Technical Report

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Report Title:	Value of data from commercial ram breeders' flocks as an industry reference population for Australian sheep
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Acknowledgements

Abstract

This report examines the value of using carcase data from industry ram breeding flocks to build upon an industry sheep reference population in Australia. Data from 1,981 lambs managed in 16 commercial ram breeder flocks were collected between 2017 and 2020 for carcass and meat quality measurements: hot carcase weight, tissue depth at the GR site, eye muscle depth, fat depth at the C site, intramuscular fat and shear force. Industry data were cross-validated with and without reference data from the MLA Resource flock. Industry data did not bias the estimation of breeding values when used in combination with the reference population. Therefore, industry data can be used to expand an industry reference population if data collection is accurate and consistent with industry standards.

Contents

1 Introduction

The MLA Resource Flock (RF) is the current Australian sheep reference population and a succession of the Sheep CRC Information Nucleus Flock (Van der Werf et al. 2010). The flock provides a well-designed and ongoing sheep reference population and is mostly funded with national levy funds. This industry investment helps subsidise the high cost for progeny testing and measuring expensive traits such as shear force and intramuscular fat of lamb meat.

Historically most Resource Flock sites were well-resourced research stations and Resource Flock data has been used for research as well as in routine genetic evaluation to produce Australian Sheep Breeding Values (ASBVs). Large reference populations lead to increased accuracy of genomic predictions (Habier et al., 2010) which can be further enhanced by collecting phenotypic and genotypic information from additional animals. As part of expanding the reference population, a series of companion projects were established where breeders funded data collection from their own flocks with co-investment support from industry funds. These projects allowed for more animals to be genotyped and measured for carcase and meat quality traits to help build an industry reference population. This population represents a bigger proportion of the Australian sheep industry and allows for data to be collected with reduced investment per animal measured from industry funds. The quality of data collected on these projects, however, varied and procedures were not always fully comparable to data quality from the research stations used in the Resource Flock. Therefore, we investigated the value of the records collected on industry animals via the co-investment funding model as part of the reference population for sheep in Australia.

2 Methodology

2.1 Data

Data were recorded from commercial (seedstock, non-research) animals as a satellite flock to the MLA Resource flock. This process involved animals from two different sources: i) surplus animals – animals selected based on phenotypic or genetic performance, and ii) structured progeny test – when dams were joined to sires to generate progeny for testing.

This report used data from 25 different flocks measured from 4,778 animals born between 2017 and 2020. The animals selected for progeny testing were progeny of 418 sires. Sire types included Merino sires (Merino, Poll Merino), Maternal sires (White Dorper, Border Leicester, Booroola Leicester, Coopworth, Bond, Corriedale, Dohne Merino, East Friesian, Prime South African Meat Merino) and Terminal sires (Hampshire Down, Ile De France, Poll Dorset, Southdown, Suffolk, Texel, White Suffolk).

From the 4778 animals used for this report, 4122 were progeny of terminal sire types, 28 of maternal and 628 of Merino. Because of the large number variations between these three groups, only terminal animals were considered for this analysis.

Table 1. Number of records and genotypes for the seedstock flocks for the animals born between 2017 and 2020. Year: year of birth, N: number of animals with records, N/Y total number of recorded animals per year, Genotypes: number of genotyped animals, G/Y: total number of genotyped animals with records per year, N selected: number of animals selected for the analysis.

Flock code	Year	N	N/Y	Genotypes	G/Y	N selected
1		71		66		65
2		10		10		10
3		55		54		53
4		62		60		60
5		90		89		89
6	2017	24	1606	23	1554	23
7		46		44		44
8		181		178		
9		212		181		
10		466		464		
11		243		242		
12		146		143		
1		64		62		62
8		461				
9		219		220		
13	2018	89	1691	89	1110	
10		499		497		
11		244		242		
12		115				
14		20		19		17
1		101		101		100
15		41		41		38
16		48		48		42
17		24		24		24
18		49		49		49
19	2019	99	1025	99	682	65
20		15		15		15
21		87				
8		150		135		
22		235				
23		12		12		
24		134		133		
25		10		6		
19		239		239		239
8	2020	149	466	48	355	
12		68				
Grand Total			**4778**		**3701**	**995**

