



THE UNIVERSITY
of ADELAIDE

SA Merino Sire Evaluation

2024 drop – carcase outcomes

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1. Introduction

Good meat eating quality is driven by multiple traits which are influenced by genetic and environmental effects. Two key traits are intramuscular fat (IMF) and shear force after 5 days ageing (SF5).

Lean meat yield refers to the amount of lean in a carcass expressed as a percentage of hot standard carcass weight. Dual energy x-ray absorptiometry (DXA) is a precise and accurate method used to assess carcass composition, including lean, fat, and bone at chain speed in both the hot and cold carcass. DXA devices provide a lean meat yield estimate (DXA lean), with higher values indicating leaner carcasses (akin to lower fat score or GR). Lean meat yield has a high heritability in the range of 51% to 58%.

The percentage of intramuscular fat (IMF) is a major determinant of eating quality. IMF, visualised as marbling, is a measure of the chemical fat percentage in the lamb loin. An increase in IMF% has been shown to correlate with increased consumer perception of juiciness, tenderness, flavour, and overall liking with a minimum of 4% IMF preferred by consumers. The IMF range is typically between 2% and 7%. This trait is moderately to highly heritable and negatively correlated with SF5.

Shear force reflects consumer perception of tenderness and is measured as the force required to cut through a sample of cooked loin after five days ageing to allow for tenderisation from proteolytic ageing. Values for SF5 less than 3kg or 29.42N are desirable and represent more tender meat. SF5 is a moderately to highly heritable trait with a typical range from 1.1kg to 7.7kg.

Higher, or more positive values for DXA lean% and IMF% are favourable, whereas lower, more negative values are preferred for SF5. A balanced approach to selection for lean meat yield and meat quality is needed to ensure these negatively correlated traits do not work against each other.

2. Project purpose and outcomes

This project contributes to the SA Merino Sire Evaluation Site which has the outcome to provide an independent ram benchmarking service within SA for merino sires. Specifically, the purpose of this project was to enable collection of hard-to-measure meat eating quality phenotypes for IMF and SF5 from 2024 drop progeny of the 10 rams entered at the site. This will enable informed sire selection, increase breeding value accuracy of relatives, and augment the reference populations for these traits. This was achieved through completion of the following activities:

- 2024 Turretfield Research Centre drop wether lambs processed at JBS, Bordertown.
- Individual animal IMF% and SF5 samples collected and analysed.
- Collection of individual animal data for the progeny of 10 rams, including HSCW, GR tissue depth, eye muscle measurements, IMF%, SF5, and DXA carcass composition estimates.
- Fitting of a sire model to report on heritability, variance components, and sire predicted means across the sampled traits.

3. Methodology

3.1. Animal management

The South Australian Merino Sire Evaluation site at Turretfield Research Centre, Rosedale evaluated 10 rams (Table 1), each joined to 57 ewes via artificial insemination on 30 November to 1 December 2023. Ewes were pregnancy scanned and managed in one mob until just prior to lambing when they were separated into groups of single, twin-bearing, and triplet-bearing ewes until lambing commenced in late April 2024. Quadruplet bearing ewes and a single quintuplet bearing ewe were removed from the trial. Conception rate was recorded at 64%, with 57% of ewes scanned pregnant with multiples for a total of 442 progeny generated across the 10 rams. Sire pedigree was established by DNA testing.

Table 1 Summary of sires evaluated as part of the 2024 drop of the SA Merino Sire Evaluation Trial, including the sire code, the breeders flock and sire number, Sheep Genetics ID, and the sire of sire.

Sire Code	Breeders flock, sire number	Sheep Genetics ID	Sire of Sire (breeders flock, sire number)
GEL, 190140	Gelton Poll, 190140	601341-2019-190140	Unknown
GLE, 220386	Glenville Poll, 220386	600711-2022-220386	Ridgeway Advance, 190448
GUN, 220067	Gunallo Poll, 220067	600880-2022-220067	Mernowie, 200769
KEL, 221415	Kelvale Poll, 221415	600416-2022-221415	Kelvale Poll, 201309
MAL, 222357	Malleetech Poll, 222357	609533-2022-222357	Malleetech Poll, 199153
PEP, 222047	Pepper Well Poll, 222047	601351-2022-222047	Kelvale, 200022
PYR, 220220	Pyramid Poll, 220220	601381-2022-220220	Wiringa Park Poll, 200037
RIC, 170013*	Richmond, 170013	505021-2017-170013	Richmond, 130579
TRE, 210106	Trefusis Poll, 210106	601615-2021-210106	Alfoxtton Poll, 150459
WIR, 220450	Wiringa Park Poll, 220450	601445-2022-220450	Wiringa Park Poll, 200037

* indicates link sire included to provide a genetic link across years and sites.

