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Abstract

Data for progesterone concentration (a proxy measure for puberty), pre-joining weight and condition, and reproductive outcomes for pedigreed ewes joined to lamb as yearlings were obtained from 9 breeders in three states (NSW, VIC and SA) from 12 industry flocks, containing maternal, terminal and Merino breed types. The focus ewes (N=3296) were born in 2012, and were joined to first lamb as 1 year olds in 2013. Fertility levels ranged from 0% to 75% across flocks. Progesterone and fertility data combined suggest that the main factor contributing to variable yearling reproductive performance was failure to attain puberty. Progesterone concentrations were moderately heritable but not strongly correlated genetically or phenotypically with pre-joining weight or condition score. Therefore, progesterone levels were largely independent of genes controlling pre-joining weight and condition score. Low to moderate genetic correlations between pre-joining weight, condition score or progesterone and the number of lambs born (NLB) indicates that breeders cannot rely solely on these traits to provide indirect information on genetic merit for NLB in yearling ewes and that the reproductive performance itself needs to be recorded. However, estimates of genetic correlations suggest the accuracy of selection for NLB may be improved by data from these correlated traits. More accurate estimates of genetic parameters are required to evaluate the expected changes in response to selection under alternative recording strategies involving correlated traits. Phenotypically, progesterone concentration was most strongly associated with fertility, whereas pre-joining weight and condition score were most strongly associated with litter size.

Executive summary

It is becoming an increasingly common approach in the Australian sheep industry to attempt to improve ewe lifetime productivity by joining young ewes to first lamb as one year olds. This project targeted more comprehensive recording of pedigreed ewes joined to lamb as yearlings, and obtained data from 9 breeders in three states (NSW, VIC and SA), some with multiple breeds within location, totalling 12 industry flocks representing maternal, terminal and Merino breed types. The focus ewes (N=3296) were born in 2012, and a large proportion of these ewes were joined to first lamb as 1 year olds in 2013. In addition to recording reproductive outcomes, additional data were collected on either post-weaning or pre-joining condition score (N=1322+1423), pre-joining weight (N=3098) and progesterone (N=1890) early in the joining period to more closely examine the associations between pre-joining weight and condition score with hormonal status and the observed reproductive outcomes. Progesterone concentrations were measured on all ewes within a contemporary group at D14 after ram/teaser introduction, and this was used as an indirect measure for identifying the physiological attainment of puberty.

Fertility of ewes joined to lamb as yearlings varied widely between flocks, as has been observed previously, ranging from 0% (Superfine merino flock) to 75% (Terminal composite flock). Within the maternal breed types the range in fertility across flocks was 28-73%. Because flocks were located at different sites under different management, which could also affect comparisons with the limited amount of data available, the data should not be considered to infer statistically reliable breed differences, nor to provide definitive estimates for the effects of heterosis. However, Border Leicesters (which are more strongly seasonal) tended to have lower fertility than the Maternal composite flocks, which also have retained heterosis.

Several factors were identified which were significantly associated with reproductive outcomes for ewes joined to lamb as yearlings. These included contemporary group and ewe genotype within flock, the age the ewe was first exposed to rams for joining, and the age class of their dams. As there are associations between age and weight, between age and dam age, between dam age and weight, and between age, weight or dam age group and assignment to contemporary groups, disentangling these effects into independent factors is not entirely clear cut and the values obtained are therefore model dependent. However, higher age at joining and/or improved weight and condition score generally contributed to more favourable reproductive outcomes, as expected. Only some flocks restricted joining to ewes exceeding a minimum weight (35-38kg, depending on flock), but censoring on weight and contemporary group allocation could have reduced the observed associations between weight and reproductive performance. While a ewes' own birth or rear type was significantly associated with the weight and condition score achieved prior to joining, birth and rear type of the ewe joined were not ultimately significant ($P>0.05$) for reproductive outcomes in this data.

Progesterone concentrations were lowly correlated with weight and uncorrelated with condition score genetically, while weight and condition score were strongly correlated genetically with each other. Therefore, the attainment of puberty (as indicated by progesterone concentrations) is not controlled by exactly the same genes that influence pre-

joining weight or condition score, and breeders therefore cannot rely solely on pre-joining weight to be an accurate indicator of sexual maturity in their ewe lambs.

Overall, the single measurement of progesterone concentration measured on day 14 after ram (or teaser) exposure was a moderately heritable trait, but estimates of genetic correlations with reproductive traits were indicative only due to large standard errors. Based on the estimates of genetic parameters obtained, calculation of co-heritabilities demonstrated that, from a genetic perspective, pre-joining condition score was more informative than pre-joining weight or progesterone concentration for reproductive outcomes. Phenotypically, progesterone was the trait most strongly associated with fertility traits whereas pre-joining weight and condition score were the most strongly associated with litter size. Pre-joining weight, condition score and progesterone concentration all had similar phenotypic correlations (0.07 to 0.12) with the number of lambs weaned (NLW), but this explains very little (R^2<1%) of the variation observed in NLW after accounting for other factors in the model (contemporary group, age and dam age). Therefore, none of these traits is an accurate phenotypic predictor of reproductive outcomes within a flock or effective as a substitute for recording reproductive performance directly on ewes for genetic evaluation.

The attainment of puberty (as indicated by progesterone concentrations) can be seen as a limiting for reproductive outcomes in some flocks. Assuming that ewes with progesterone concentrations exceeding a threshold of 1ng/ml are pubertal, many ewes (71% of all ewes joined) considered heavy enough to join were not pubertal based on their progesterone levels by D14 into joining. Moreover, across flocks there was a strong positive association between the incidence of progesterone concentration exceeding 1ng/ml at testing and flock fertility. Ewes assessed pubertal at day 14 of joining based on a progesterone concentration >1ng/ml had overall a higher fertility rate than ewes with progesterone ≤1ng/ml (59% vs 35% fertility). The observed distributions of progesterone also differed for ewes which lambed compared to ewes which did not. Therefore, some of the variation in reproductive performance observed between flocks was almost certainly due to variability in the incidence of ewes attaining puberty prior to or within the joining period.

However, a single evaluation of progesterone concentration at day 14 is associated with errors in detecting puberty for an individual ewe, relative to continuous sampling strategies. Approximately 35% of the ewes which had progesterone <1ng/ml on D14 subsequently produced lambs, whereas about 41% of the ewes with progesterone >1ng/ml produced no lambs. This equates to 25% and 12% of all ewes joined respectively. The first group includes both false negatives (ie pubertal ewes measured for progesterone at the wrong stage of oestrus cycle) and ewes which were correctly identified as not pubertal on D14 but subsequently went on to first cycle and become pregnant within the joining period after D14. The second group includes false positives (because the threshold itself comes with some error attached) and also pubertal ewes which failed to get pregnant during joining, or which lost their pregnancy. Based on the sample of ewes recorded for both progesterone and lambing outcomes, 46% of the ewes joined showed no evidence of having attained puberty before or during the joining period (progesterone ≤1ng/ml at D14, no lambs produced), 42% were pubertal and lambed, and 12% of ewes appeared pubertal based on progesterone levels but produced no lambs. Therefore, the most limiting factors for lambing performance of yearling ewes were, in order, failure to attain puberty prior to or within the joining period (46%) followed by failure to join and/or maintain a pregnancy to lambing (12%). The latter is probably similar to what is typically observed for infertility in adult (post-pubertal) ewes, with the additional complications that ewe lambs appear more likely to have disrupted cycles and also to lose their pregnancy (Thompson and Paganoni, 2013).