Within the data set there were variations in the number of animals recorded across different flocks and years (Table 1 and Table 3) and in the trait distribution (Figure 1 and Figure 2). The terminal data set was filtered to use animals from flocks with consistent recording. Therefore, 995 lambs born between 2017 and 2020 were selected (Table 1). These lambs came from 15 seedstock ram breeding flocks and were the progeny of 281 sires across 3 breeds (Poll Dorset, White Suffolk and Southdown). For clarity, this data set will be referred as seedstock data. A second dataset with 4,027 Resource Flock (RF) animals was used for validation. The Resource Flock animals (Table 2) were born between 2015 and 2020 and were the progeny of 445 sires across the same three breeds (Poll Dorset, White Suffolk and Southdown).

Carcase traits for seedstock and Resource Flock animals were measured after slaughter in commercial abattoirs. Weight (HCWT) and tissue depth at the GR site (GRFAT, total tissue depth measured with a GR knife on the 12th rib) were measured on the hot carcase. After overnight chilling (3 – 4 º C), at a cut between the 12th and 13th ribs of each carcase, eye muscle (M. longissimus thoracis et lumborum, LL) depth (EMD), and fat depth at the C site (CFAT) were measured. The percentage of intramuscular fat (IMF) at the LL was determined using a near infrared procedure (NIR) as described by (Perry et al. 2001). Shear force (SF5) at 5 days after slaughter was measured at a section of the LL as described by Hopkins et al. (2010). Number of animals from each flock and year are shown on Table 1, trait mean values for each flock and year on Table 3 and number of animals with completed records for each flock and trait on Table 4.

The distribution for each trait and flock for all terminal animals in Figure 1. Distributions for each trait and year of birth can be seen in Figure 2.

Table 2. Number of animals (N) for each year of birth (Y) for the Resource flock data set. HCWT: hot carcase weight (Kg), CEMD: eye muscle depth (cm), IMF: intramuscular fat (%), SF5: shear force 5 days after slaughter (N), CFAT: fat at the c-side (cm), GRFAT: fat at the GR site (cm).

Y	N	HCWT	CEMD	IMF	SF5	CFAT	GRFAT
2015	738	22.76 (3.55)	32.41 (4.74)	4.3 (1)	39.87 (14.2)	3.51 (1.74)	13.29 (6.29)
2016	672	26.04 (3.93)	34.25 (4.81)	4.61 (1.07)	37.77 (10.33)	5.94 (2.95)	17.56 (5.46)
2017	1105	26.05 (3.58)	35.42 (4.08)	4.35 (0.98)	34.95 (10.3)	4.48 (2.28)	18.3 (5.34)
2018	648	27.17 (2.86)	35.05 (4.21)	4.87 (1.29)	31.01 (8.87)	5.4 (2.31)	21.34 (5.57)
2019	817	27.51 (3.52)	35.01 (4.08)	4.78 (1.11)	29.58 (9.46)	5.68 (2.91)	22.42 (5.8)
2020	47	25.44 (3.47)	34.4 (3.88)	3.8 (0.94)	31.5 (6.92)	4.74 (2.18)	14.91 (5.73)
Total	**4027**	**25.91 (3.87)**	**34.52 (4.48)**	**4.55 (1.1)**	**34.56 (11.36)**	**4.94 (2.61)**	**18.54 (6.47)**

Table 3. Number of records and mean values (± SD) for each trait for all the carcase traits recorded in the seedstock animals born between 2017 and 2020.Y: year of birth, N: number of records, 0 indicates no records collected for the specific trait. HCWT: hot carcase weight (Kg), CEMD: eye muscle depth (cm), IMF: intramuscular fat (%), SF5: shear force 5 days after slaughter (N), CFAT: fat at the c-side (cm), GRFAT: fat at the GR site (cm).

