synchronised and mated by artificial insemination in April of 2017-2019 inclusive. The aim was for 20 ewes to be inseminated per ram (300 ewes per year) with the aim of achieving 20 lambs per ram (300 lambs per year). The aim was to grow lambs to an average of 24kg carcass as it is expected there will be more variation between lambs at that weight than 19kg sucker lambs. It was planned that lambs would be slaughtered in April the following year (2018-2020) and that we could get DXA measurement of lean meat yield.

Lambs were mothered up with the primary aim of recording date of birth and birth type (single vs twin and triplet). Weight was recorded at weaning, post-weaning and multiple times pre-slaughter. Fat and muscle depth was recorded by ultrasound scanning following Sheep Genetics protocols.

While the lambs were alive, as many traits as possible were recorded. This included wrinkle, face cover, wool colour, wool character, fleece rot, black spots and skin pigment, and structural defects such as shoulders, feet, legs and jaws. The plan was for lambs to be shorn pre-slaughter to get wool growth and fibre diameter measures. In 2018 the project was the basis of one of the major presentations at the Corriedale World Congress, Bendigo, Wednesday 18th July. It was planned that the site be used for field days to promote Sheep Genetics and educate about the value of genomics for increasing rates of genetic improvement. The field day did not occur due to changes in lease arrangements at Cressy and COVID-19.

Carcass weight, GR Fat, eye muscle width and depth, C-fat, and lean meat yield were recorded at the abattoir. Meat samples were purchased for measurements of intramuscular fat and shear force. Fat melting point was not recorded as it is not a currently recognised trait by Sheep Genetics and no Honours students chose that as a project. All carcass and meat measurements were collected using standard protocols written by the UNE and Murdoch meat teams as part of the Sheep CRC and MLA Resource Flock.

3. Results

3.1 Measurements live and at slaughter of third cohort

Semen was supplied for 15 rams and 300 ewes (20 per sire) were mated by artificial insemination in 2017. There were a number of ewes that did not conceive to the AI so, despite high weaning rates, there were just 212 lambs available for subsequent analyses.

The 2nd joining in April 2018 comprised 200 ewes mated by artificial insemination to 10 rams plus 80 ewes naturally mated to 4 rams including use as backups. Thus, a total of 14 sires. This resulted in 235 lambs for slaughter, bringing the total to 447 which was a fair way short of the target of 600.

To address the shortfall in lamb numbers, an additional joining of 191 ewes using natural mating was conducted in February 2019. The season has been better and they have scanned at 151% although we expected this to result in about 270 lambs and actually resulted in 197 slaughtered.

The 3rd AI joining was conducted on 24th April 2019 and used 14 sires from 8 studs. Backup sires were not used and so the scanning result suggests we will get 149 lambs, although 130 was more likely and there were 103 survive to slaughter.

Thus, the aim was for 900 lambs but changes in lease arrangements at Cressy prevented sufficient ewes being available to achieve that. There were 764 lambs (Table 1) and 745 lambs with carcass records (Table 2).

Table 1. Range of birth dates of lambs (758 of 764 with records)

Birth Year / CG	Mean DOB	Min	Max	Lambing period (days)
2017	21/9/17			assigned
2018	21/9/18	8/9/18	3/10/18	25
2019A1	5/8/19	25/7/19	31/8/19	37
2019A2	11/8/19	27/7/19	31/8/19	35
2019B	19/9/19	17/8/19	22/9/19	36

The additional naturally mated 2019A cohort were joined in November 2018 and born in April 2019. Due to natural mating, there was a large range of ages and therefore weights so it was decided the lightest 22 would be finished with the 2019B AI lambs and so were managed this way for at least 3 months. Thus, the 2019A cohort was split into 2019A1 and 2019A2 with the 2019A2 group slaughtered on the same day (29/4/20) as the 2019B AI cohort (Table 2).

Table 2. Numbers of lambs slaughtered for four birth groups and five slaughter days

Birth Year and contemporary group	18/4/2018	19/4/2018	10/4/2019	1/4/2020	29/4/2020
2017	104	104			
2018			228		
2019A1				176	
2019A2					22
2019B					104

The fixed effects of sex, type of birth and type of rearing were recorded on the majority of lambs as presented below:

Female	Male	NA	Total
371	353	40	764

Type	Single	Twin	Triple	NA	Total
Birth	222	450	82	10	764
Rearing	291	398	45	30	764

3.2 Genotypes provided to Resource flock

During the trial tissue sampling units (TSUs) were taken from all the lambs. These were sent to Neogen in Nov 2020 for Genotyping (50K SNP). At the same time TSUs or semen samples from most of the

sires in the trial were sent for genotyping on high density (600k) chips. The genotyping has recently been completed and is being used to verify sire. 37 out of 44 sires have been genotyped with progeny numbers listed (Table 3). After receiving the genotype data and processing, there were 36 sires genotyped on Ovine-HD 600K, 764 progeny genotyped on GGP Ovine 50K and a single additional sire genotyped on GGP Ovine 50K. Advances in the genotyping chips enabled the sires to be genotyped at much higher density than originally planned.