Based on results from this study, some observations can be made:

- Pre-joining weight, condition score and progesterone each explain relatively little, phenotypically, of the variation between ewes in reproductive performance within contemporary groups. The maximum phenotypic correlation between these traits and NLB was generally <0.20.
- In the absence of very high estimates for genetic correlations between traits, it is important to record reproductive performance directly for genetic evaluation purposes and to not rely solely on data from other traits, because accuracy of breeding values for reproductive traits will be low where only correlated data are available. This is also true for adult ewes.
- The current recommendations to improve the reliability of lambing performance of yearling ewes are largely based on obtaining a minimum weight at joining. These recommendations should be expanded to include assessment of condition, which is relatively easily scored on farm. Ewes with condition scores of 4 & 5 had the highest NLB, but were at low frequency in the data. High condition scores could suggest that these ewes achieved higher growth and/or intakes prior to joining and/or were physiologically more mature than their contemporaries. The latter possibility might be confirmed when data become available for mature ewe weight.
- Since progesterone measured from a single field sample was moderately heritable and associated with fertility and reproductive outcomes, both across and within flocks, the method used in this study is considered adequate for evaluating differences between sires in the progesterone levels of their daughters measured early in the joining period. However, the usefulness of this information for genetic evaluation of yearling reproductive performance needs to be evaluated further by obtaining more accurate estimates of genetic correlations. Current estimates indicate that genetically, progesterone concentration appears to be largely independent of weight and condition.
- Because of the relatively low number of records, resulting in large standard errors for parameter estimates, more data are required to obtain accurate estimates of genetic correlations between pre-joining weight or condition score and progesterone with reproductive outcomes. Index calculations are then required to evaluate the overall benefits in response to selection from including additional traits (PJWT, PCOND and PROG) in the genetic evaluation for yearling reproductive performance. The utility of using these measures can then be evaluated against the costs of the additional recording for progesterone.
- Significant service sire effects were evident (not reported in detail here) for fertility and the composite traits NLB and NLW. Choice of service sires (age, experience), use of syndicates, and joining paddock characteristics might have a bigger impact on yearling reproductive performance compared to adult ewes. This should be investigated further.
- Based on limited data from 1 flock only, the efficacy of pharmaceutical intervention could be investigated experimentally for improving commercial flock outcomes. However, this strategy would not seem sensible for selection purposes since it will almost certainly mask early natural early attainment of puberty.

- Extension and pipeline development has only been partially successful. However, MLA are able to promote the use of existing “repro ready” software to improve the quality of reproductive data entering Sheep Genetics analyses. AGBU staff will be able to conduct further breeder visits when more “repro ready” software becomes available to Industry.

The data collated from participating breeders in this project will contribute towards the ability to produce more accurate Australian Sheep Breeding Values (ASBVs) for yearling ewe reproductive performance through Sheep Genetics, and demonstrate that age at joining, pre-joining weight, condition score and the attainment of puberty are all important for successful joining of ewes to lamb as yearlings.

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1 Background

This project was intended to build upon B.SGN.0127 (Genetic Evaluation for the Australian Sheep Industry: Better targeted and faster genetic gain) in specific areas. These were to:

- Investigate reproductive performance of ewes which are first joined to lamb as yearlings, and to
- Improve data collection systems and procedures to improve the quality of data presented for genetic evaluation of reproductive traits from industry flocks.

Previous work under B.SGN.0127 identified that the reproductive performance of yearling ewes was not the same trait genetically as reproductive performance of older ewes (Bunter and Brown, 2013). This resulted in an extension of OVIS (Brown et al, 2007) to separate genetic evaluation of yearling from adult performance, and has motivated further work in this area to better understand the factors that influence yearling reproductive performance, which has been observed to be very variable between flocks (Fogarty et al, 2007; Bunter and Brown, 2013; Newton et al, 2014). This should enable improved models for genetic evaluation to be applied to the yearling reproductive data.

This project extended the existing arrangements under B.SGN.0127 to specifically facilitate data collection, collation and analyses for yearling reproductive performance in pedigreed populations, the sourcing of reliable industry reproductive data for further analyses, and communication of requirements for improving accuracy of data collection for reproductive traits within Industry flocks.

2 Project objectives

The primary project objectives were:

- To obtain a better understanding of the factors contributing to successful yearling lambing outcomes and the models that will be required for genetic evaluation purposes.
- To assist breeders to better understand how to collect high quality data on reproductive traits. Improved performance recording practices by breeders leads to better data quality for genetic evaluation.
- To ultimately contribute to the development of improved genetic evaluation models for reproduction traits and implement them using better industry data in OVIS. Improved accuracy of ASBVs for reproductive traits will lead to better adoption of data based selection on reproductive ASBVs.

3 Methodology

Target Flocks. In this project we specifically targeted the collection of more detailed data on ewes joined to lamb as yearlings from independent breeders with a strong interest in improving reproductive performance generally, and with motivation to mate ewes to lamb as yearlings, if they were not already doing so. Breeders contributing to this project were already receiving Australian Sheep Breeding Values (ASBVs) for the number of lambs weaned (NLW) from Sheep Genetics (SG), indicating that they have already met data quality requirements. Reproductive data included information usually collected via Sheep Genetics through pedigree of lambs, as well as collation of data not currently routinely available in Sheep Genetics databases. Data were therefore from pedigreed populations with relatively complete recording based on mothering up of lambs.

The approach of targeting specific flocks complements the alternative approach of performing analyses across large (but incomplete) data sets to develop improvements for the genetic evaluation system, because it generated the capacity to provide clearer interpretation of the results obtained. Moreover, additional traits were also recorded in these flocks specifically under this project. For example, joining details (dates and service sires), pre-joining weights and condition score (see www.lifetimewool.com.au/conditionscore.aspx) and ultrasound pregnancy scan data. Therefore, preliminary associations between a range of traits routinely evaluated in SG can be estimated from this data, along with the additional traits recorded. Concurrently, a database was developed within AGBU, which this more detailed data can be submitted to.

Diverse breeds were targeted, and included Merinos (predominantly medium prolific and some superfine), a maternal breed (Border Leicester) and two lines of maternal composites, along with a smaller sample of terminal breeds (Poll Dorset, White Suffolk) and terminal composites. With the exception of the Merinos, all of these breeds have been used in the development of existing maternal composites analysed by Sheep Genetics. Participating flocks were located across the Eastern seaboard (NSW and Victoria) and in South Australia.

Yearling performance has been observed to be widely variable across flocks and years within flocks even within breed type (Fogarty et al., 2007; Bunter and Brown, 2013; Thompson and Paganoni, 2013; Newton et al, 2014). Recommendations to Industry to improve outcomes have mostly been based on achieving sufficient weight prior to joining. However, the aetiology of low and variable fertility in yearling ewes is relatively poorly understood. For example, is performance hindered by failure to attain puberty, failure to mate, or failure to maintain the pregnancy? To establish whether attainment of physiological maturity (puberty) was a limiting factor, and genetically correlated with reproductive outcomes, a protocol was established to measure progesterone of young ewes 14 days into the joining period. This protocol was intended to be achievable in the field, and did not involve repeated sampling, which is costly, disruptive and of limited practicality when recording for genetic evaluation purposes.

Progesterone sampling procedure. Progesterone was chosen as the most useful hormone to assay as an indirect indicator of puberty because levels are only elevated post-puberty, secretions are non-pulsatile in nature and progesterone is also elevated for a significant amount of time (11/16 days=69%) during a normal oestrus cycle (Goodman and Inskeep, 2006). Ewe lambs were bled for progesterone sampling only on D14 after their introduction to a teaser or rams at the start of a joining period. This timing was chosen to maximise the chance of correctly detecting pubertal ewes with a single sampling opportunity. The stimulation of puberty or synchronisation of oestrus cycles from the resulting “ram effect” (Martin et al, 1986; Rosa and Bryant, 2002) would further reduce the percentage of cycling ewes which would not be detected with elevated progesterone from a single sample (termed false negatives).

Plasma samples were subsequently analysed at a single laboratory by a single operator using a commercially available enzyme linked immunosorbent assay (ELISA) (Demeditec DE1561, Demeditec Diagnostics GmbH Germany). A 4-point logistic equation was used to estimate progesterone concentrations from absorbance values. Sensitivity of the assay is 0.045ng/ml for human progesterone samples. Progesterone is a highly conserved molecule and though this is an ELISA kit for human samples, it has previously been validated for use in camels (Moghiseh 2008), 5 wild ungulate species including Barbary sheep (Conception Borque 2011) and Kermani ewes (Nasroallah Moradi kor 2012). A validation was conducted to determine that the kit was sensitive enough to differentiate in sheep between progesterone levels of positive controls, using samples from 10 mature cross-bred ewes known to be pregnant and negative controls, 10 Merino wethers aged approximately 1 year. A two-sample t-test confirmed that the mean progesterone levels were significantly different ($P < 0.001$) in the two test groups, whilst comparison of the duplicates showed intra-assay variation to also be within acceptable limits.

For the purposes of parameter estimates presented here, progesterone concentration was treated as a continuous trait. For comparison, progesterone was also converted to a binary trait using a 1ng/ml threshold, or log-transformed.

Statistical analyses. All data were analysed with linear mixed models using ASREML (Gilmour et al, 2006). Systematic effects evaluated for each trait included contemporary group, sire and dam breed, birth type-rear type and dam age class, along with measurement age fitted as a covariate (linear and quadratic tests). Contemporary group construction differed according to trait. Contemporary groups for reproductive and weight traits were defined by flock, date of observation, dam age group and allocation of ewes to management groups by breeders. For example, ewes managed separately are defined by separate management groups within some flocks. Contemporary group for progesterone also included date of bleeding along with assay batch and plate. Significant ($P<0.05$) terms were retained in final models for analyses. Trait heritabilities were estimated using an animal model, with and without service sire fitted as an additional random effect. The likelihood ratio test was used to determine the significance of random effects separately for each trait. Heritability estimates were obtained from univariate analyses, whereas correlations between traits were estimated using a series of bivariate analyses.