Flock	Y	N	HCWT	CEMD	IMF	SF5	CFAT	GRFAT
1		71	38.13 (5.1)	43.16 (4.0)	5.12 (1.0)	38.40 (10.6)	8.48 (3.4)	25.55 (4.9)
2		10	27.47 (1.8)	36.27 (2.8)	2.72 (0.5)	48.36 (11.9)	3.61 (1.6)	14.75 (3.7)
3		55	23.19 (2.1)	33.36 (3.1)	3.30 (0.9)	36.86 (9.1)	2.50 (1.1)	8.90 (2.5)
4		62	27.07 (3.1)	37.26 (4.0)	4.51 (0.8)	38.49 (9.3)	3.87 (1.9)	14.71 (4.2)
5		90	23.19 (3.5)	36.82 (3.9)	2.82 (0.8)	56.16 (17.6)	3.10 (1.4)	12.21 (3.5)
6	2017	24	23.32 (2.6)	37.67 (4.2)	3.78 (0.4)	43.69 (14.5)	2.96 (1.2)	11.12 (3.9)
7		46	24.55 (3.7)	36.70 (4.0)	3.02 (0.7)	31.95 (6.7)	3.91 (1.6)	14.07 (3.9)
8		181	23.72 (3.3)	36.18 (3.7)	3.96 (0.8)	36.19 (9.7)	3.83 (2.0)	14.96 (4.0)
9		208	19.60 (2.9)	28.40 (3.1)	4.30 (1.6)	34.00 (9.3)		2.30 (0.7)
10		467	24.40 (1.9)	27.58 (2.7)	3.90 (1.3)	28.08 (5.7)	4.10 (2.2)	10.79 (4.0)
11		243	23.78 (2.7)	27.70 (2.8)	3.99 (1.1)	23.52 (4.7)	4.93 (1.8)	13.78 (3.8)
12		146	24.95 (4.1)	36.70 (4.9)	4.59 (0.9)	41.39 (10.2)	5.00 (2.4)	15.82 (4.9)
1		64	24.40 (3.3)	34.11 (2.8)	4.20 (0.6)	50.35 (14.8)	3.08 (1.4)	11.09 (4.3)
8		464	21.32 (2.3)	31.86 (3.8)	4.12 (0.7)	35.31 (9.5)	3.73 (1.8)	11.67 (4.0)
9		228	19.02 (2.5)	30.16 (3.1)	3.85 (0.8)	44.25 (13.5)		12.19 (3.5)
13	2018	89	18.83 (2.6)	26.64 (4.0)	4.84 (0.8)	32.08 (7.8)	3.72 (2.6)	10.36 (3.5)
10		499	25.88 (1.9)	27.45 (2.7)	4.67 (1.4)	24.59 (5.4)	5.15 (1.8)	14.39 (3.3)
11		245	29.46 (3.4)	31.01 (3.2)	4.46 (1.3)	23.92 (4.7)	6.07 (2.3)	21.71 (5.1)
12		115	24.93 (4.1)	34.77 (3.8)	4.34 (0.7)	37.99 (10.3)	3.90 (1.9)	16.10 (5.8)
14		20	24.57 (2.6)	35.65 (2.6)	3.85 (0.6)		4.32 (2.1)	16.73 (3.7)
1		101	25.42 (3.1)	36.51 (3.5)	3.80 (0.6)	51.32 (15.4)	2.26 (1.4)	11.10 (3.0)
15		41	23.43 (2.8)	34.88 (3.5)	4.22 (0.9)		3.67 (1.3)	14.90 (3.0)
16		48	24.43 (2.6)	36.96 (3.5)	3.48 (0.8)	36.21 (9.7)	1.92 (0.9)	14.19 (4.1)
17		24	24.02 (2.8)	36.21 (3.9)	3.49 (0.7)	30.92 (6.0)	1.79 (1.1)	15.38 (4.4)
18		49	25.93 (2.0)	38.83 (4.3)	3.80 (0.7)	40.63 (10)	2.15 (1.2)	15.20 (4.3)
19		99	26.05 (3.8)	38.10 (4.3)	4.47 (0.9)	31.77 (7.5)	5.23 (2.5)	17.95 (4.9)
20	2019	15	24.52 (1.4)	34.07 (5.0)	3.96 (0.8)	27.88 (5.8)	2.40 (1.4)	15.80 (4.3)
21		87	22.98 (4.9)	36.23 (4.7)	3.22 (0.9)	36.03 (10.8)	1.86 (1.2)	8.78 (4.0)
8		150	26.10 (3.4)	36.13 (3.7)	4.66 (0.6)	38.83 (8.7)	4.66 (2.2)	17.74 (4.1)
9		302	22.57 (3.7)		5.50 (1.3)	39.78 (14.3)		
22		241	25.88 (3.9)	35.82 (4.2)	3.65 (0.9)	31.49 (7.7)	3.41 (2.3)	15.17 (4.0)
23		12	22.04 (2.5)	32.75 (3.7)	3.34 (0.6)	38.08 (13.9)	2.33 (1.0)	13.42 (4.5)
24		134	27.67 (2.9)	27.22 (3.3)	5.72 (1.5)	30.28 (6.1)	4.21 (1.7)	12.54 (3.3)
25		10	24.82 (3.1)		3.10 (1.0)	35.50 (9.0)		
19		239	29.70 (3.9)	36.91 (4.6)	4.00 (0.9)	26.05 (5.4)	6.73 (1.9)	22.43 (5.4)
8	2020	149	25.09 (3.5)	34.93 (3.8)	3.91 (1.0)	30.51 (7.7)	4.79 (1.9)	14.78 (4.7)
12		68	23.64 (4.1)	33.66 (3.4)	3.32 (0.9)	31.74 (6.8)	4.32 (1.9)	12.66 (4.3)