All progeny in the dataset were imputed from 45,740 SNPs to high density (570,293 SNPs) utilising the 36 high density genotyped sires as the reference population. Duplicated SNP positions and X and Y chromosome SNPs were removed prior to imputation. Imputation was completed using Fimpute3 (Sargolzaei *et al.* 2014). The imputed dataset, including the reference sires, was then filtered to remove SNPs with a minor allele frequency less than 0.01 and was checked for duplicate samples. Two separate samples were found to have the same tag, but different genotypes, so due to the possibility of miss labelling, these two samples were removed to give a total of 798 samples for GRM construction.

Homozygous genotypes for the major allele were coded as 0, for the minor allele as 2, and heterozygous genotypes as 1. The GRM with 798 animals was constructed as per VanRaden's first method (VanRaden 2008);

$$\boldsymbol{G} = \frac{\boldsymbol{ZZ'}}{2\sum_{i=1}^{n} p_i(1-p_i)}$$

Where **Z** denotes a centred matrix of allele effects with a mean of zero, p_i is the frequency of the minor allele at locus i and division by $\mathbf{2}\sum p_i(1-p_i)$ scales the **G** matrix to be similar in magnitude (so that diagonal elements average 1) to the numerator relationship matrix constructed from genealogy (VanRaden 2008).

Table 3. Studs, sires and numbers of progeny

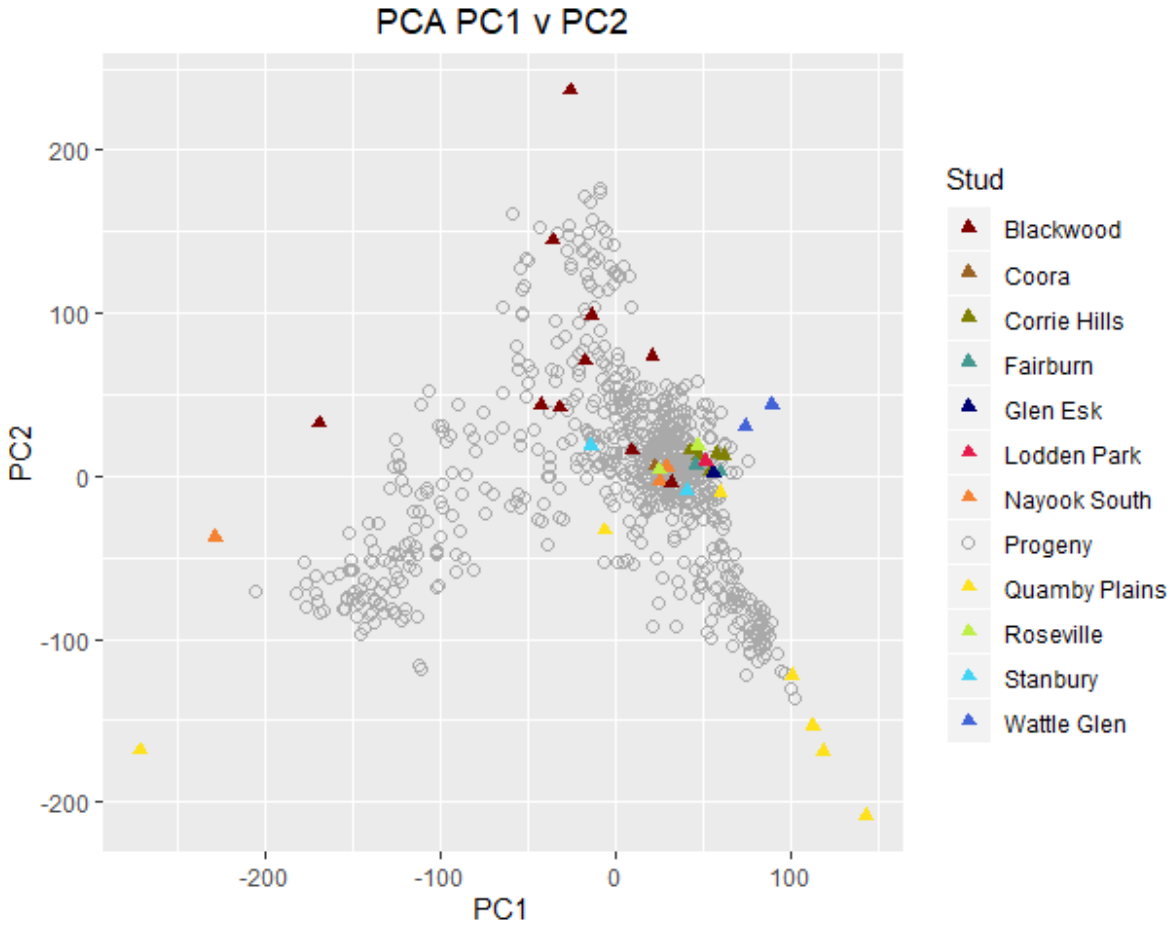
Stud	Sire Sheep Genetics ID	No. of Progeny	Genotyped
Quamby Plains	030036-2010-100650	16	Yes
Quamby Plains	030036-2011-110270	13	Yes
Quamby Plains	030036-2013-130393	15	Yes
Quamby Plains	030036-2014-140276	7	Yes
Quamby Plains	030036-2016-160064	27	Yes
Quamby Plains	030036-2016-160325	26	Yes
Quamby Plains	030036-2016-160334	12	Yes
Quamby Plains	030036-2016-160001	42	Yes
Quamby Plains	030036-2014-140060	?	No
Quamby Plains	030036-2017-170066	60	Yes
Quamby Plains	030036-2017-170150	24	Yes
Corrie Hills	030106-2014-140145	14	Yes
Corrie Hills	030106-2015-150159	15	Yes
Corrie Hills	030106-2016-160176	15	Yes
Corrie Hills	030106-2017-170057	16	Yes
Corrie Hills	030106-2017-170251	18	Yes
Fairburn	030136-2011-110021	17	Yes
Fairburn	030136-2017-171005	24	Yes
Glen Esk	031315-2015-155235	19	Yes
Stanbury WCH	031460-2012-120308	14	Yes
Stanbury WCH	031460-2012-121211	21	Yes
Coora	031897-2006-060262	18	Yes
Lodden Park	032062-2012-120534	19	Yes
Wattle Glen	032145-2015-150004	12	Yes
Wattle Glen	032145-2016-160094	32	Yes
Nayook South	032272-2014-140059	18	Yes
Nayook South	032272-2015-150160	1	Yes
Nayook South	032272-2016-160010	12	Yes
Nayook South	032272-2016-160213	15	Yes
Roseville	032361-2006-060209	19	Yes
Roseville	032361-2015-150423	15	Yes
Roseville	032361-2016-160049	17	Yes
Sweetfield	032382-2017-170076	1	Yes
Blackwood	032401-2012-120085	17	Yes
Blackwood	032401-2014-140033	19	Yes
Blackwood	032401-2014-140093	7	Yes
Blackwood	032401-2015-150175	11	Yes
Blackwood	032401-2017-170049	27	Yes
Blackwood	032401-2017-170030	26	Yes
Blackwood	032401-2017-170055	15	Yes
Blackwood	032401-2017-170113	43	Yes
Blackwood	032401-2016-160002	?	No
Blackwood	032401-2016-160128	?	No
Blackwood	032401-2016-160128	?	No