4 Results and discussion

4.1 Data characteristics and traits recorded

Nine breeders representing diverse breeds and localities (Table 1) participated in the PhD project of Jo Newton, which facilitated more detailed and supervised on-farm data collection for pedigreed ewes joined to lamb as yearlings. A description of the traits recorded and the breakdown of records by breed type are shown in Tables 2 and 3. Early and pre-joining condition scores were recorded on separate subsets of animals, using a five score scale and based on the procedures outlined in the Lifetime Wool Project. The timing of condition scoring relative to joining was determined by individual flock management practices. The relatively limited number of half scores was rounded up for PCOND. A small proportion of ewes were scanned for fertility only (not scanned for litter size), and these ewes were not assigned a record for SNLB (Table 3) because the values obtained do not indicate the variation in litter size.

The wide variation in fertility of ewe lambs across flocks is also illustrated in Table 1, ranging from 0% to 75%. Low fertility was generally limiting to the subsequent number of records generated for litter size and lamb survival. Raw data characteristics, along with the age at recording for each event, are shown for all other traits by breed group in Table 4. Only two breeders had multiple breed groups, so it is not statistically accurate to directly compare means between breed types. However, it is clear from Table 4 that in the participating flocks, the Merinos were observed to be both older and lighter at weaning and post-weaning, but younger at commencement of joining. It is also observable that synchronisation of young ewes followed by hand mating did not result in more consistent reproductive performance of yearling ewes (flocks 8_S, 9_S and 10_S, Table 1), given the resultant wide range in fertility observed (13 to 43% fertility) for the flocks treated identically within a single location.

Table 1. Overview of industry flocks involved in data collection including breed type, location, number of ewe lambs mated (no. mated), mean fertility level and the number of ewe lambs sampled for progesterone (no. sampled)

Flock No.	**Breed type**	**Breed**	Location*	Weight threshold	No. mated	Mean fertility %	No. sampled
1	Merino	Merino-M	South-West Slopes, NSW	35kg	619	42%	503
2	Merino	Merino-S	Northern Tablelands, NSW	No	54	0%	53
3	Maternal	BL	Central-West, NSW	No	127	28%	111
4	Maternal	BL	Mount Lofty Ranges, SA	No	327	34%	317
5	Maternal	Composite	Riverina, NSW	No	532	55%	408
6	Maternal	Composite	Lower South East Coast, SA	No	783	58%	301
7	Maternal	Composite	South West, VIC	38 kg	473	73%	0
8_S	Terminal	PD	Lower South East, SA	?	70	33%	65
9_S	Terminal	Composite	Lower South East, SA	?	70	43%	66
10_S	Terminal	WS	Lower South East, SA	?	68	13%	66
11	Terminal	WS	South West, VIC	38 kg	101	51%	0
12	Terminal	Composite	South West, VIC	38 kg	65	75%	0

*location as per the forecast regions defined by the Australian Bureau of Meteorology; $_S$ indicates synchronised for hand mating after blood sampling; ?: unknown.

Table 2. A description of traits and their abbreviations

Trait name (units)	Description	Abbreviation
Early condition score (1-5)	Condition score 6-8 weeks prior to joining	ECOND
Pre-joining weight (kg)	Weight at ram in date	PJWT
Pre-joining condition score (1-5)	Condition score at ram in date	PCOND
Progesterone (ng/ml)	Circulating progesterone at Day 14 after exposure to rams/teasers	PROG
Fertility (0=no/1=yes)	Fertility assessed by lambing outcomes Fertility assessed by pregnancy scanning	FERT SFERT
Litter size (N)	Number lambs born per ewe lambed Number of foetus scanned per pregnant ewe	LSIZE SLSIZE
Number of lambs surviving (N)	Number of lambs alive at weaning	LSURV
Percentage lamb survival (%)	LSURV/LSIZE	PLSURV
Number of lambs born (N)	Number of lambs born per ewe joined Number of foetus per ewe joined	NLB SNLB
Number of lambs weaned (N)	Number of lambs weaned per ewe joined	NLW

Table 3. Summary of records by trait group and breed group

Trait group	Maternal	Merino	Terminal	Combined
ECOND	1143	0	179	1322
PJWT	2250	571	277	3098
PCOND	1292	0	131	1423
PROG	1203	564	131	1888
FERT/NLB/NLW	2312	680	304	3296
LSIZE/LSURV/PLSURV	1264	281	133	1678
SFERT	1713	641	294	2648
SNLB	1314	641	294	2249

All flocks were managed by individual breeders at the different locations, with additional traits recorded where possible. Therefore, not all flocks have all traits recorded and the management was not identical across flocks – typical of Industry data. Of the ewes known to be joined, 97% had pre-joining weights recorded, but only 56% had condition scores (Merino's were not scored). The average age at the commencement of joining varied from 217 days (Merino) to 231 (Maternal) to 244 days (Terminal). The corresponding average ages at conception (back-calculated from lambing dates using a standard gestation length of 150 days) were 233, 257 and 261 days, giving a mean interval from the start of joining to conception of 16, 26 and 16 days, and mean lambing ages of 383 days (Merino), 407 days (Maternal) and 411 days (Terminal). The full length of the joining interval at one location (208 animals in 3 flocks) was 2-5 days only due to use of synchronisation and pen mating of ewes. Joining length was between 31 and 62 days for the remaining naturally mated flocks. Assuming a normal oestrus cycle length, a joining interval of only 31 days limited a proportion of ewes to presenting with potentially <2 cycles within the joining period, which would not support maximum fertility rates (130 ewes in flock 5 affected). Most breeders joined ewe lambs to single sires; the exceptions were the Merino flock on the South-West

Slopes, NSW (flock 1, 42% fertility), and the Border Leicester flock in Central-West NSW (flock 3, 28% fertility) who mated in syndicate.

Table 4. Overview of traits recorded on industry flocks by breed type (Maternal, Merino and Terminal) and across breed (combined)

		Maternal	Merino	Terminal	Combined
ECOND	N	1143	0	179	1322
	x_{age}	171 (28.3)		169 (22.8)	171 (27.7)
	mean(sd)	3.03 (0.30)		3.23 (0.42)	3.06 (0.33)
	range	2 - 4.5		2.5 - 4.5	2 - 4.5
PJWT	N	**2250**	**571**	277	3098
	x_{age}	222 (30.5)	214 (11.8)	222 (28.2)	221 (28.0)
	mean(sd)	42.2 (7.85)	38.5 (4.42)	46.0 (7.58)	41.8 (7.56)
	range	18.0 - 73.5	20.5 - 51.5	31.5 - 71.5	18.0 - 73.5
PCOND	N	**1292**	0	131	1423
	mean(sd)	3.07 (0.71)		3.29 (0.57)	3.09 (0.70)
	range	1 - 5		2.5 - 4.5	1 - 5
PROG	N	**1203**	**554**	131	1890
	x_{age}	237 (29.8)	231 (6.91)	211 (33.14)	234 (26.4)
	mean(sd)	1.22 (1.49)	1.13 (1.38)	0.45 (0.64)	1.14 (1.43)
	range	0.00 – 5.0	0.00 – 5.0	0.03 – 5.0	0.00 – 5.0
PROGB	mean(sd)	0.33 (0.47)	0.28 (0.45)	0.08 (0.27)	0.30 (0.46)
	range	0/1	0/1	0/1	0/1
PROG-Log	mean(sd)	-0.22 (0.52)	-0.21 (0.46)	-0.52 (0.33)	-0.24 (0.50)
	range	-1.55 – 0.70	-2.22 – 0.70	-1.53 – 0.70	-2.22 – 0.70
SFERT	N	**1713**	**641**	294	2648
	x_{age}	313 (25.5)	317 (12.0)	325 (32.8)	315 (24.3)
	mean(sd)	0.63 (0.48)	0.38 (0.49)	0.58 (0.49)	0.56 (0.50)
	range	0 / 1	0 / 1	0 / 1	0 / 1
SNLB	N	**1314**	**641**	294	2249
	mean(sd)	1.12 (0.86)	0.49 (0.70)	0.78 (0.76)	0.90 (0.85)
	range	0 - 3	0 - 3	0 - 2	0 - 3
FERT	N	**2312**	**673**	304	3289
	mean(sd)	0.55 (0.50)	0.39 (0.49)	0.44 (0.50)	0.50 (0.50)
	range	0 / 1	0 / 1	0 / 1	0 / 1
LSIZE	N	**1264**	261	133	1658
	mean(sd)	1.50 (0.54)	1.28 (0.46)	1.23 (0.42)	1.44 (0.53)
	range	1 - 3	1 - 3	1 - 2	1 - 3
LSURV	N	**1264**	261	133	1658
	x_{age}^	257 (23.6)	233 (8.01)	261 (27.2)	254 (23.9)
	mean(sd)	1.17 (0.65)	0.75 (0.74)	0.85 (0.57)	1.08 (0.68)
	range	0 - 3	0 - 2	0 - 2	0 - 3
NLB	N	**2312**	**673**	304	3289
	mean(sd)	0.82 (0.84)	0.49 (0.68)	0.54 (0.67)	0.73 (0.81)
	range	0 - 3	0 - 3	0 - 2	0 - 3
NLW	N	**2312**	**673**	304	3289