Table 4. Number of animals with completed data for each farm and year of birth for all measured carcase traits. HCWT: hot carcase weight (Kg), CEMD: eye muscle depth (cm), IMF: intramuscular fat (%), SF5: shear force 5 days after slaughter (N), CFAT: fat at the c-side (cm), GRFAT: fat at the GR site (cm).

Flock	Y	HCWT	CEMD	IMF	SF5	CFAT	GRFAT
1		71	67	71	71	71	71
2		10	10	10	10	10	10
3		55	55	55	55	55	55
4		62	62	62	61	62	62
5		90	90	90	90	90	90
6	2017	24	24	24	24	24	24
7		46	46	46	46	45	45
8		181	181	181	181	181	180
9		208	208	208	208	0	208
10		466	464	464	464	464	463
11		243	242	241	242	242	242
12		146	145	146	144	146	146
1		64	64	64	64	64	64
8		461	464	348	464	464	464
9		226	228	228	212	0	227
13	2018	89	89	89	89	89	89
10		499	499	499	499	499	499
11		244	244	234	234	244	244
12		115	115	115	115	115	115
14		20	20	20	0	20	20
1		101	101	101	101	101	101
15		41	41	41	0	41	41
16		48	48	48	48	48	48
17		24	24	24	24	24	24
18		49	48	48	48	48	49
19		99	99	99	99	99	99
20	2019	15	15	15	15	15	15
21		87	87	87	85	87	87
8		150	150	150	150	150	150
9		302	0	296	294	0	0
22		235	151	234	234	151	152
23		12	12	12	12	12	12
24		134	134	134	134	134	134
25		10	0	10	10	0	0
19		239	239	239	239	239	239
8	2020	149	147	149	147	147	149
12		68	68	68	68	68	68