Lamb marking occurred on 21 May 2024 and lambs were managed in the same lambing mobs until weaned at 12 weeks of age on 23 July 2024. Lambs were then managed in one mob on grass-based pasture and supplementary fed due to dry conditions. Lambs were crutched in October 2024, visually classed on 1 March 2025, shorn on 2 March 2025, and scanned for carcass traits on 26 March 2025. Following carcass scanning, lambs were split into sex groups and managed as two mobs. The wether lamb cohort was sold on 29 July, 2025 with approximately fifteen progeny per sire selected for meat eating quality evaluation. For some sires, avoiding selection of lambs of multiple birth type was not possible. A summary of sire's wether progeny is provided in Table 2.

Table 2 Summary of number of wether progeny per sire by birth (BT) and rearing type (RT), where 0 indicates non-survival, 1 indicates single, 2 indicates twin, and 3 indicates triplet.

	BT	1	1	2	2	2	3	3	3
	RT	0	1	0	1	2	0	1	2
<i>Sire Code</i>									Total
<i>GEL,, 190140</i>			1	1	4	13		3	22
<i>GLE, 220386</i>			8		2	8		3	21
<i>GUN, 220067</i>			11		3	8		3	25
<i>KEL, 221415</i>			9	1	9	4			23
<i>MAL, 222357</i>		1	8	1	4	8		4	29
<i>PEP, 222047</i>			4	1	2	12		2	21
<i>PYR, 220220</i>			12		5			1	18
<i>RIC, 170013*</i>			4		5	10		1	20
<i>TRE, 210106</i>			10		5	11	1	1	30
<i>WIR, 220450</i>			5		5	4		3	19

* indicates link sire included to provide a genetic link across years and sites.

3.2. Abattoir assessment

The wether cohort were consigned together and transported from Turretfield Research Centre, Rosedale to JBS, Bordertown on Tuesday 29th July 2025. Lambs were rested in lairage overnight then harvested on Wednesday 30th July 2025 and fabricated on Thursday 31st July 2025. All lambs consigned (n = 216) were subject to basic chiller assessment, and a subset (n = 152) representing approximately 15 lambs from each of the 10 sires entered were selected for further evaluation of eating quality traits. The basic chiller assessment on all 216 lambs included rib count, GR tissue depth, Hot Standard Carcase Weight (HSCW), palpated fat score, and DXA carcase composition estimates for lean, fat, and bone. In addition, loin eye width, loin eye depth, loin fat depth, loin eye muscle area (EMA), shear force after 5 days aging (SF5), and intramuscular fat content (IMF) were also recorded for the eating quality subset.

Electronic identification was scanned at the point of slaughter and carcasses were manually tagged to enable tracking through harvest and fabrication, and subsequent linkage to Sheep Genetics identification. Carcasses were trimmed to AUS-MEAT specifications and then weighed to determine HSCW. All carcasses were then subjected to electrical stimulation before entering the chiller where they remained overnight at 0-4°C. Approximately two hours after chiller entry tissue depth (mm) was recorded using a GR knife inserted over the 12th rib 110mm from the midline.

Carcasses were DXA scanned to assess lean, fat and bone composition then fabricated after approximately 24 hours of active chilling. The left-side loin sample was collected following preparation to AUS-MEAT specifications for short loin (H.A.M. item number 4881). Samples were vacuum sealed and refrigerated at approximately 4°C until further preparation. Samples were transported to the laboratory where loin eye measurements were recorded prior to deboning. Measurements at the cranial end of the loin included loin eye width, loin eye depth, and fat depth over the loin 45mm from the midline using digital calipers (150mm digital vernier, Kincome, Scoresby, Australia). This was followed by preparation of a denuded eye of short

loin (H.A.M. item number 5150), which was separated into a cranial and caudal piece for IMF and SF5 testing, respectively. A sample of approximately 45g was diced into 5mm cubes and placed in 50ml polypropylene tubes (Screw cap tube, Sarstedt, Nümbrecht, Germany), then frozen at -20°C until IMF analysis. Each SF5 sample was prepared with dimensions 60-70mm length, 40-50mm width, and 20-25mm depth to produce a weight of approximately 65g then individually vacuum sealed, aged at 4°C until day 5 post-slaughter, then frozen at -20°C until analysis (Sheep CRC, 2009).