Sires with unknown progeny numbers were naturally mated in teams and did not have progeny clearly assigned to them.

Team scoring visual traits. Feb 2020

Relationships between animals are represented by plotting the first and second principal component (Figure 1). There were some surprises in the relationships shown. The ewes in the trial were sourced from Blackwood and Quamby Plains and both studs have been selecting for similar breeding objective. Thus, they were expected to be more closely related than is evident from the graph. Other studs such as Wattle Glen have been a closed flock for some time and were expected to be quite different. They were not close to other sires, but closer than expected. Many of the other studs grouped similarly demonstrating close relationships between Stanbury, Roseville, Corriedale Hills, Fairburn, Glen Esk, Loddon Park and two of Nayook South's sires.

Figure 1. Principal component plot of relationships from imputed 600k HD data between animals showing which studs the sires came from



1.4 Live animal measurements

The project has a very committed and active team from NSW, Victoria, SA and Tasmania. On 14-19th Feb 2018 the group met at Cressy Research Farm, Tasmania, and collected measurements/scores on 28 traits on the 212 lambs that survived to weaning. This was conducted again on 1-3rd March 2019 and 28-29th February 2020. Many (23) traits have been recorded by the group plus additional regular liveweights (Table 4).

Sarah Welsh recording data, February 2020.