Figure 1. Carcase trait distributions for all terminal animals used in the analysis. Different colours indicate different flocks. CEMD: eye muscle depth, CFAT: fat at the c-side, GRFAT: fat at the GR site, HCWT: hot carcase weight, IMF: intramuscular fat, SF5: shear force 5 days after slaughter.
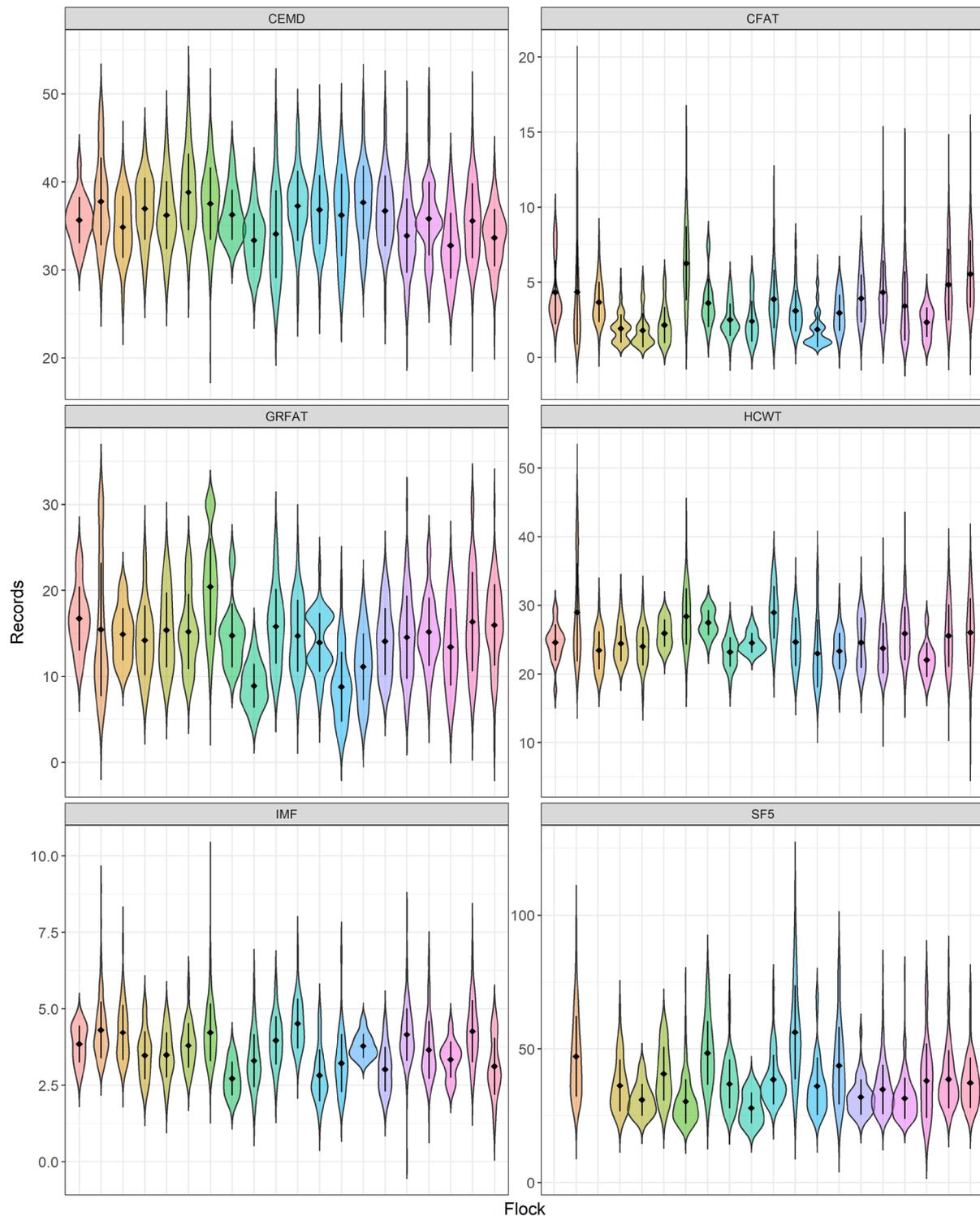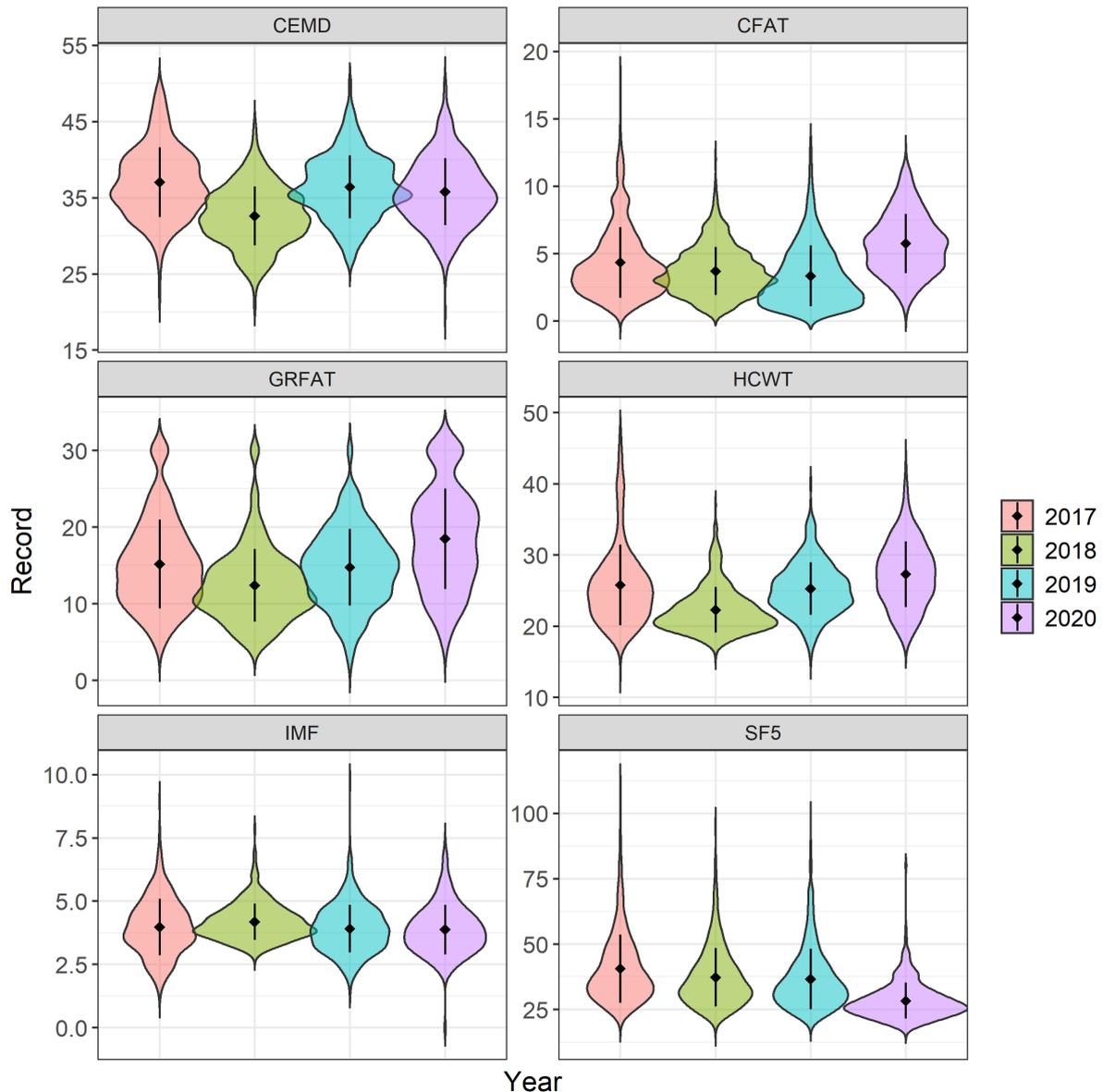
Figure 2. Carcase trait distribution for each year of birth. Different colors indicate different years. CEMD: eye muscle depth, CFAT: fat at the c-side, GRFAT: fat at the GR site, HCWT: hot carcase weight, IMF: intramuscular fat, SF5: shear force 5 days after slaughter.