3.3. Laboratory measured traits

Frozen IMF samples were appropriately packaged and transported to University of New England, Armidale for analysis. Samples were freeze dried and IMF% was determined using the procedure of near infrared reflectance spectroscopy (NIR). SF5 analysis was conducted following the Sheep CRC method (Sheep CRC, 2009). Briefly, frozen samples were weighed then cooked in a bag in batches using a water bath set at 71°C for 35 mins. Following cooking, samples were cooled in their bag under cold running water for 30 mins then removed from the bag, dried with paper towel, weighed, and stored in the refrigerator at 4°C until testing. Shear force after 5 days aging was determined using a Lloyd LRX texture analyser fitted with a Warner-Bratzler blade attachment programmed with a crosshead speed of 100.00mm/min. Samples were cut into 10mm thick pieces that were then sliced parallel to the muscle fibres into pieces approximately 8mm by 12mm. Six replicates from each sample were loaded into the Lloyd cutting chamber for testing such that the cutting line was perpendicular to the muscle fibres. Each of the six measurements were recorded (Newtons) and the mean, standard deviation, and coefficient of variation were calculated for each sample. The mean SF5 value was used for analysis unless the coefficient of variation was 24% or greater, in which case the median value was used.

3.4. Statistical analysis

Data were collated in Excel (Microsoft Corporation, 2018) then summarised, visualised, and analysed in R (R Core Team, 2021) using readxl (Wickham and Bryan, 2019), ggplot2 (Wickham, 2016), dplyr (Wickham *et al.*, 2021), tidyr (Wickham, 2021), biometryassist (Nielson *et al.*, 2025) and asreml (Butler, 2020). Asreml was used to fit linear mixed models to estimate heritability and generate sire predicted means for all traits. Basic chiller assessment traits included data from 216 lambs, and eating quality traits included data from the representative subset of 152 lambs. For all models, the trait being examined and birth type were fit as fixed effects, with sire included as a random term. The standard error is reported for each trait. In this trial only observations on sires were obtained, therefore due to the sire making up ¼ of additive genetic variance the following equation was used to estimate heritability:

$$h^2 = \frac{(4 \times \text{sire variance})}{(\text{sire variance} \times \text{residual variance})}$$

4. Results and discussion

4.1. Descriptive statistics

Descriptive statistics for the unadjusted live weight, chiller assessment, eating quality, carcass composition, and eye muscle area data are provided in Table 3. For each trait, the mean, minimum, maximum, standard deviation, and coefficient of variation (a measure of variability calculated by standard deviation/ mean and multiplied by 100) are reported. As expected in a progeny test, there was large variation across the cohort. This is important and demonstrates differences in performance between individuals within the same lifetime management group. Lambs weighed between 37.4kg and 82.4kg at the time of slaughter and 44.55% yielding carcasses with HSCW from 15.4kg to 39.0kg. GR tissue depth ranged from 3.00mm (fat score 1) to 30.00mm (fat score 5). Intramuscular fat and SF5 were variable traits, indicated by high coefficient of variation values, ranging from 3.22% to 12.46% and 23.94 N to 102.07 N, respectively, which are similar to values reported elsewhere (Mortimer *et al.*, 2014). An IMF above 4% is considered preferable and an impressive 93% of lambs sampled for eating quality traits exceeded this value. Only four lambs where eating quality traits were collected had a shear force below 29.42 N (3 kg), which is sought after to achieve tenderness. DXA lean averaged 49.47% with a range from 39.84% to 55.07%. DXA fat and DXA bone were more variable traits with a comparatively higher CV, and average of 39.62% and 10.98%, respectively. Loin EMA averaged 1635.99 mm² with a range from 964.42 mm² to 2523.74 mm². Loin eye depth was more variable than loin eye width as indicated by coefficient of variation. Loin fat depth ranged from 0.96mm to 8.81mm and was a highly variable trait, following the large variation observed in other fatness traits.

Table 3 Summary statistics for unadjusted carcass, eating quality, composition, and eye muscle measurements including mean, minimum, maximum, standard deviation (SD), and coefficient of variation (CV).

	Mean	Minimum	Maximum	SD	CV (%)
<i>HSCW (kg)</i>	25.72	15.40	39.00	3.50	14
<i>GR (mm)</i>	15.13	3.00	30.00	4.96	33
<i>IMF (%)</i>	6.39	3.22	12.46	1.88	29
<i>SF5 (N)</i>	53.88	23.94	102.07	15.10	28
<i>DEXA lean (%)</i>	49.47	39.84	55.07	2.62	5
<i>DEXA fat (%)</i>	39.62	31.57	53.44	3.76	9
<i>DEXA bone (%)</i>	10.98	6.83	13.40	1.13	10
<i>Loin eye depth (mm)</i>	25.25	17.20	34.10	3.53	14
<i>Loin eye width (mm)</i>	64.59	52.10	97.90	5.95	9
<i>Loin fat depth (mm)</i>	3.82	1.00	14.90	1.72	45
<i>EMA (mm²)</i>	1635.99	964.42	2523.74	305.69	19

4.2. Sire predictions

The predicted mean \pm standard error by sire for carcass traits where sire resulted in significant variation are presented in Figure 1 and include HSCW and GR tissue depth.