Table 4. Summary of live data collected and prepared for analysis (the primary differences in number of measurements are due to the numbers of cohorts where they were measured)

Trait	n	Mean	SD	Min	Max
Weaning weight (kg)	745	32.7	7.6	13.6	54.5
Post weaning weight (kg)	644	39.6	5.5	21.0	55.0
Height (cm)	341	65.3	3.5	53.0	73.0
Greasy fleece weight (kg)	551	1.81	0.39	0.60	3.00
Fibre diameter (um)	551	23.1	1.8	18.2	29.3
Staple length (cm)	316	4.92	0.88	2.50	7.00
Comfort factor (%)	551	93.4	6.2	55.8	99.9
PEMD Scan (mm)	731	26.4	2.7	17.5	37.0
PFAT Scan (mm)	731	3.52	0.92	2.00	7.50
Pigment nose	366	3.7	0.8	1.0	5.0
Pigment hooves	366	4.1	0.7	1.7	5.0
Face cover	571	2.7	1.0	1	4.8
Jaw conformation	365	1.0	0.7	1.0	3.7
Leg conformation	573	2.1	0.8	1.0	4.0
Back conformation	366	1.6	0.6	1.0	3.7
Body Wrinkle	574	1.3	0.5	1.0	4.0
Staple structure	574	2.6	0.6	1.0	4.3
Wool colour	573	2.3	0.8	1.0	5.0
Wool character	573	2.7	0.6	1.0	4.3
Crimps	208	57.2	1.1	54	60
Breech wrinkle	233	1.2	0.2	1.0	1.7
Breech cover	233	4.0	0.3	2.0	4.8

1.5 Carcass and meat measurements

Unfortunately, getting the lambs booked into an abattoir with DXA measurement of lean meat yield in 2018 was not possible due to the large number of research kills being conducted at JBS. Thus, we killed the lambs at Frewstal, Stawell Vic 17-19th April 2018. The team of staff at Frewstal were superb which made processing relatively straight forward. In 2019, after discussion with Sheep Genetics, it was decided that it was better to foster the relationship with Frewstal than get yield on just a portion of the lambs.

Lambs were killed one day, hot standard carcass weight is recorded, GR fat depth recorded, pH is measured at 3 times and then are boned out the next day. There is quite a lot of work in the boning room on day 2 as the team recorded ultimate pH, collected loin samples, measured fat depth (C-Fat) and eye muscle depth and width, and meat colour. Three samples were then packed for measurement of intramuscular fat content and shear force. Given the large amount of work in the boning room the 212 lambs were killed over 2 days in 2018. In 2019, the 235 lambs were killed on a single day, but processed over 2 days. In 2019 it was decided that holding lambs in lairage would have a greater impact on meat quality than killing on a single day and processing in the boning room over 2 days. Kill day or processing day are included in the models as contemporary group definitions for analysing meat quality data. Samples were then transported to University of Adelaide for subsequent testing. All protocols matched the Sheep CRC standards and kill and processing day was recorded.

At Adelaide University there is a meat science laboratory with shared equipment with SARDI. Emma Winslow from SARDI led the team for the slaughter in 2018 but was on maternity leave in 2019. MEQ probe (meat eating quality) is a spin-out company from University of Adelaide's Centre for NanoScale BioPhotonics (CNBP). They are commercialising a probe for testing IMF and other meat quality factors in beef and lamb. During 2019 the MEQ team joined our meat science laboratory which provided additional equipment and people with experience in meat science. Thus, in 2019 the MEQ team were used to help support them financially and provide an opportunity for MEQ measurement on an additional cohort of lambs. The MEQ probe measurements were part of MLA project P.PSH.1132 and our IMF measurements have been supplied to them also. In 2020 MEQ left the Campus and moved to Gundagai so the IMF samples from final two slaughter groups were processed at UNE.

Initially the aim was to have carcasses averaging 24kg and so the plan was to kill lightest half of the lambs a month later to give them time to grow out. However, due to changes in management at Cressy, it became difficult to grow lambs out as heavy as desired with 35 (8%) being less than 16kg (Figure 1). The average was 19.5kg with a range from 12.6-26.7kg and lambs in 2019 were slightly heavier than 2018.

The difference in slaughter date between 2019A1 and 2019A2 was only 4 weeks so separating the light lambs appears unnecessary. However, this was right at the start of COVID-19 restrictions and there were significant delays in that slaughter. The upside of this was that the 2019A1 lambs were heavier than other groups but the downside of COVID-19 was that we could not get our research teams into the abattoirs. There was a real risk of losing all the slaughter data and definitely no chance of getting pH decline and other abattoir measurements.

We were very fortunate to have developed a strong working relationship with staff at Frestal abattoir. Specifically, Dale Flanagan and Robert Frews and his staff and livestock buyers have been incredibly helpful. Dale organised for tracking of body number and boned out shortloins to be collected from the boning room, cryovacced, body number written on the bag, packing in boxes, ageing for five days, freezing and then transporting to SA. Our correlation between liveweight and carcass weights suggests identification has remained intact. The industry owes a lot to the priority placed on the information by Dale and colleagues. The DXA scanner was not installed at Frewstal in time for our slaughters and no other plant with DXA would take the lambs so we do not have accurate lean meat yield data. Many traits have been recorded (Table 5), but not fat melting point as planned, due to difficulty and cost.

