PERFORMANCE CORRIEDALE GROUP GENOMICS PROJECT

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SUMMARY

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 project achieved 764 carcasses from 44 sires (12 studs) from 3 AI and 1 natural mating in 2017-19. Lambs were slaughtered at 6-7 months with carcass and meat quality data, wool and type traits recorded. The data from the project will contribute to the Sheep Genetics database. The project also provides a model for engagement of breeds which are lower in number but still significant in impact.

INTRODUCTION

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 and there is ongoing recording through the MLA Resource Flock, there are insufficient records for the genomic tests to be valuable to Corriedale breeders.

The project was initiated by the Performance Corriedale Group who only account for 11% of registered Corriedales, but accounted for over 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 45 sires representing 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.

MATERIALS AND METHODS

In April of 2017-19, approximately 300 Corriedale ewes were synchronised and 20 inseminated to each sire provided. An additional natural mating was conducted in late 2018 to generate additional lambs for the project so lambs were born in four cohorts (2017, 2018, 2019A, 2019B). In total there were 44 sires from 12 studs used, some across years so the number of lambs per sire ranged from 1-60.

Lambs were slaughtered in April the following year. For the 2017 cohort, there were consecutive slaughter days. The 2019 born lambs were slaughtered in two groups where a small number (22) of the lightest 2019A born lambs were finished and slaughtered with the 2019B, so there are five slaughter cohorts (2017, 2018, 2019A1, 2019A2, 2019B). The number of carcasses in 2017 cohort was 212, 2018 was 233, 2019A1 was 175, 2019A2 was 22 and 2019B was 103.

Ewes were scanned for number of fetuses (0-3) and lambs were mothered up for recording type of birth (1-3) and rearing (1-3) with four combined classes resulting (11, 21, 22, 33). The very few triplet born lambs not raised as triplets were treated as multiples for type of birth and grouped with

classes 21 and 22 for those raised as singles or twins respectively. Lamb survival rates were good with carcasses comprising 30% singles, just 11% born multiple raised single, 54% twins and 6% triplets.

Live traits included multiple weights, height, scanned fat and eye muscle depth, greasy fleece weight, fibre diameter, comfort factor and staple length, scores for nose and hoof pigment, face cover, jaw and leg conformation, back conformation, body and breech wrinkle, breech cover, wool staple structure, wool colour and character. Carcass and meat traits included carcass weight, GR fat depth, loin eye muscle depth, width and calculated area, calculated lean meat yield, pH decline and ultimate, meat colour (L, a, b), cooking loss, shear force and intramuscular fat content. Not all traits were measured on all cohorts either because it was not possible to enter the abattoir in 2020 due to COVID-19 (e.g. loin dimensions and pH decline), slight differences in laboratory procedures (e.g. meat colour), not shorn (e.g. greasy fleece weight), or the scores lacked variation and were of limited value (e.g. jaw confirmation and breech wrinkle and cover). Muscle and fat depths presented herein have not been adjusted for weight (live or carcass).

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. 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 800 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);

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

Where $\mathbf{Z}$ 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 $\mathbf{G}$ matrix to be similar in magnitude (so that diagonal elements average 1) to the numerator relationship matrix constructed from genealogy (VanRaden 2008).

The model fit to most traits included the random genomic relationship matrix and fixed effects of cohort (2017, 2018, 2019A1, 2019A2, 2019B), sex (ewe, wether) and type of birth and rearing (11, 21, 22, 33). Kill day within 2017 was added to carcass traits and birth group (2017, 2018, 2019A, 2019B) was used for weaning weight as it was recorded before the 2019A drop were split.

RESULTS AND DISCUSSION

The phenotypic variances herein (Table 1) are similar to those reported by Mortimer et al. (2017, 2018) so it is assumed the lower heritability estimates are primarily due to small numbers. However, 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 lower. That said, the mean was close to the maximum and so this could also be a function of a very small number of highly inbred animals.

The wool and scored traits were similar with many slightly more heritable than reported by Mortimer et al. (2017). Examples are GFW (0.76 vs 0.57) and FD (0.82 vs 0.74). Of the scored

traits, colour (0.47) was similar to yellowness (0.80) but wrinkle was lower (0.16 vs 0.34), likely reflecting the much plainer body of Corriedales than Merinos.