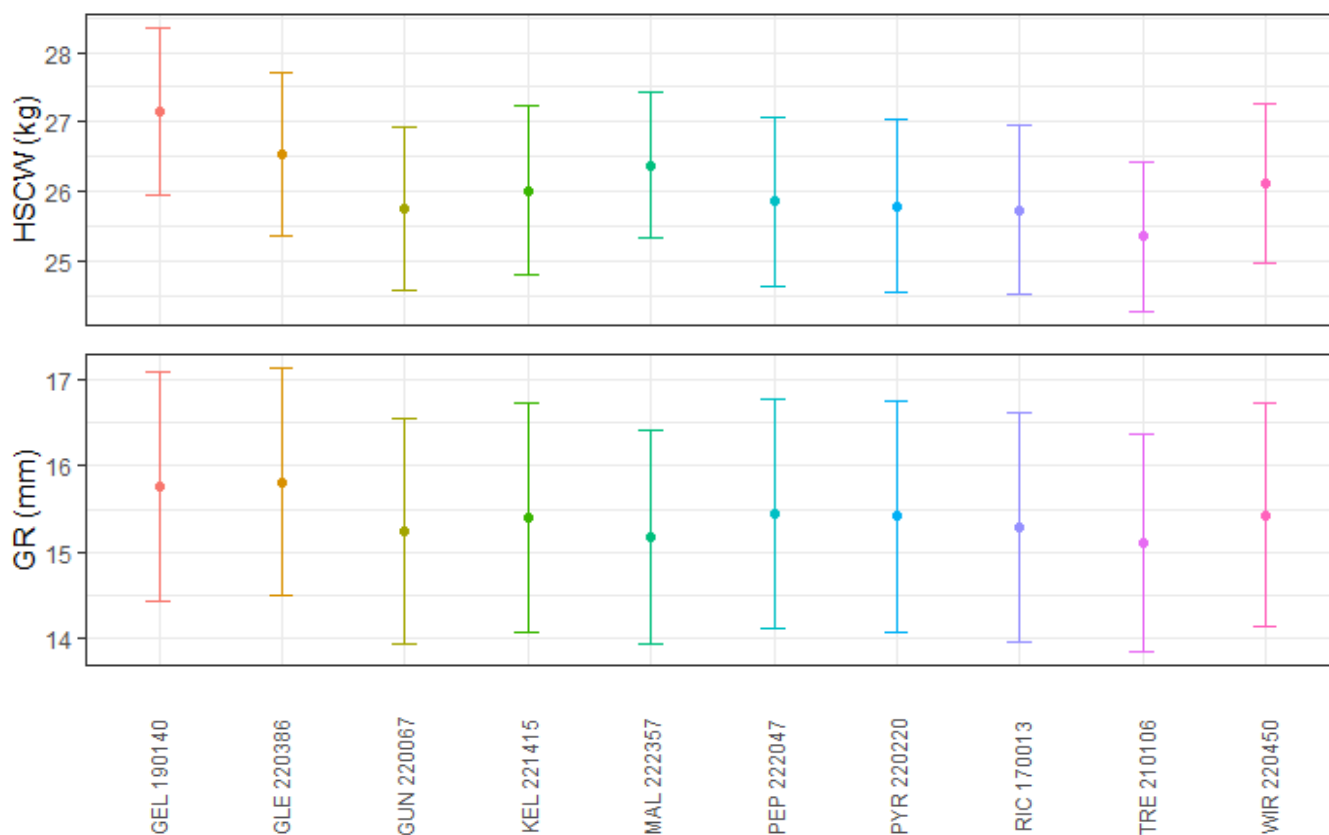


Figure 1 Summary of predicted means (\pm standard error) for carcass traits including Hot Standard Carcass Weight (HSCW), and GR tissue depth (GR), separated by sire.

Figure 2 summarises the predicted mean \pm standard error for loin eye traits by sire where sire had a significant effect on variation. Sire resulted in significant variation in loin eye depth, which was likely the driver for the similar variation observed in loin EMA.