	mean(sd)	0.64 (0.76)	0.29 (0.59)	0.37 (0.57)	0.55 (0.73)
	range	0 - 3	0 - 2	0 - 2	0 - 3
PLSURV	N	**1264**	261	133	1658
	mean(sd)	0.72 (0.45)	0.57 (0.50)	0.68 (0.47)	0.69 (0.46)
	range	0 - 1	0 - 1	0 - 1	0 - 1

4.2 Progesterone data

The ELISA assay was first validated with samples from negative controls (wethers) and pregnant ewes (not presented). The progesterone data from industry flocks, sampled on D14 of joining, were distributed with a skewed appearance (Figure 1), with a peak in the distribution below 1ng/ml and another (arbitrary) peak at 5ng/ml for samples with progesterone levels exceeding the maximum value of the standards. Pubertal ewes are expected to have progesterone levels >1ng/ml, but not all pubertal ewes will be detected with a single sample because the timing of testing for already cycling ewes may not coincide with their elevated progesterone during a normal oestrus cycle (ie. a false negative). As noted previously, the strategy of measuring at 14 days after the introduction of males was an attempt to make use of the “ram effect” to synchronise ewes and to maximise the opportunities for identifying elevated progesterone throughout both shortened and/or normal cycling patterns. The false negative rate of approximately 24% with a single sample from random sampling within a flock can be reduced to about 12%, even if only 50% of the ewes become naturally synchronised, and falls further as a higher percentage of ewes becomes synchronised. However, the degree of synchronicity could not be accurately established from this data.

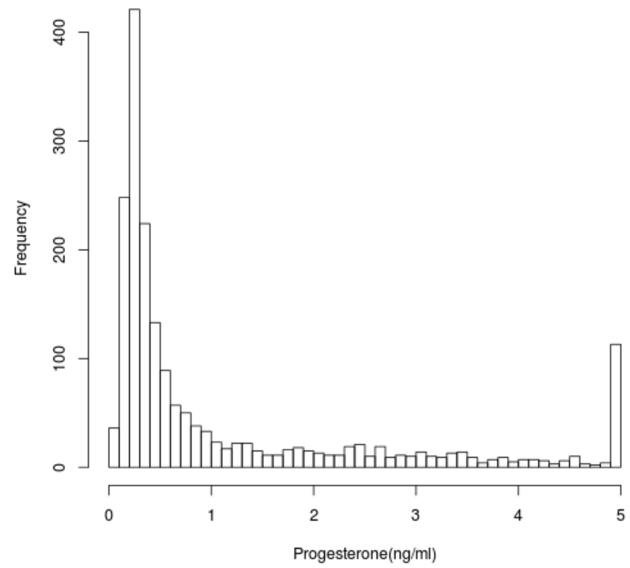

Figure 1: Progesterone levels of young ewes exposed to rams (teasers) for 14 days.

The distributions of progesterone by flock (Figure 2) shows the very different types of distributions which were observed across flocks. A relatively flat distribution with few animals below 1 ng/ml implies that the ewes were already cycling prior to joining (eg flock 6) whereas distributions dominated by samples <1ng/ml (eg flocks 8 & 9) contained many ewes with no evidence of having attained puberty at D14 of the teasing/joining period. The overall distribution of progesterone for ewes which became pregnant (N=786) compared to ewes which did not get pregnant (N=1089) is shown in Figure 3. Ewes which did not become pregnant throughout the entire joining period were most strongly represented at D14 with progesterone levels below 1ng/ml, which suggests that despite being considered an acceptable weight to join, they had not reached puberty at joining and/or did not respond to the "ram effect" by becoming pubertal and successfully mating. A relatively smaller proportion of ewes with progesterone >1ng/ml measured at D14 also did not become pregnant. These ewes appear to have been pubertal, but either failed to mate or maintain a pregnancy. This phenomenon is also true for a percent of adult ewes, since flocks generally do not have 100% fertility. Ram failure was also a strong possibility for some this group (flock 2 had zero fertility). Finally, a proportion of ewes with low progesterone also became pregnant. This group of ewes would contain both the false negatives noted above, as well as ewes which had sufficient time during the joining period to become pubertal and successfully mate.

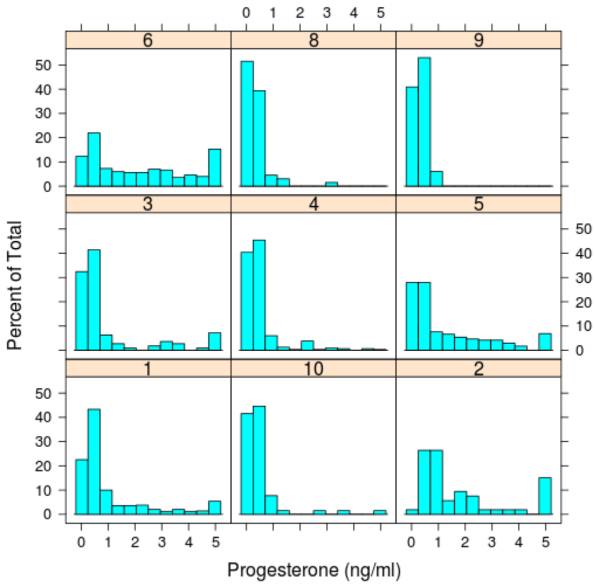

Figure 2. Progesterone by flock

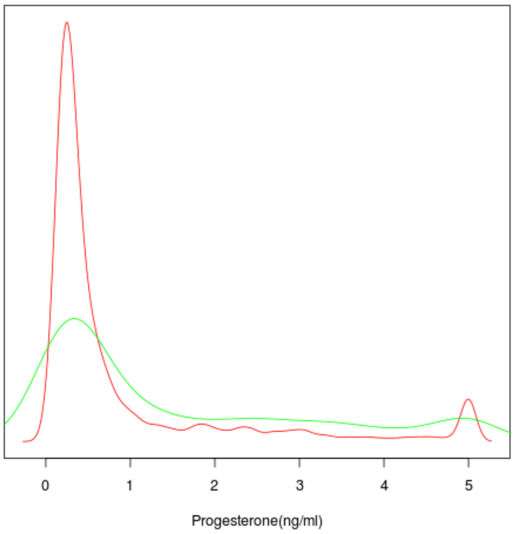

Figure 3. The distribution of progesterone for ewes which became pregnant (green line) compared to ewes which did not become pregnant (red line) at joining

The association between adjusted progesterone levels and pregnancy rates across flocks is illustrated in Figure 4. As the percent of ewes assessed as pubertal rose above the predicted false discovery rate of 24% for unsynchronised ewes, the percent of ewes which became pregnant also increased. Based on the progesterone levels from this assay, 29% of ewes were considered pubertal and 71% were not. Ewes assessed pubertal at day 14 of joining had overall a higher fertility rate than ewes with progesterone <1ng/ml (59 vs 35%).

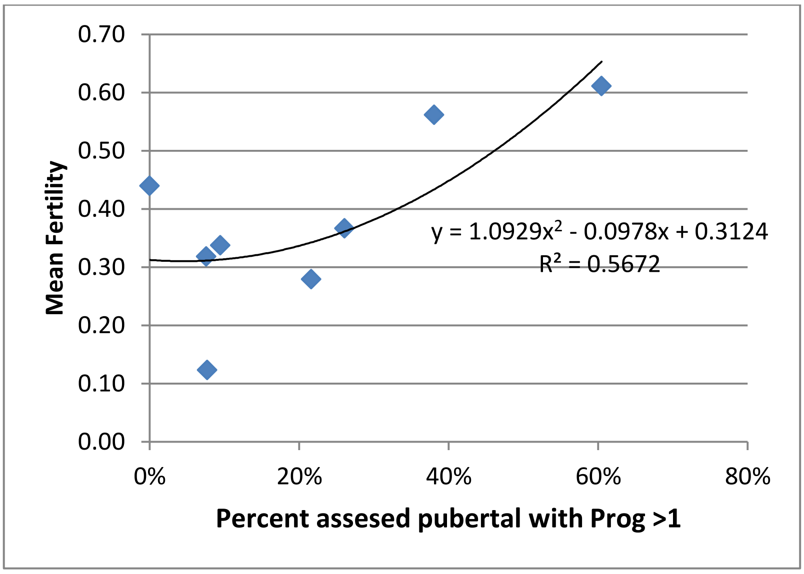

Figure 4. A scatterplot of the % pubertal by % fertile across flocks (excluding flock 2).