Table 5. Summary of carcass traits prepared for analysis

Trait	n	Mean	SD	Min	Max
Hot std. carcass weight (kg)	736	20.6	3.5	11.3	32.90
GR Fat (mm)	435	7.5	5.6	0.5	25.0
Eye muscle depth (mm)	436	41.4	12.8	21.5	63.0
Eye muscle width (mm)	436	42.3	13.2	20.0	66.0
Eye muscle area (cm^2)	436	12.8	1.8	7.7	18.4
Lean meat yield (%)	366	58.6	2.1	53.1	61.4
pH ultimate LL	601	5.79	0.18	5.18	6.66
Temp ultimate LL	601	2.39	2.54	-0.70	12.9
pH ultimate ST	208	5.96	0.23	5.47	6.93
Temp ultimate ST	208	1.59	0.36	0.50	2.8
L	204	33.4	2.2	27.6	40.6
a	204	16.4	1.4	12.6	19.9
b	204	5.3	1.0	2.4	8.3
Carcass marbling score	171	1.3	0.7	0.0	3.0
Lab marbling score	123	2.2	0.5	1.0	4.0
Lab temp (^oC)	123	8.69	2.62	1.00	15.30
Lab pH	123	5.89	0.27	5.50	6.66
Cooking loss (%)	122	27.6	2.6	21.8	36.1
Shear Force (N)	715	39.5	13.4	17.0	99.3
Intramuscular fat (%)	732	4.66	1.48	1.43	11.61

The two traits that are measured as primary indications of carcass quality are intramuscular fat content (IMF, %) and tenderness measured as shear force in Newtons. The aim for heavy carcass weights was to achieve maximum expression of variation in intramuscular fat (IMF), but there was still ample variation (1.4-11.6%, Figure 2) with a mean of 4.7% at a mean carcass weight of 20.6kg. It is expected that the lighter and leaner lambs were more susceptible to cold shortening which is likely the cause of some very high shear force values at low IMF (Figure 2). The spread of data is completely in line with similar industry data sets being collected at present including those presented at the annual ALMTech review in April.