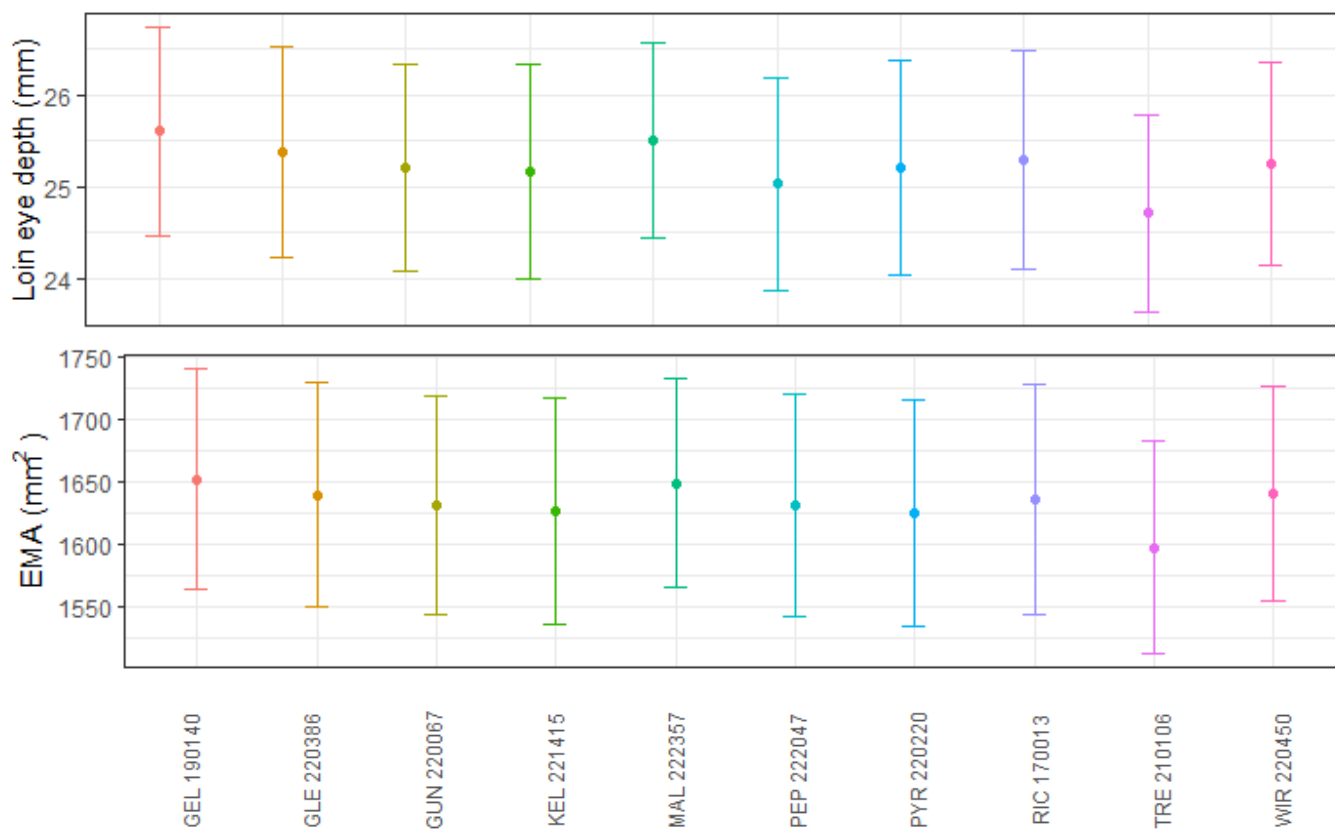


Figure 2 Summary of predicted means (\pm standard deviation) for the loin eye traits of loin eye depth and eye muscle area (EMA), separated by sire.

Sire resulted in significant variation in IMF and the predicted mean \pm standard deviation are summarised in Figure 3. All sires had a predicted mean above 4% IMF which is the minimum value considered preferable by consumers.