The exception to this pattern was flock 2 (Superfine Merinos) where 49% of the ewes recorded for progesterone appeared to be pubertal, but no ewes became pregnant. This flock was single sire mated, but sire failure was not identified even though it is implied by an outcome of zero fertility. On the other hand, very poor fertility of ewes joined to lamb as yearlings has also been observed previously in the INF flock at Kirby research station (Newton et al, 2014), which was also predominantly of the fine-superfine ewe type. Therefore, it could be that speculated that Superfine Merino ewes become physiologically pubertal (as suggested by progesterone levels), but there are other factors at play which result in poor fertility. This possibility could be investigated further for Superfine Merino's if breeders of this Merino type feel that joining ewes to lamb as yearlings is an economically viable management practice, because the sample size for Superfine merinos was very low in this study.

It is also possible to exclude flocks which were synchronised for pen-mating after progesterone was measured on Day 14 (Figure 5), because these ewes had pharmaceutical intervention to assist their reproductive performance prior to mating, and were supervised for mating, once only. The association between puberty and flock fertility across flocks was improved when considering results from only naturally mated flocks (Figure 4 vs Figure 5: R^2 57% vs 78%), and the coefficient of 0.57 (Figure 5) shows that the change in the proportion of ewes considered pubertal was strongly mirrored by the change in the proportion of ewes which were fertile across flocks, consistent with the observed frequency (59%) of pubertal ewes which lambed. Moreover, the accompanying change in y-intercept (Figure 4 vs Figure 5: 0.31 vs 0.24) implies that pharmaceutical intervention was successful in slightly elevating the fertility rate of young ewes. However, since this possibility is based solely on the change in the estimated relationship between puberty and fertility (Figure 4 vs Figure 5) using data solely from one location, this management option needs to be investigated further using a controlled trial where the reproductive performance of ewes with and without pharmaceutical intervention can be directly compared.

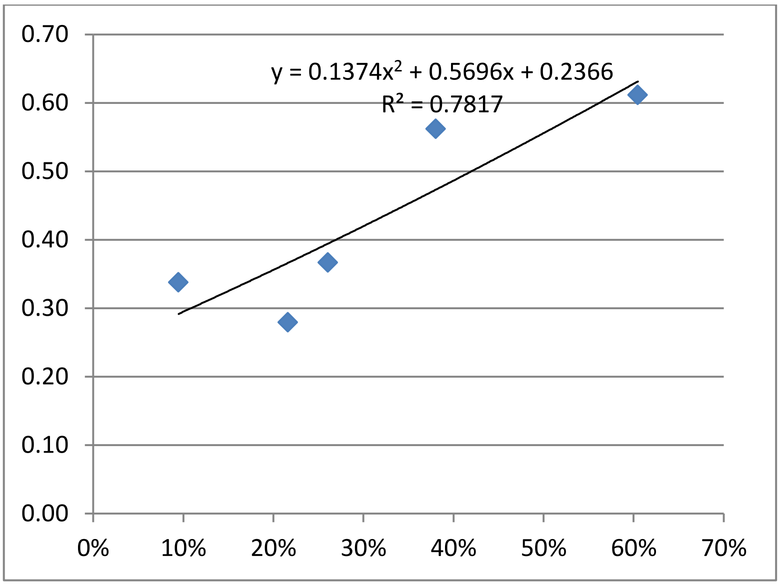

Figure 5. A scatterplot of the % pubertal by % fertile across flocks (excluding flock 2 and the synchronised flocks).

Overall, approximately 41% of the ewes which were considered physiologically pubertal based on progesterone levels did not produce any lambs (~12% of all ewes joined), which could indicate false positives, failed behavioural oestrus resulting in no mating, mating but no pregnancy, or pregnancy loss. The failure of pubertal ewes to become pregnant appears much higher in young compared to adult ewes (eg 41% vs 5-10%), and this observation is consistent with other studies. In a relatively small experiment involving 224 Merino ewes, Thompson and Paganoni (2013) observed that while 93% of ewes reached puberty by the end of the 68 day joining period, only 81% of ewes mated and only 34% became pregnant. The low pregnancy rate was observed because successful matings (resulting in pregnancy) occurred in <40% of cases from each mating round, 7% of ewes skipped a cycle before there was an opportunity for rebreeding, with similarly low success, and 27% of ewes cycled only once within the 68 day breeding period. Moreover, 6.7% of ewes lost their pregnancy between scanning and lambing. These observations illustrate why a percentage of young pubertal ewes produce no lambs. Using a simple threshold of 1 ng/ml will also introduce some false positives with respect to identification of puberty, since ELISA assays also have some variability. However, the extent of false positives and the relative contributions of all effects to outcomes were not known in this data.

Conversely, approximately 35% of the ewes considered not to be pubertal based on progesterone levels at D14 produced lambs (25% of all ewes joined). As noted previously, these ewes include false negatives (ie. pubertal ewes measured in an uninformative part of their reproductive cycle) and also ewes which first became pubertal and then successfully mated within the joining period after D14. In the work of Thompson and Paganoni (2013), it was also reported that the percent of Merino ewe lambs identified as pubertal increased from 16 to 60% over a two week teasing period (compared to 83% by D49 and 93% by D82 after first exposure to males), suggesting that ewes achieving puberty after D14 will contribute significantly to this 35%. The percent of ewes which subsequently lambed is also consistent with the low fertility rate/mating noted above. These observations should be confirmed with data from more flocks, but the high percentage on non-pubertal ewes at D14, along with the association between a single assessment of puberty at D14 and overall flock fertility, supports the concept that failure to attain puberty (and synchronicity?) prior to or early in the joining period is probably the major problem which creates variation in lamb production from young ewes joined to lamb as yearlings in field data.

4.3 Systematic and random effects

The significance of systematic effects for each trait is shown in Table 5. The amount of variation in the raw data explained by the full model is illustrated by the R^2. Significant model terms explained a lot of the variation observed in PJWT (66%) or PCOND (47%), but R^2 were lower for PROG, SFERT and SNLB (28-31%), and lower still (<17%) for all reproductive traits recorded at or after lambing. For all traits, contemporary group was the main factor describing variation (CGP accounted for between 52-86% of variation explained by the full model), while contributions from other factors were comparatively less. There was generally a lot of unexplained variation for reproductive traits recorded at lambing, which is only partly to do with the distributions of these traits (ie they are largely categorical in nature). The other cause of low R^2 values is an inability to identify significant contributing factors.

While birth type and/or rear type of the young ewe were significant factors affecting pre-joining weight and early or pre-joining condition score, as expected, they were not consistently significant factors affecting progesterone levels or reproductive outcomes in these models. The lack of significant service sire effect for PJWT, PCOND and PROG (which an animal's subsequent mate cannot directly influence) simply illustrates that individual service sires were not systematically allocated to ewe groups varying in their characteristics for these traits. Therefore, service sire effects for reproductive traits should not be influenced by variation between mating groups in weight or condition of the young ewes presented to the sires at joining.

Table 5: Summary of significance of fixed effects and random effects for traits from the combined data.

	Systematic Effects							Random effect
Trait	CG	SB/DB	BTRT	Measurement age	(measurement age)^2	Dam Age Class	R^2 %	ssire
ECOND	***	*	***	***	ns	ns	10.6	nr
PJWT	***	***	***	***	***	***	66.2	nr-ns
PCOND	***	***	***	***	***	***	46.9	nr-ns
PROG	***	ns	ns	***	ns	***	30.8	nr-ns
SFERT	***	***	ns	***	***	***	27.7	sig
SNLB	***	***	*	***	***	***	28.8	sig
FERT	***	***	ns	***	***	***	17.5	sig
LSIZE	***	ns	ns	ns	ns	ns	8.7	ns
LSURV	***	ns	ns	ns	ns	ns	11.3	sig
NLB	***	***	ns	***	***	***	17.0	sig
NLW	***	***	ns	***	***	***	15.5	sig
PLSURV	***	***	ns	ns	ns	ns	13.3	sig

*P<0.05;**P<0.01;***P<0.001; nr: not relevant; sig & ns: significant or not significant at P<0.05; CG: contemporary group; SB/DB: sire and dam breed; BTRT: birth and rear type

Solutions for systematic effects are shown in Table 6. In the base model, ewe lambs which were older at the commencement of joining were significantly heavier, had better condition score, had higher progesterone and improved NLB. Based on these estimates of solutions, a 60 day difference in age would be equivalent to differences of +9.6kg in pre-joining weight, +0.84 change in condition score and +0.72 ng/ml progesterone (base model), which is quite considerable.