Figure 2. Distribution of carcass weights for lambs processed across all cohorts

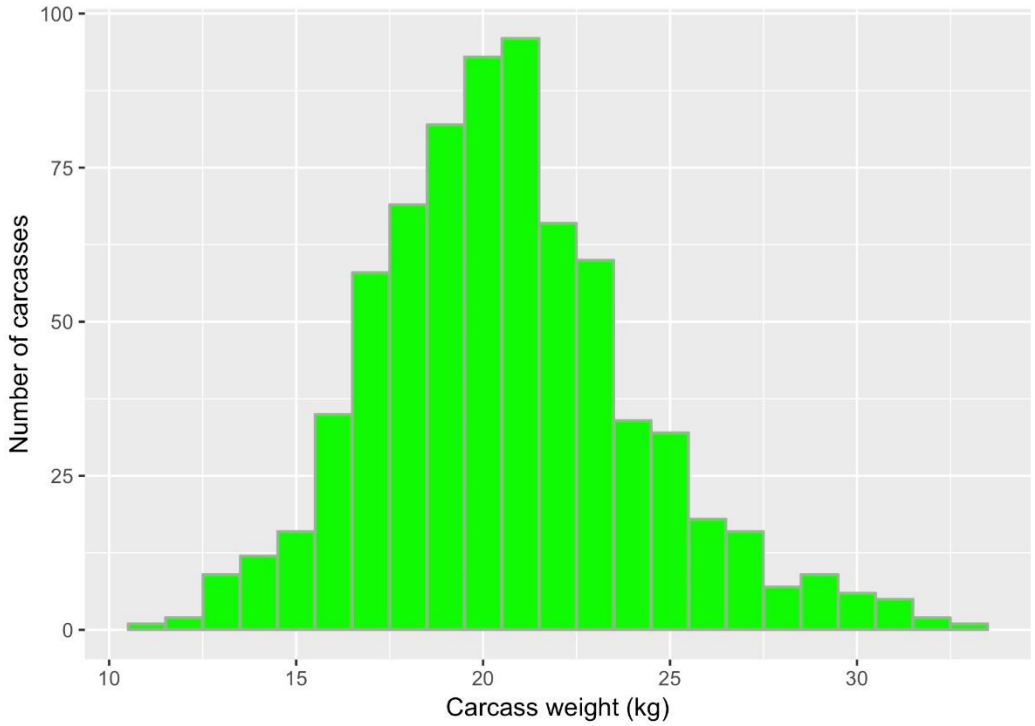


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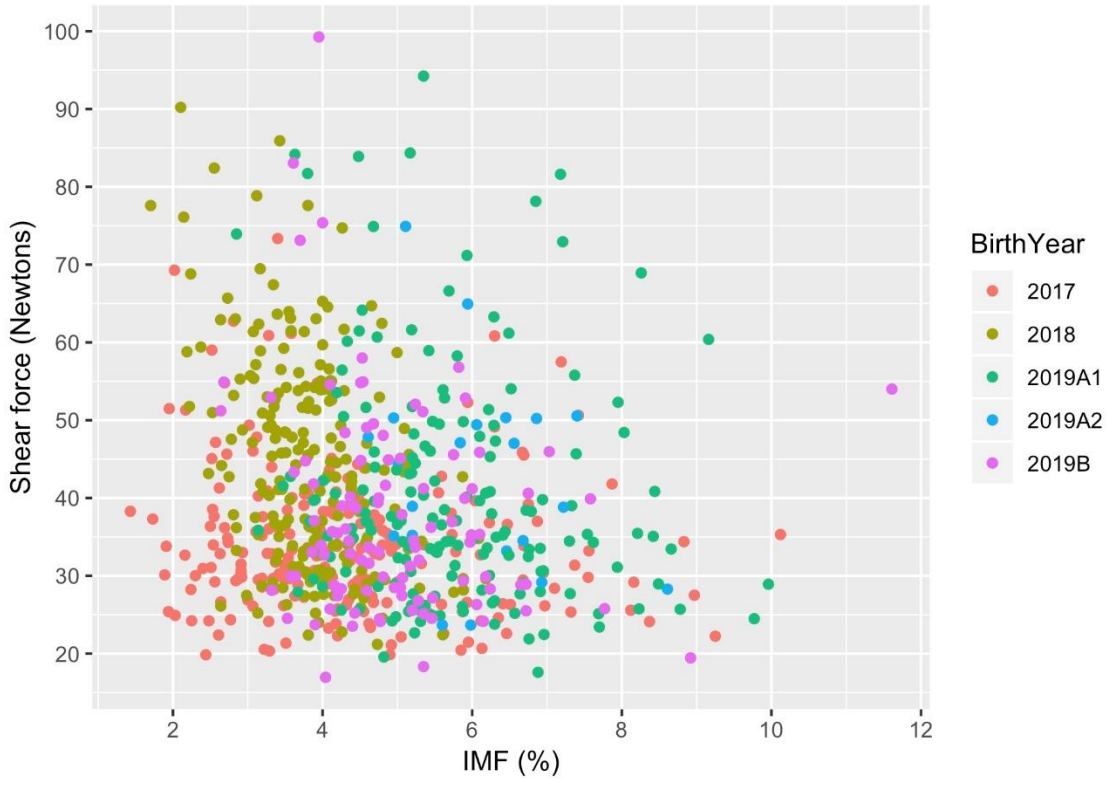
Figure 3. Relationship between tenderness (shear force after 5 days ageing) and intramuscular fat content (IMF) with different contemporary groups shown



1.6 Sheep Genetics data submission and reporting

We have been careful not to release any data to breeders other than through Sheep Genetics so that we can 1) encourage breeders to use the Australian Sheep Breeding Values (ASBV's) reported by Sheep Genetics; and 2) only one estimated breeding value is presented to prevent confusion.

There have been many traits measured as outlined in Table 1. Data for core Sheep Genetics traits were supplied to Sheep Genetics in September 2018 and throughout the trial. Sheep Genetics have been working on improving the pipeline of flow of data from research and resource flocks. There are relatively simple issues such as 16 digit codes on all lambs and sires. This is simple for sires currently in Sheep Genetics as they already have 16 digit code data. Sires that are from studs which are not part of Sheep Genetics can have codes formed based on the same logic as others (i.e. breed, flock, year, number). The issue of how breeders who submitted sires but are not members of Sheep Genetics will receive data and, therefore, value from the project still needs to be resolved. Project values (not ASBVs but calculated similarly) for all traits have been reported to all contributing breeders.

1.7 Genomic analysis

The data was analysed with three different models:

1. Birth group (2017, 2018, 2019A, 2019B) as there were two drops born in 2019, 2019A was naturally mated and2019B like 2017 and 2018 were by AI. This was fitted to weaning and post-weaning weight, height, scan eye muscle depth, scan fat depth and wool traits.
2. Contemporary Group (2017, 2018, 2019A1, 2019A2, 2019B) as the 22 lightest lambs from the 2019A drop were not going to make market weights in time and so were finished with the 2019B group. This was fitted to all live scores and traits other than those above.
3. Contemporary group (2017, 2018, 2019A1, 2019A2, 2019B) plus kill day (April 2018 day 1&2, April 2019 day 1&2, April 2020a, April 2020b) as the first two birth groups were killed across two days. Note that the 2019A2 and 2019B contemporary groups were finished and processed together. This was fitted to all carcass and meat quality traits.

All models also included type of birth and rearing (4 levels: born and raised single, born multiple raised single, born multiple raise twin or born and raised triplet), sex (ewe, wether), heterozygosity fraction (range 1.7-34.8, mean =34.2%) and the random genomic relationship matrix based on imputed genotypes from the progeny 50K to sire 600k HD. Day of birth was not recorded for the 2017 drop and was not significant for carcass traits so was not included in the models.