2.2 Statistical analyses

Estimated Breeding values (EBVs) were estimated using the LAMBPLAN genetic evaluation software OVIS (Brown et al. 2018) for all animals (both seedstock and Resource Flock datasets). All data was pre-adjusted for birth and rear type (single, twins, triplets and quadruplets or more lambs), lamb age and age of dam. Contemporary group, defined by breed, flock, management group, sex, date of measurement and kill group, was used as a fixed effect. Hot carcase weight was included as a covariate to adjust other carcase traits to a weight constant. All models included the random effects of animal, genetic group (Swan et al. 2016) and sire × flock interaction. To estimate the differences in accuracy of prediction an internal cross-validation procedure was used for each data set as described by Legarra and Reverter (2018). Resource Flock (RF) data were separated into four data sets with approximately the same size as the seedstock data. Resource Flock animals were randomly

assigned to groups one to four based on their sires so that half-sib families were not represented in multiple groups. All seedstock animals were assigned to group five. Numbers of records, sires and unadjusted trait means for each group are shown on Table 5.

Following analysis of the full data set, three different validation scenarios were investigated:

1. EBVs were calculated and validated in Resource Flock. EBVs were estimated using 3 of the RF groups as the training population and validated in the remaining Resource Flock group (RF – RF analysis, performed four times).
2. Prediction of seedstock animals was carried out using only Resource Flock data as the training population (groups one to four) and the seedstock group as the validation data set (RF – seedstock analysis, replicated four times).
3. Prediction of Resource Flock animals was performed using four different replicated combinations of Resource Flock (groups one to four) and industry animals (group five) (combined analysis). For each replication of this analysis, three of the combined groups were used as the training population, and the fourth as the validation data set.