Trends for age of dam effects were less clear, and this might be due to some confounding between age of dam and subsequent management of their ewe lambs. Ewe lambs born to yearling dams were generally lighter and had lower condition scores prior to joining relative to offspring of older ewes. They also had significantly lower progesterone early in the joining period (-0.853 ng/ml, base model), but these trends were not reflected in a significantly reduced NLB for daughters of ewe lambs (Table 6). However, large standard errors for the yearling dam age class show that there were relatively few daughters of yearling ewes in this data.

Adding pre-joining weight to the base model (base + weight model) illustrated that in addition to the effect of increasing age at joining, increasing weight (for age) was associated with increased progesterone at joining and also increased NLB. However, a difference of 10kg of weight would alter progesterone by 0.29 ng/ml (base+weight model) after correction for age, which is a fairly small effect. Without concurrent correction for age, which is auto-correlated with weight, the regression on weight and dam age effects were increased (not presented). This result indicates that there was some association between age of ewe and/or age of the ewe's dam in this data, and the magnitude of regressions on weight were reduced by accounting for variation in age. In some flocks, very light ewe lambs were not joined (or recorded for progesterone), which might also have reduced the magnitude of solutions for weight. Nevertheless, both age and weight were significantly associated with each other and with progesterone levels.

The more extended models including condition score are predominantly relevant to Maternal breeds only, because Merinos were not condition scored and there were also relatively few Terminal ewes present in the data. Extension of the model for progesterone to include condition score showed a biologically sensible but statistically insignificant ($P>0.05$) association between condition score and progesterone level: ranging from -0.271 to 0.182 ng/ml from scores 1 to 5 (deviated around score 3); with the biggest change from score 3 to 4. This suggests that after accounting for age and weight, increasing condition score could be associated with an increasing likelihood of a ewe achieving puberty. However, the number of ewes with records for both pre-joining condition score and progesterone was limited in this data, reducing experimental power. In support of this, condition score pre-joining was significantly ($P<0.05$) associated with the NLB in a similar pattern, and this association was consistent with the results of Hatcher et al (2007a, b) for maiden and mature Merino ewes.

In models extended to include condition score, the overall solution for the regression of progesterone on weight was not reduced, whereas the regression of NLB on weight was reduced by accounting for pre-joining condition. The combined solutions for weight and the deviation from the average regression on weight demonstrated that weight was a less significant factor affecting progesterone levels or NLB for maternal breed ewe lambs within condition scores of 4 or 5 achieved shortly prior to joining. However, these are also very high scores. It could be speculated that ewes with very high condition scores at a young age might be earlier maturing than ewes with lower scores. However, it is unclear whether increasing condition score through nutritional management prior to joining would improve NLB in ewes joined to lamb as yearlings in a similar manner, because these ewes might still not be physiologically mature (ie non-pubertal) even if condition score is nutritionally increased. Condition score has been suggested as an alternative to recording live weight to monitor nutritional outcomes for ewes (van Burgel et al 2011), but these traits are not identical genetically or phenotypically (Tables 7 & 8) and therefore do not provide identical information. The role of photoperiod for the timing of puberty relative to the growth achieved (indicated by both weight and condition score) might also be important (Foster at al 1988).

Table 6: Solutions for some systematic effects from the combined data (solutions exceeding 2xSE are in bold)

Effect	Levels	Trait			
		PJWT	PCOND	PROG	NLB
Base model					
Measurement age***	1 2	**0.16 (0.01)** ns	**0.014 (0.001)** ns	**0.012 (0.002)** ns	**0.010 (0.001)** **-0.0001 (0.0000)**
Dam age class***	1	-0.379 (0.564)	-0.020 (0.075)	**-0.853 (0.193)**	0.077 (0.076)
	2	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
	3	0.323 (0.258)	0.079 (0.045)	0.113 (0.089)	-0.030 (0.040)
	4	**0.614 (0.282)**	0.053 (0.049)	0.142 (0.096)	-0.035 (0.044)
	5	0.436 (0.320)	0.007 (0.059)	0.213 (0.115)	-0.050 (0.050)
	6	-0.126 (0.482)	-0.071 (0.084)	**0.391 (0.163)**	-0.143 (0.077)
	7	**1.156 (0.558)**	-0.072 (0.102)	0.141 (0.190)	**-0.234 (0.089)**
	8	1.452 (0.881)	0.124 (0.254)	-0.015 (0.301)	-0.293 (0.144)
Base + weight model†					
PJWT***	1	na	na	**0.029 (0.007)**	**0.016 (0.003)**
Base + condition score model†					
CS ns/***	1	na	na	-0.271 (1.213)	-0.739 (0.373)
	2	na	na	-0.127 (0.119)	**-0.301 (0.059)**
	3	na	na	0.00 (0.00)	0.00 (0.00)
	4	na	na	0.240 (0.122)	0.098 (0.056)
	5	na	na	0.182 (0.258)	0.201 (0.135)
Base + weight + condition score + wt × condition†					
PJWT.CS**/*	1.1	na	na	0.00 (0.00)	0.027 (0.169)
	1.2	na	na	0.019 (0.017)	**0.021 (0.008)**
	1.3	na	na	0.00 (0.00)	0.00 (0.00)
	1.4	na	na	**-0.046 (0.014)**	-0.010 (0.007)
	1.5	na	na	-0.033 (0.040)	-0.003 (0.023)
CS */ns	1	na	na	-0.151 (1.208)	-0.051 (3.59)
	2	na	na	0.094 (0.150)	-0.083 (0.086)
	3	na	na	0.00 (0.00)	0.00 (0.00)
	4	na	na	**0.349 (0.140)**	0.109 (0.064)
	5	na	na	0.225 (0.445)	0.178 (0.251)
PJWT***	1	na	na	**0.032 (0.008)**	**0.012 (0.003)**

*P<0.05; **P<0.01; ***P<0.001; †Age and dam age class included in model (solutions not presented).
CS: condition score with 0.5 scores rounded up to the next score.

4.4 Estimates of heritabilities

Estimates of heritabilities from the combined breed analyses are shown in Table 7. Within breed group estimates are available elsewhere, along with estimates from alternative models, but were generally low accuracy because of low N and are not presented here. There were considerably fewer records for condition scores than for pre-joining weight.

Therefore, estimates involving ECOND or PCOND, and LSIZE, LSURV or PLSURV are based on substantially fewer records than for the other traits.

Pre-joining weight was highly heritable (0.42±0.07) and this estimate is likely biased upwards through both the diverse population used for parameter estimation and an inability to accurately estimate the maternal genetic component for this trait with the prevailing data structure. Condition score was moderately heritable (0.18±0.07), but with more variation observed in pre-joining scores compared to an earlier (post-weaning) assessment. Parameter estimates for the reproductive traits were generally low (occasionally negligible), compared to studies involving cross-bred ewes (Afolayan et al 2008), but were similar to other estimates from purebred maternal (eg Brash et al 1994a,b) or Merino (Herbart et al 2010) populations and within expectation given the relatively limited amount of data available.

Progesterone concentration measured in young ewes under the applied protocol had a heritability of 0.28±0.07. Progesterone treated as a binary (threshold) trait was also lowly heritable (PROGB: 0.08±0.04), while estimates for PROG-Log were intermediate. PROGB has a lower heritability than PROG because of the conversion of continuous PROG values to a binary scale; the calculated estimate for the underlying scale of PROGB is actually higher at 0.15, similar to that of PROG-Log. The heritability for PROG is much higher than date of first oestrus in sheep established using raddle marks. For example, Beef and Lamb NZ (2011) reported a heritability of 9-10% for date of first oestrus in ewe hoggets. The heritability of PROG in this study is closer to heritability estimates for other traits indicative of puberty, such as age at first egg (poultry) or age at first corpus-lutea (beef cattle, Johnston et al, 2009), which can be observed accurately without a male presence, and which do not require expression of either behavioural oestrus of females or mating behaviour of males to obtain the trait observation.