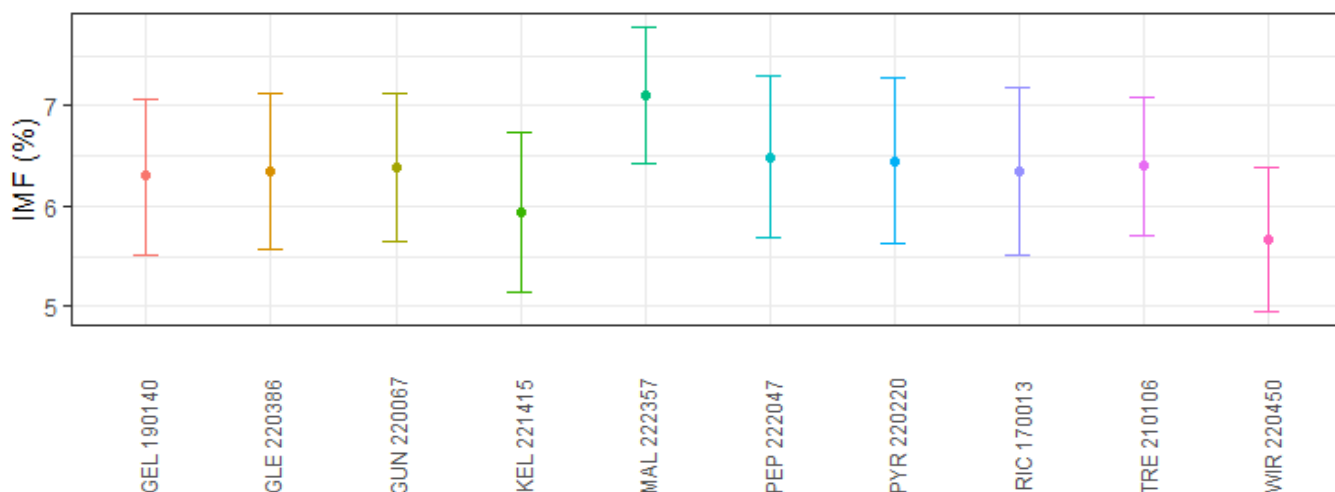


Figure 3 Summary of predicted means (\pm standard deviation) for the eating quality trait intramuscular fat (IMF), separated by sire.

Sire had a significant effect on DXA carcass composition estimates which are summarised in Figure 4 with the predicted mean \pm standard error by sire. Sires with a low DXA lean value had correspondingly high DXA fat predictions, and vice versa. DXA bone had the least variation of the DXA carcass composition estimates.

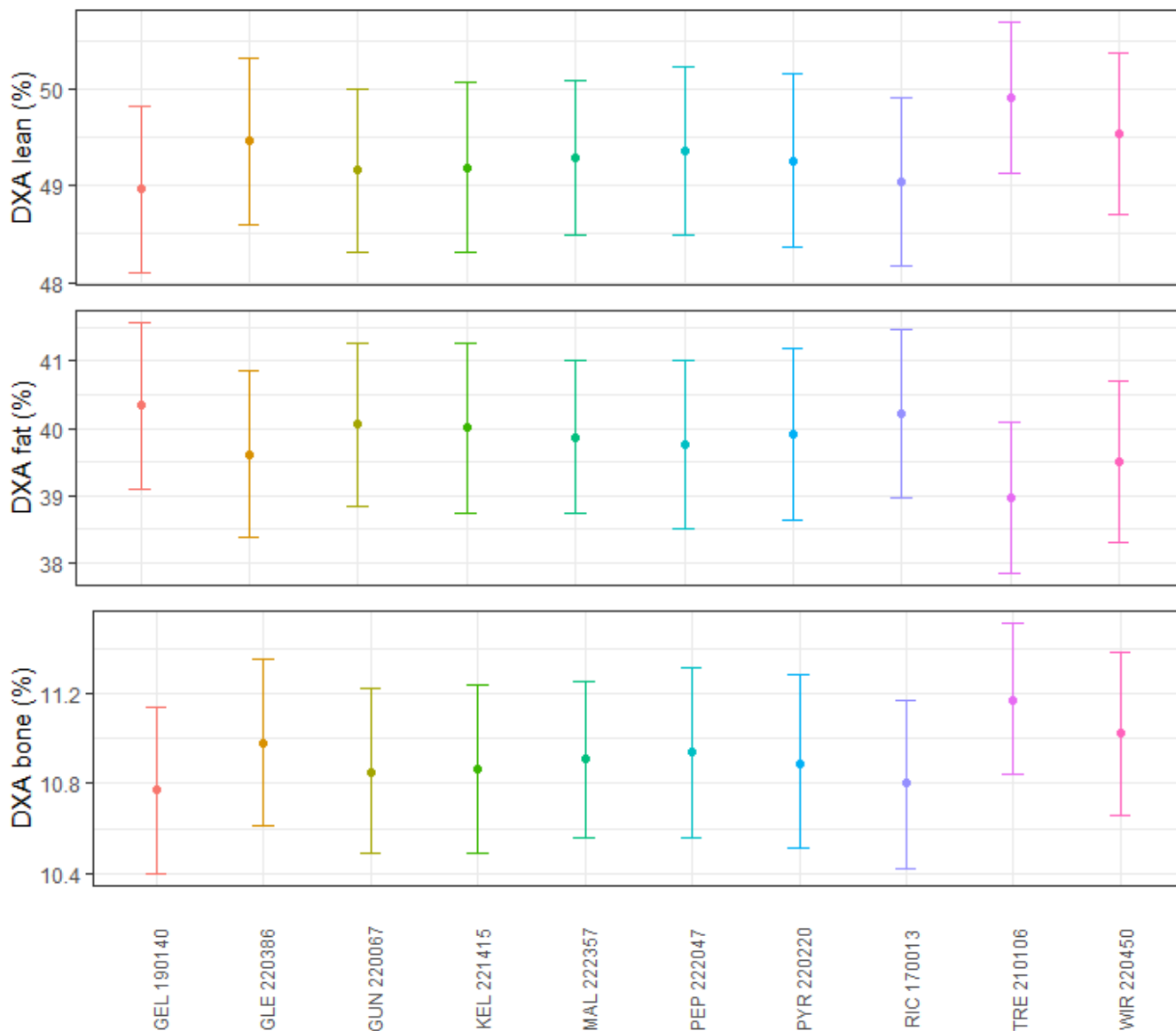


Figure 4 Summary of predicted means (\pm standard deviation) for the carcass composition traits including DXA lean, DXA fat, and DXA bone, separated by sire.