For each trait, four validation metrics were calculated and averaged across replicates. Accuracy and dispersion metrics were calculated using the LR method (Legarra and Reverter 2018) as the correlation and regression slopes between the EBVs from each of the three analyses (RF – RF, RF – seedstock, combined) with EBVs from the full analysis. The regression slopes between EBVs are expected to have a value close to one if there is no over or under dispersion. Accuracy and dispersion were also calculated as the correlation and regressions for EBVs on phenotypes adjusted for fixed effects, with regressions performed in ASReml (Gilmour et al. 2015).

Table 5.Number of animals (N), sires (Sires), sires per contemporary group (Sires/CG) and unadjusted mean record values (standard deviation) for all traits and validation groups used in the validation analysis. CWT: hot carcase weight (kg), CEMD: carcase eye muscle depth (cm), CFAT: fat depth at the C-site (cm), GRFAT: tissue depth at GR-site (cm), IMF: intramuscular fat (%), SF5: shear force 5 days after slaughter (N).

Group[1]	N	Sires	Sires/CG	HCWT	CEMD	CFAT	GRFAT	IMF	SF5
1	1,100	112	16.7	23.6 (3.8)	32.9 (4.8)	4.3 (2.4)	14.5 (6.2)	4.4 (1.0)	39.3 (12.9)
2	1,162	110	17.7	26.3 (3.7)	35.1 (4.2)	4.8 (2.6)	18.0 (5.1)	4.4 (1.0)	35.3 (10.1)
3	953	111	15.4	26.7 (3.1)	35.4 (4.2)	5.2 (2.4)	20.7 (5.8)	4.7 (1.2)	32.9 (10.3)
4	812	112	26.4	27.5 (3.5)	34.9 (4.1)	5.7 (2.9)	22.3 (6.0)	4.7 (1.1)	29.0 (8.9)
5	995	140	9.6	26.9 (5.2)	37.0 (4.5)	4.4 (2.8)	16.4 (6.7)	3.9 (1.0)	38.3 (15.0)

[1] Data for groups 1 to 4 came from Resource Flock animals, group 5 included seedstock data

3 Results and discussion

Record numbers varied for different traits across seedstock flocks for different years of birth (Table 4). For example, there were no CFAT records for flock 9 across different years, while flock 22 had only 151 out of 235 lambs recorded for CEMD, CFAT and GRFAT. Of all traits HCWT had the most consistent recordings and it was present for all animals in different flocks. Trait means and distribution also varied within seedstock data (Table 3 and Figure 1), and between seedstock and Resource Flock animals (Table 2). Seedstock animals used in the validation came from flocks with consistent recordings across years but still exhibited higher variation for HCWT, CEMD GRFAT and SF5 compared to the Resource flock data. The mean number of sires for each contemporary group was lower for the seedstock animals (9.6) compared to the resource flock data set (15.4 – 26.4, Table 5). Inconsistencies in recording and lower representation of the flock's diversity can influence predictive performance, and the validation analysis results reflect differences in recoding between seedstock and Resource Flock data.

Validation results followed similar patterns for two of the three different validation scenarios. For the RF – RF and combined scenarios LR EBV dispersion metrics had values close to one for HCWT and CFAT and greater than one for CEMD, GRFAT, IMF and SF5 (Table 6). Better LR EBV dispersion values for these scenarios indicated it is possible to combine RF and seedstock data for genetic evaluation, as the addition of seedstock data did not influence the predictive ability of the RF data set. LR EBV correlations ranged from 0.36 (EMD, combined) to 0.52 (GRFAT for RF – RF and combined, SF5 for RF – RF). Phenotypic dispersions for the same validation scenarios (RF – RF and combined) were close to one for GRFAT (0.95 and 0.94 respectively) and CFAT (0.87 for both). However, estimates greater than one were observed for EMD, IMF and SF5 for both analyses. Correlations between EBVs and phenotypes were consistent between the two analyses ranging from 0.19 (EMD) to 0.45 (CWT).