Table 7. Estimates of heritabilities from the base model (univariate analyses)

Trait	h^2	ss^2	σ^2p
ECOND	0.18 (0.07)	Ne	0.10
PJWT	0.42 (0.07)	Ne	20.6
PCOND	0.18 (0.07)	Ne	0.26
PROG	0.28 (0.07)	Ne	1.55
PROGB	0.08 (0.04)	Ne	0.19
PROG-Log	0.18 (0.06)	Ne	0.18
SFERT	0.08 (0.04)	Ne	0.18
SNLB	0.04 (0.03)	Ne	0.53
FERT	0.07 (0.03)	0.04 (0.02)	0.21
LSIZE	0.10 (0.05)	Ne	0.26
LSURV	0.06 (0.04)	0.02 (0.01)	0.43
NLB	0.04 (0.03)	0.03 (0.01)	0.56
NLW	0.04 (0.03)	0.04 (0.02)	0.46
PLSURV	0.01 (0.03)	0.03 (0.02)	0.19

4.5 Correlations between traits

Correlations between traits from bivariate analyses are shown in Table 8. Genetic correlations with other traits were not estimated for PLSURV, which was not heritable in this data. Residual covariances (and therefore phenotypic correlations) were not estimated when no animals had both traits recorded, or no variation was present in one trait when both traits were recorded, or when trait values were identical for animals with both trait records. There were no significant changes to estimates of genetic correlations between traits from models where service sire effects were included compared to those presented here, where service sire effects were not considered. All estimates of genetic correlations involving the lowly heritable reproductive traits are accompanied by large standard errors.

Pre-joining weight and condition scores were moderately correlated phenotypically (rp: 0.45±0.02), very highly correlated genetically (rg: 0.84±0.09), and had similar low phenotypic correlations (0.12±0.03 and 0.07±0.04) with progesterone. Corresponding genetic correlations between PJWT or PCOND with PROG were 0.31±0.15 and -0.06±0.29 indicating that progesterone was genetically correlated with weight.

Both pre-joining weight and condition score were positively associated phenotypically with fertility and/or litter size, resulting in overall phenotypic correlations between PJWT or PCOND with NLB or NLW of between 0.01 to 0.12. Corresponding genetic correlations ranged between 0.09 and 0.51, but standard errors were large (0.2 to 0.3). Genetic correlations suggest overall that the genetic control of condition score, which combines an assessment of muscle and fat cover, might be a slightly better indicator of a young ewes' ability to produce and rear lambs successfully compared to weight alone. However, estimates of parameters are not very accurate and also represent different sub-samples of the study population. Neither PJWT nor PCOND were phenotypically associated with the percentage of lambs which survive until weaning (which was not heritable), but they were associated with the number of lambs at weaning through their associations with fertility and litter size.

Progesterone, when treated as either a continuous or binary trait, was highly correlated phenotypically (rp about 0.75±0.02) and genetically (rg: 0.99) regardless of the model fitted, as expected (not presented). Including PJWT or PCOND as covariates in the progesterone model slightly reduced trait heritability (0.22-0.26 vs 0.28), which supports non-zero genetic correlations between progesterone and weight or body condition. Progesterone (PROG) had positive phenotypic correlations with FERT (0.15±0.02), NLB (0.12±0.02) and NLW (0.06±0.02); the accompanying genetic correlations were also positive and of larger magnitude, but had large standard errors. As indirect traits, phenotypic correlations indicate that progesterone was more strongly associated with fertility that PJWT or PCOND, whereas PCOND and PWT were (relative to PROG) more strongly associated with litter size.

Estimates of co-heritabilities (CoH) are provided in Table 9, and indicate approximately how much genetic information an indirect trait (eg PJWT, PCOND and PROG) provides towards estimates of genetic merit for the reproductive traits of interest, such as FERT, LSIZE, LSURV, NLB and NLW. Coheritabilities are calculated as h_1h_2rg and can therefore take a negative value if the estimated genetic correlation between traits is negative. Estimates of coheritabilities demonstrate that PCOND provided useful information on the genetic merit for FERT because the estimated coheritability is larger than the corresponding heritability for

FERT. This suggests that PCOND is a useful indirect trait which can contribute to improved accuracy for estimates of breeding values for reproductive performance; fertility in particular. Pre-joining weight and PROG also provided some genetic information towards these traits, but genetic correlations were comparatively lower. However, since all parameter estimates had large standard errors, and not all animals had all of the same traits recorded, establishing the relative contribution of different indirect traits on reproductive outcomes is imprecise. In particular, progesterone was only recorded on a subsample of animals.

Coefficients of determination were almost negligible between PJWT or PCOND and PROG, which indicates that these traits were largely not associated with each other phenotypically, such that the progesterone assay essentially provided information on hormone status which was largely independent of phenotypes for weight and condition. In contrast, the R^2 of 0.25 between PJWT and PCOND showed that a significant proportion of variation in one trait was associated with variation in the second.

Table 8: Correlations between traits (h^2 diagonal; phenotypic above diagonal; genetic below diagonal; bold values exceed 2×se)

TRAITS	ECOND	PJWT	PCOND	PROG	PROG +WT	PROG+CS	PROG +BO	PROG-B	PROG-Log	SFERT	SNLB	FERT	LSIZE	LSURV	NLB	NLW	PLSURV
ECOND	**0.18**	**0.27 (0.04)**	ne*	ne*	ne*	ne*	ne*	ne*	ne*	0.05 (0.05)	0.00 (0.04)	0.02 (0.04)	-0.02 (0.05)	0.00 (0.05)	0.01 (0.04)	0.01 (0.04)	0.05 (0.05)
PJWT	0.45 (0.28)	**0.42**	**0.45 (0.02)**	**0.12 (0.03)**	**0.08 (0.03)**	**0.11 (0.03)**	**0.08 (0.03)**	**0.10 (0.03)**	**0.08 (0.03)**	**0.11 (0.02)**	**0.12 (0.02)**	**0.08 (0.02)**	**0.07 (0.03)**	0.04 (0.03)	**0.10 (0.02)**	**0.07 (0.02)**	-0.01 (0.03)
PCOND	0.93 (0.60)	**0.84 (0.09)**	**0.18**	0.07 (0.04)	0.03 (0.04)	**0.11 (0.05)**	**0.42 (0.04)**	**0.11 (0.04)**	0.06 (0.04)	**0.12 (0.03)**	**0.12 (0.03)**	0.05 (0.04)	**0.14 (0.03)**	0.01 (0.04)	0.01 (0.04)	**0.12 (0.03)**	-0.02 (0.04)
PROG	0.01 (0.50)	**0.31 (0.15)**	-0.06 (0.29)	**0.28**	ne*	ne*	ne*	ne*	ne*	**0.16 (0.03)**	**0.17 (0.03)**	**0.15 (0.02)**	-0.03 (0.04)	-0.07 (0.04)	**0.12 (0.02)**	**0.06 (0.02)**	-0.04 (0.04)
PROG + WT	0.00 (0.51)	0.27 (0.16)	-0.12 (0.29)	ne*	**0.26**	ne*	ne*	ne*	ne*	**0.15 (0.03)**	**0.16 (0.03)**	**0.14 (0.02)**	-0.04 (0.04)	-0.07 (0.04)	**0.12 (0.02)**	**0.06 (0.02)**	-0.04 (0.04)
PROG + CS	-0.02 (0.51)	0.29 (0.15)	-0.04 (0.29)	ne*	ne*	**0.27**	ne*	ne*	ne*	**0.16 (0.03)**	**0.17 (0.03)**	**0.15 (0.02)**	-0.03 (0.04)	-0.07 (0.04)	**0.12 (0.02)**	**0.06 (0.02)**	-0.04 (0.04)
PROG + BO	-0.07 (0.53)	0.21 (0.17)	0.18 (0.27)	ne*	ne*	ne*	**0.22**	ne*	ne*	**0.15 (0.03)**	**0.16 (0.03)**	**0.14 (0.02)**	-0.04 (0.04)	-0.07 (0.04)	**0.11 (0.02)**	**0.06 (0.02)**	-0.04 (0.04)
PROG- B	0.14 (0.78)	-0.10 (0.27)	-0.71 (0.50)	ne*	ne*	ne*	ne*	**0.08**	ne*	**0.19 (0.03)**	**0.22 (0.03)**	**0.16 (0.02)**	-0.04 (0.04)	-0.04 (0.04)	**0.13 (0.02)**	**0.08 (0.02)**	-0.01 (0.04)
PROG-Log	-0.02 (0.63)	0.24 (0.18)	-0.27 (0.35)	ne*	ne*	ne*	ne*	ne*	**0.18**	**0.18 (0.03)**	**0.21 (0.03)**	**0.16 (0.02)**	-0.05 (0.04)	-0.07 (0.04)	**0.14 (0.02)**	**0.08 (0.02)**	-0.03 (0.04)
SFERT	**0.92 (0.27)**	0.12 (0.24)	**0.78 (0.28)**	0.23 (0.25)	0.21 (0.26)	0.21 (0.26)	0.19 (0.26)	0.19 (0.37)	0.18 (0.30)	**0.08**	**0.84 (0.01)**	**0.86 (0.01)**	-0.03 (0.04)	**-0.14 (0.04)**	**0.75 (0.01)**	**0.57 (0.01)**	**-0.14 (0.04)**
SNLB	0.17 (0.40)	-0.16 (0.27)	0.34 (0.36)	0.38 (0.29)	0.37 (0.29)	0.37 (0.29)	0.36 (0.30)	0.53 (0.40)	0.26 (0.35)	**0.77 (0.12)**	**0.07**	**0.74 (0.01)**	**0.84 (0.01)**	**0.45 (0.03)**	**0.85 (0.01)**	**0.64 (0.01)**	**-0.13 (0.03)**
FERT	-0.03 (0.42)	0.12 (0.19)	**0.79 (0.22)**	0.26 (0.22)	0.25 (0.23)	0.25 (0.23)	0.25 (0.23)	0.21 (0.32)	0.25 (0.26)	**0.71 (0.13)**	**0.80 (0.13)**	**0.09**	ne*	ne*	**0.87 (0.00)**	**0.71 (0.01)**	**-0.08 (0.04)**
LSIZE	-0.22 (0.42)	0.12 (0.23)	-0.28 (0.38)	0.08 (0.31)	0.07 (0.31)	0.08 (0.31)	0.07 (0.32)	0.04 (0.44)	-0.14 (0.34)	0.08 (0.40)	**0.93 (0.09)**	0.11 (0.28)	**0.10**	**0.58 (0.02)**	ne*	**0.58 (0.02)**	**-0.17 (0.03)**
LSURV	-0.40 (0.55)	0.04 (0.30)	-0.14 (0.46)	0.13 (0.38)	0.11 (0.38)	0.13 (0.38)	0.13 (0.39)	0.01 (0.54)	0.04 (0.43)	0.16 (0.54)	**0.76 (0.34)**	0.46 (0.37)	0.96 (0.23)	**0.06**	**0.71 (0.01)**	ne*	**0.66 (0.02)**
NLB	-0.12 (0.39)	0.15 (0.20)	0.51 (0.28)	0.28 (0.24)	0.26 (0.24)	0.27 (0.24)	0.26 (0.25)	0.22 (0.35)	0.21 (0.28)	**0.55 (0.20)**	**0.97 (0.08)**	**0.91 (0.05)**	0.04 (0.46)	**1.00 (0.08)**	**0.08**	**0.82 (0.01)**	**-0.24 (0.03)**
NLW	-0.23 (0.39)	0.09 (0.20)	0.43 (0.28)	0.14 (0.25)	0.12 (0.25)	0.13 (0.25)	0.12 (0.26)	0.00 (0.36)	0.10 (0.29)	**0.62 (0.21)**	**0.99 (0.15)**	**0.92 (0.07)**	**0.84 (0.16)**	0.05 (0.56)	**0.98 (0.05)**	**0.08**	**0.67 (0.02)**
PLSURV	ne*	ne*	ne*	ne*	ne*	ne*	ne*	ne*	ne*	ne*	ne*	ne*	ne*	ne*	ne*	ne*	**0.00**