4.3. Relationship between traits

The relationship between unadjusted traits HSCW, GR tissue depth, DXA fat, IMF, and SF5 are presented in Figure 5. All traits and their relationships followed trends as expected and reported in other literature. There was a positive relationship between HSCW and GR, with GR tissue depth increasing as carcass weight increased. There was also a trend for GR tissue depth to increase as DXA fat increased. This was

not as strong a relationship and highlights the ability of DXA to capture whole carcass fatness over measures using a single location. As DXA lean increased, indicating less carcass fat, IMF decreased. There was a negative relationship between IMF and SF5 as expected, such that as IMF increased, SF5 decreased, both of which are desirable values for eating quality.

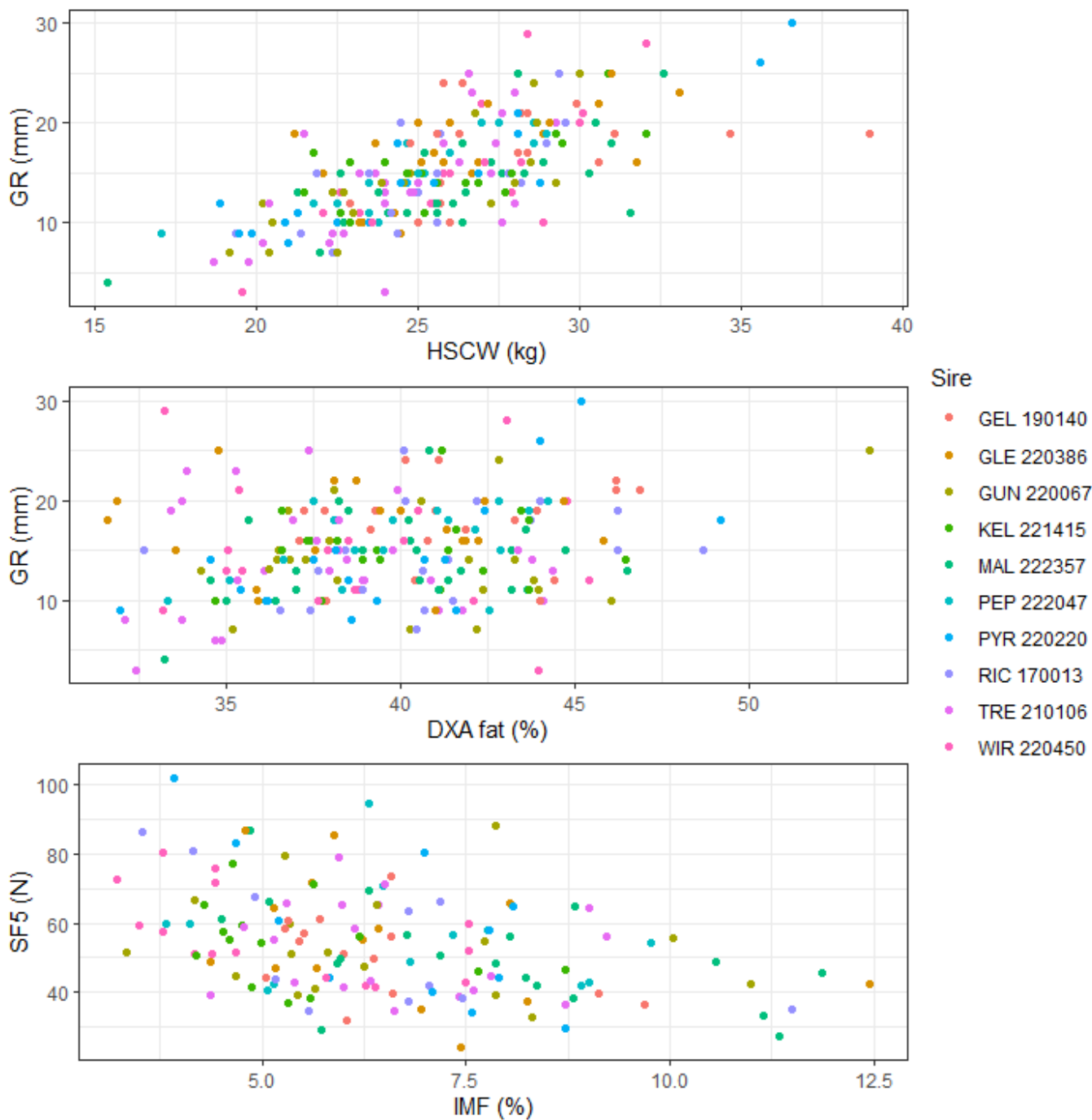


Figure 5 The relationship between recorded traits including Hot Standard Carcass Weight (HSCW), GR tissue depth (GR), DXA fat, intramuscular fat (IMF), and shear force after 5 days ageing (SF5). Colours indicate sire with the sire code and colour summarised in the legend.