Differences were observed in the metrics when Resource Flock data was used to predict into industry animals (scenario RF – seedstock). LR EBV dispersions were better and closer to one for GRFAT (0.94), HCWT (0.85) and CFAT (0.73) although for the last two traits the values observed were lower than the other two validation scenarios (Table 5). LR EBV accuracies were higher for all traits ranging from 0.49 (CFAT) to 0.64 (CEMD). Higher phenotypic dispersions were observed for all traits ranging from 0.67 (HCWT) to 1.67 (SF5). Phenotypic accuracies were similar to other validation analyses for CEMD and CFAT but higher for the rest of the traits. In general, validation patterns were very similar when using RF data to predict RF progeny (RF – RF) and combined RF and seedstock data (combined) were used to validate RF phenotypes but over-dispersion was observed when RF data was used to predict industry phenotypes (RF – seedstock).

Accuracy of genomic predictions can benefit from larger reference populations (Habier et al. 2010). In this study the value of expanding the Australian sheep reference population by using data from seedstock ram breeding flocks for carcase and meat quality traits was explored. Cross validation results showed that it was possible to use data from seedstock ram breeding flocks to expand the industry reference population for traits recorded using common protocols. Comparison between observed and predicted performances in a cross-validation analysis is important to measure the efficiency of the application of the analysis to specific data sets

(Legarra et al. 2008). Our results show that for reference and seedstock data, phenotypic and EBV dispersions can be similar when seedstock data are used in combination with a well recorded reference population (Analyses RF – RF and combined, Table 2). Using seedstock and reference data together does not introduce further bias to breeding values estimation.

Table 6. Validation metrics for each validation scenario averaged across replicates. CWT: hot carcase weight, EMD: carcase eye muscle depth, CFAT: fat depth at the C-site, GRFAT: tissue depth at GR-site, IMF: intramuscular fat, SF5: shear force 5 days after slaughter.

Metric	Trait						Scenario[1]
	HCWT	**CEMD**	**CFAT**	**GRFAT**	**IMF**	**SF5**	
LR EBV dispersion	0.93	1.16	0.94	1.07	1.28	1.14	RF – RF
	0.85	1.56	0.73	0.94	1.13	1.07	RF – seedstock
	0.92	1.15	0.94	1.08	1.27	1.13	Combined
LR EBV correlations	0.46	0.37	0.44	0.52	0.49	0.52	RF – RF
	0.50	0.64	0.49	0.57	0.56	0.60	RF – seedstock
	0.45	0.36	0.43	0.52	0.48	0.50	Combined
Phenotypic dispersion	0.61	1.21	0.87	0.95	1.33	1.12	RF – RF
	0.67	1.61	1.25	1.01	1.06	1.67	RF – seedstock
	0.58	1.19	0.87	0.94	1.31	1.10	Combined
Phenotypic - EBV correlations	0.45	0.19	0.24	0.40	0.30	0.40	RF – RF
	0.49	0.19	0.24	0.43	0.59	0.65	RF – seedstock
	0.45	0.19	0.24	0.40	0.30	0.40	Combined

[1] RF-RF: prediction using different datasets of Resource Flock animals, RF – seedstock: using Resource Flock animals to predict into seedstock animals, Combined: using different combinations of Resource Flock animals.

When Resource Flock data was used to predict seedstock phenotypes results depended upon the recorded traits. For example, CEMD presents higher biases than other carcase traits both for EBV and phenotypic dispersions (Table 6) but also exhibits higher mean values in the seedstock animals compared to the reference data sets (Table 5). Moreover, data structure is different between RF and seedstock animals. The number of sires per contemporary group is typically lower for seedstock data (Table 5) and RF data also normally represents a bigger range of breeds and diversity of sires (van der Werf et al. 2010). This highlights the importance of recorded data quality; the establishment of an industry reference population can benefit from accurate and consistent data recording.

4 Conclusions

Data collected from seedstock ram breeding flocks can be used to complement managed progeny test sites to create an industry reference population. The effectiveness of commercial data depends on the trait measured (completeness of data and good representation of the flock's diversity) and the influence of fixed effects recorded on the flock. Co-investment into industry recorded carcase traits using levy funds was found to be beneficial to the growth of the reference population. However, these projects should be carried out with caution as there is a risk of reduced sire diversity, less consistent data collection, and reduced data quality if they are not managed properly.

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