In the absence of other data from Sheep Genetics, this trial lacks numbers to achieve accurate parameter estimation. Genetic variance was not able to be estimated for six traits: scanned fat depth, jaw structure, shear force, eye muscle depth from dissected loin, calculated eye muscle area and ultimate pH. For traits like fat depth and jaw structure, there was likely simply insufficient variation. Eye muscle depth and area were likely not measured sufficiently accurately. pH is commonly lowly heritable with large impacts from processing. Unfortunately shear force (toughness) which is a primary trait of interest was not heritable. This is likely due to variable cooling within the chiller resulting in large variation (Figure 2) due to cold-shortening (processing factors) that has dwarfed the genetic variation.

The phenotypic variances herein are similar to those reported by Mortimer et al. (2017, 2018). The wool and scored traits were more heritable than reported by Mortimer et al. (2017). Examples are

GFW (0.755 vs 0.57) and FD (0.821 vs 0.74). Wool colour (0.47, Table 6) was also higher than brightness (0.19) but breech wrinkle was lower (0.164 vs 0.33), likely reflecting the much plainer body of and less variation among Corriedales than Merinos.

Heritabilities for growth traits were consistently higher than those reported by Mortimer et al. (2017), 0.542 and 0.589 (Table 6) vs 0.14 and 0.31 (Mortimer et al. 2017) for weaning and post-weaning weights respectively. The heritability of post-weaning eye muscle depth herein (0.472) was higher to Mortimer et al. (2017) estimate (0.14).

Mortimer et al. (2018) reported genetic parameters for carcass and meat quality traits similar to those herein but most were lower. The Corriedale heritability estimates for HSCW herein (0.63 and 0.464) a stark example (0.35). Mortimer et al. (2018) did report similar heritability for intramuscular fat (0.58) and shear force (0.10) with the estimates herein were 0.464 and 0.154 respectively.

The heterozygosity on some animals (e.g. minimum 1.7% was lower than other livestock data sets we have analysed and potentially indicates a higher level of inbreeding in Corriedale than other livestock. If there is genuinely less genetic diversity than for other breeds, then the heritability would be expected to be lower but there was not strong evidence of that.

The genetic correlations were able to be estimated for most traits. Carcass weight was very highly genetically correlated with weight at other times (0.91 and 0.93) and with eye muscle depth (0.74), fat depth (0.62) and height (0.59, Table 6). It was also strongly correlated with shear force (-0.83) so heavier carcasses had more tender meat. Correlations between carcass weight and wool traits were low (0.04-0.20) although staple structure score was much higher (0.56).

Intramuscular fat was correlated with growth (0.42) and carcass weight (0.39) and scanned fat depth (0.64). It was moderately correlated with fibre diameter (0.35), staple length (-0.48) and surprisingly strong negatively with hoof pigment (-0.60) and breech wrinkle (-0.51). It was also negatively correlated with pH indicating higher IMF was associated with favourable pH, presumably because of the correlation with increased fat cover.

Table 6. Phenotypic variation, heritability and genetic correlations with carcass weight and intramuscular fat

TRAIT	Phenotypic SD	Heritability	h^2 SE	r_G with HSCW	r_G with IMF
Weaning wt (kg)	4.6	0.542	0.094	0.91	0.28
Post Weaning wt (kg)	4.9	0.589	0.104	0.93	0.42
Height (cm)	2.4	0.485	0.158	0.59	0.36
Scan EMD (mm)	2.4	0.472	0.091	0.74	0.31
Scan fat (mm)	0.9	0.489	0.102	0.62	0.64
Greasy fleece wt (kg)	0.3	0.755	0.105	0.17	0.19
Fibre diameter (μm)	1.8	0.821	0.097	0.14	0.35
Staple length (cm)	0.8	0.214	0.138	0.20	-0.48
Comfort factor (%)	6.1	0.610	0.110	0.04	-0.28
Nose pigment (score)	0.77	0.571	0.151	-0.16	-0.25
Hoof Pigment (score)	0.71	0.533	0.160	-0.39	-0.60
Face cover (score)	0.55	0.383	0.108	-0.26	-0.18
Jaw structure (score)	0.05	0	0	-	-
Leg structure (score)	0.38	0	0.056	-0.29	0.27
Back structure (score)	0.33	0.232	0.105	-0.31	-0.39
Breech wrinkle (score)	0.46	0.164	0.086	-0.06	-0.51
Staple structure (score)	0.58	0.275	0.095	-0.56	0.14
Colour (score)	0.63	0.470	0.104	0.14	-0.06
Character (score)	0.58	0.408	0.109	0.02	0.25
HSCW (kg)	2.7	0.630	0.093	1	0.39
Shear force (N)	12.9	0.154	0.074	-0.83	-0.33
IMF (%)	1.26	0.464	0.096	0.39	1
GRFat (mm)	2.6	0.504	0.139	0.47	0.44
EMD (mm)	3.1	0.388	0.120	0.72	0.23
EMW (mm)	3.3	0.352	0.132	0.60	-0.50
EMA (cm^2)	1.7	0.448	0.137	0.81	0.13
LMY (%)	0.81	0.437	0.131	0.07	-0.25
pHuLL	0.150	0.063	0.063	-0.04	-0.60