Heritabilities for growth traits were consistently higher than those reported by Mortimer et al. (2017) but there was no maternal effect fitted herein: 0.54 vs 0.14 for weaning weight, 0.59 vs 0.31 for post-weaning weight, 0.49 vs 0.11 for scanned fat depth and 0.47 vs 0.14 for scan eye muscle depth.

Compared to Mortimer et al. (2018), carcass traits herein were also often more highly heritable. Examples include carcass weight (0.63 vs 0.35), GR fat (0.50 vs 0.23), lean meat yield (0.55 vs 0.29), intramuscular fat (0.46 vs 0.58), shear force (0.15 vs 0.10), and pH (0.06 vs 0.15).

Table 1. Data description, summary and heritabilities

Trait	Mean	Min	Max	σ_P	h^2	h^2 SE
Weaning Weight (kg)	32.6	13.6	54.5	4.6	0.54	0.09
Post Weaning Weight (kg)	39.6	21.0	55.0	4.9	0.59	0.10
Height (cm)	63.4	51.9	73.0	2.4	0.49	0.16
Scan Eye Muscle Depth (mm)	26.4	17.5	37.0	2.4	0.47	0.09
Scan Fat depth (mm)	3.5	2.0	7.5	0.9	0.49	0.10
Greasy Fleece Weight (kg)	1.81	0.6	3.0	0.3	0.76	0.11
Fibre Diameter (um)	23.1	1.8	18.2	1.8	0.82	0.10
Comfort Factor (%)	93.5	55.8	99.9	6.1	0.61	0.11
Staple Length (cm)	4.83	0.7	2.5	8.4	0.21	0.14
Nose Pigment Score	3.7	1	5	0.8	0.57	0.15
Hoof Pigment Score	4.1	1	5	0.7	0.53	0.16
Face cover Score	2.7	1	5	0.6	0.38	0.11
Jaw Structure Score	1.0	1	4	0.1	0.00	0.06
Leg Structure Score	2.1	1	4	0.4	0.00	0.06
Back Structure Score	1.9	1	4	0.3	0.23	0.11
Body Wrinkle Score	1.3	1	4	0.5	0.16	0.09
Staple Structure Score	2.6	1	5	0.6	0.28	0.10
Colour Score	2.3	1	5	0.6	0.47	0.10
Character Score	2.7	1	5	0.6	0.41	0.11
Hot Std. Carcass weight (kg)	20.6	11.3	32.9	2.7	0.63	0.09
Shear Force (N)	39.5	17.0	99.3	12.9	0.15	0.07
Intramuscular fat (%)	4.66	1.43	11.61	1.3	0.46	0.10
GR Fat depth (mm)	10.9	1	25	2.6	0.50	0.14
Eye Muscle Depth (mm)	41.1	21	63	3.1	0.39	0.12
Eye Muscle Width (mm)	42.6	20	66	3.3	0.35	0.13
Eye Muscle Area (cm^2)	12.8	7.7	18.4	17.1	0.45	0.14
Lean Meat Yield (%)	55.3	50.8	60.1	1.1	0.55	0.21
pHuLL	5.79	5.13	6.66	0.2	0.06	0.06

CONCLUSIONS

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 breed 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 (aim $45,000) to be tested. This was then matched with funds from the Davies Livestock Research Centre and MLA Donor Company. 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.

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. The project trained two Honours students (HG and SW).

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. Sire genomic values for all traits have been reported to breeders. 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.

ACKNOWLEDGEMENTS

REFERENCES

Mortimer S.I., Hatcher S., Fogarty N.M., van der Werf J.H.J., Brown D.J., Swan A.A, Greef J.C., Refshauge G, Hocking Edwards J.E. and Gaunt G.M. (2017) *J. Anim. Sci.* **95**: 1879.

Mortimer S.I., Fogarty N.M., ven der Werf J.H.J., Brown D.J., Swan A.A., Jacob R.H., Geesink G.H. Hopkins D.L., Hocking Edwards J.E., Ponnampalam E.N., Warner R.D., Pearce K.L. and Pethick D.W. (2018) *J. Anim. Sci.* **96**: 3582.

Sargolzaei M, Chesnais J.P. and Schenkel F.S. (2014) *BMC Genomics* **15**: 478.

VanRaden. P.M. (2008) Efficient methods to compute genomic predictions. *J Dairy Sci.* **91**:4414.