4.4. Heritability estimates and sire predicted means

Table 4 presents the heritability estimates for traits included in this report. Intramuscular fat and HSCW had the highest heritability's of the traits sampled, but were moderate at 29% and 18%, respectively. DXA carcass composition estimates, loin eye traits, and GR tissue depth had low heritability of 12%-13%, 6%-9%, and 5%, respectively. Calibration data for the DXA unit was not available and may have contributed to the low heritability of these traits in this study compared to those reported elsewhere. Previous studies have reported heritability of GR tissue depth, lean meat yield, IMF% and SF5 at 32%, 35-58%, 48% and 27%, respectively (Jacob and Calnan, 2018; Mortimer *et al.*, 2014; Safari and Fogarty, 2003). The variation in heritability from expected values for many of the traits reported here is likely a function of the small size of the data set with only 10 sires sampled (Jacob and Calnan, 2018; Massender *et al.*, 2019; Mortimer *et al.*, 2014; Safari and Fogarty, 2003). Birth and rearing type had a significant effect on HSCW ($p = 0.02$), loin eye width ($p = 0.01$), and loin eye muscle area ($p = 0.01$, Table 4). Variance components and sire predicted means are also presented in Table 4. Predictions for GR tissue depth ranged from 15.12 mm to 15.81 mm placing predictions for all sires at the low end of a fat score 4. Sire predicted means for IMF were high, ranging from 5.66% to 7.10%, exceeding the benchmark of 4% IMF associated with good eating quality.

Table 4 Variance components and sire predicated means for carcass traits. Heritability of traits with a * were low and could not be accurately calculated.

	HSCW (kg)	GR (mm)	DEXA Lean (%)	DEXA Fat (%)	DEXA Bone (%)	IMF (%)	Loin eye width (mm)	Loin eye depth (mm)	Loin fat depth (mm)	Loin EMA (mm ²)	SF5 (N)
Variance components											
<i>Heritability</i>	18%	5%	12%	12%	13%	29%	*	9%	*	6%	*
<i>Sire variance</i>	0.53	0.28	0.20	0.41	0.04	0.26	0.000003	0.27	0.0000003	1339.75	0.00002
<i>Residual variance</i>	11.28	24.19	6.62	13.66	1.23	3.28	33.27	12.14	2.96	87508.76	234.11
<i>Birth type</i>	0.02	0.19	0.30	0.30	0.30	0.34	0.01	0.21	0.34	0.01	0.91
Sire predicted means											
<i>GEL 190140</i>	27.14	15.76	48.97	40.34	10.77	6.30		25.60		1651.92	
<i>GLE2 220386</i>	26.54	15.81	49.46	39.62	10.98	6.34		25.38		1639.05	
<i>GUN 220067</i>	25.75	15.24	49.16	40.06	10.85	6.39		25.20		1630.93	
<i>KEL 221415</i>	26.00	15.40	49.19	40.01	10.86	5.93		25.16		1627.00	
<i>MAL 222357</i>	26.37	15.18	49.29	39.87	10.91	7.10		25.51		1648.73	
<i>PEP 222047</i>	25.85	15.45	49.36	39.77	10.94	6.49		25.03		1631.03	
<i>PYR 220220</i>	25.79	15.42	49.26	39.91	10.89	6.45		25.21		1624.66	
<i>RIC 170013</i>	25.73	15.28	49.04	40.23	10.80	6.35		25.29		1635.59	
<i>TRE 210106</i>	25.35	15.12	49.91	38.98	11.17	6.40		24.71		1597.09	
<i>WIR 220450</i>	26.12	15.43	49.54	39.50	11.02	5.66		25.25		1640.50	

5. Conclusion

Carcase performance was high in relation to IMF results across the sire cohort indicating high eating quality outcomes. This was balanced by weaker SF5 performance with most values exceeding the maximum indicated for good eating quality, and lower carcase yield outcome predictions indicated by DXA carcase composition predictions. Balanced selection for carcase yield and meat quality traits can be achieved by incorporation of lean meat yield, IMF%, and SF5 breeding values into decisions when selecting sires to simultaneously improve lean meat yield and eating quality. This highlights the importance of informed genetic selection coupled with management of growth path to maximise cohort performance relative to consumer expectations.

6. References

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