4. Honours students associated with P.PSH.1001

One of the delights of this project is the involvement of Honours students. Both the students and producers have greatly enjoyed the interaction at the Performance Group meetings and the project is an ideal training opportunity. In 2018 we had Hannah Gordon and she also presented at the Corriedale World Congress in Ballarat in July 2018. Hannah was a tremendous advocate for the trial and recruited Sarah Welsh for 2019. Both students have competed in Intercollegiate Meat Judging during their 3rd year and helped with coaching the team during their Honours year. Hannah is now working at Cox Rural as a livestock production specialist in her local town (Coonalpyn, SA) and is able to continue close involvement in her family farm. Sarah has not come from a farming background but is very keen and a passionate advocate for the sheep industry. She is currently doing a Masters in Education and planning to be a High School Agriculture teacher.

5. Conclusions

5.1 Key findings and industry benefits

Data were collected for live, carcass and meat quality traits. The data will be supplied to Sheep Genetics to increase accuracy of ASBVs for Corriedale breeders as well as provide information on traits that are not part of routine reporting. Work with the Performance Corriedale Group has been a good experience for the researchers, students and breeders. It is hoped that the project will lead to other Corriedale breeders joining Sheep Genetics and the Performance Corriedale Group.

5.2 Model of engagement of smaller breeds

This project provides a model for engagement with small breeds and we have been asked to specifically comment on the merits of such a model. The starting point should be a description of the history and model.

All breeds societies that aspire to breed sheep for production need a group of breeders committed to performance recording. Performance groups provide a forum for sharing ideas, challenging each other, critical mass to engage Sheep Genetics staff and other advisors, and a collection of people who inform innovation opportunities. The Corriedale Performance Group has all of those attributes.

Smaller breeds, almost by definition, sell less rams and generally receive less for rams than those from more numeric breeds and so have less ability to invest cash in projects. The model for this project was to charge $1000 plus semen for each sire (total $45,000) to be tested. This was then matched with $1778/sire (total $80,000) from the Davies Livestock Research Centre and $2778/sire (total $125,000) from the MLA Donor Company. The MDC retains 12% ($26,763 or $595 per sire) as an access fee but operationally breeders leveraged an additional $4 to their $1 invested. Overall, the project was industry initiated, provided valuable data for Sheep Genetics, leveraged funds and captured significant in-kind contribution from the University, Corriedale Performance Breeder Group and especially Peter and Claire Blackwood (Blackwood Corriedales) who ran the trial during some difficult times.

It is good for researchers to work with producer groups like the Performance Corriedale Group. Often there is some history that initiates the connection as in this case, but it is wise for all early career livestock researchers to try and link with such a group. The benefits for the group are links to

researchers and their networks and the benefit for researchers is ground truthing research and an ideal format for testing new ideas and ways of communicating findings.

This project was excellent for training Honours students and it should be an aim for all Agricultural and Animal Science Honours students to be involved in projects with industry to build networks and skills in addition to research skills. Hannah Gordon was involved in 2018 and Sarah Welsh in 2019. Hannah was able to present initial results at the World Corriedale Conference in Bendigo in 2018.

It was hoped that the trial would attract new breeders to Sheep Genetics and reporting of results is primarily through Sheep Genetics to ensure the most accurate ASBVs are reported. ASBVs are published by Sheep Genetics for all animals owned by members and sires and dams of those animals. Ensuring value for breeders who are not part of Sheep Genetics but submitted sires and invested in the project by reporting performance still needs to be resolved..

As stated above, there is no doubt that it is good for researchers to be working with producer groups and for Honours students to be trained in a commercial environment. However, there are three realities that should be raised and worthy of consideration when establishing future projects.

1. The in-kind contribution of Peter and Claire Blackwood into the project has been outstanding and well above the level that should be expected.
2. If there is not a clear mechanism for achieving a research publication then the researchers have effectively been providing a subsidised technical service rather than being genuine collaborators.

The system is not perfect but partnerships between producers and researchers are incredibly rewarding for both and going beyond the call of duty is common for good reason. Funding bodies should not trade on good–will, but equally economic rationalists should not get in the way of committed people with a common purpose. Thus, it is exciting to see increasing numbers of projects being funded through resource flock coordination and this should be extended as broadly as possible, especially when there are groups of producers collecting performance information in a coordinated way.

6. References

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