Table 9: Coefficients of determination between indirect traits calculated from estimates of phenotypic correlations, along with coheritabilities between indirect traits and target reproductive traits, calculated from estimates of heritabilities and genetic correlations (all from Table 8).

		Coefficient of determination between indirect traits (r^2)			
Trait	h^2	PJWT	PCOND	PROG	PROG+WT
ECOND	0.18				
PJWT	0.42		0.20	0.01	ne
PCOND	0.18			<0.01	<0.01
PROG	0.28				ne
		Coheritabilities			
FERT	0.09	0.02	**0.10**	0.04	0.04
LSIZE	0.10	0.03	-0.04	0.01	0.01
LSURV	0.06	0.00	-0.02	0.02	0.01
NLB	0.08	0.03	0.06	0.04	0.04
NLW	0.08	0.02	0.05	0.02	0.02
PLSURV	0.00	0.00	0.00	0.00	0.00

4.6 Extension and pipeline development work

Jo Newton visited all breeders during the data collection process for her PhD project involving yearling ewes, which has ultimately contributed towards their improved understanding of what is required for accurate recording of reproductive performance generally. Several participating breeders were already major contributors of reproductive data to the SG analyses via mothering up of lambs, so there will be a direct benefit of the education process in this area.

Jo also provided customised spreadsheets as templates suitable for recording the required data, but they were very poorly utilised on farm. For example, breeders preferred to provide additional weights directly from automated weighing with electronic tag files, or condition score separately in excel or “visuals” files from Pedigree Master, or joining details verbally, etc. This is the second time AGBU have (unsuccessfully) attempted to get more complete data from breeders by providing pre-formatted spreadsheets which are not part of their normal performance recording software or procedures. Therefore, an interim approach to data collection within the Australian sheep industry without appropriate herd recording software routinely available to breeders is unlikely to be successful, because breeders are not sufficiently motivated to duplicate their recording efforts. This is completely understandable, but also highlights that strong prioritisation needs to be given to enabling routinely used software to record and validate all data intended for use in genetic evaluation systems.

Simultaneously, SG and AGBU have worked with several private software developers to progress the capabilities of commercially available recording software. This was identified and reported as a problem to Sheep Genetics by AGBU in 2007. Since the majority of data contained in the SG databases had been recorded using Pedigree Wizard, it is the lack of capabilities in this software which have limited improvement in the quality of reproductive data used for genetic evaluation. However, the joining module for Pedigree Master (formerly called Pedigree Wizard) is scheduled for release in January 2015. BreedElite software is now functional to enable accurate recording of joining details and provide output in the .xml format specified by SG. This includes capabilities for pregnancy scan data, the utility of which has been examined under project B.SGN.0127. Practical systems and Sapien are estimated to be about 80% towards achieving full capability for recording reproductive data accurately and providing it to Sheep Genetics. However, the full pipeline can only be tested as data enter the SG databases from the .xml files provided.

With respect to the INF database, AGBU has developed a more comprehensive database capable of storing the information required for reproductive performance, which should be used. The spreadsheets provided by Jo Newton to breeders were set up to be compatible with the increased database functionality, but the failure of breeders to provide data on these spreadsheets means that this data has not yet been uploaded to the database. We propose to do so when Jo's data are considered complete. She will also be obtaining some more data from the second drop of the focus ewes in this project.

The deficiencies of the current INF database with respect to completeness of reproductive outcomes for followers will be addressed, where possible.

In summary:

- MLA (Sheep Genetics) should continue to actively promote the use of "repro ready" flock recording software already available in Industry which is capable of accurate recording of reproductive data. At the time of this report, the only fully "repro ready" software is BreedElite.
- Further extension can be conducted by staff at AGBU for clients of all "repro ready" software as the software becomes available, to directly facilitate the entry of improved quality reproductive data and pregnancy scan data into the SG databases.
- Resource flocks need to be reminded/updated on their obligations and procedures to obtain accurate reproductive data.

5 Conclusions

In this project, considerable progress was made with respect to collecting more detailed data on the reproductive performance of ewes joined to lamb as yearlings through the PhD project of Jo Newton. The data supported highly variable reproductive performance between flocks. Ewe age, pre-joining weight and condition score, and progesterone levels were all factors associated with subsequent lambing outcomes within and across flocks. Therefore, recommendations based solely on pre-joining weight might be limited in their utility, since weight and progesterone concentrations (a proxy for the attainment of puberty) are largely uncorrelated. Progesterone recorded in the field on young ewes 14 days after exposure to males was a moderately heritable trait. However, confounding between model terms (eg contemporary group with other factors, such as weight, dam age etc) influences the magnitude of estimates of solutions for fixed effects along with correlations between indirect traits and reproductive outcomes.

The relatively low number of records generated within this study (which was partly due to low lambing percentages) limited the accuracy of parameter estimates. Therefore, further data should be obtained if more accurate genetic parameters are required. For progesterone in particular, the assessment of utility requires a cost-benefit analysis based on the predicted improvements in response to selection through recording progesterone, and identification of cheaper, more farmer friendly methods for measuring progesterone levels. Currently the genetic correlations do not look sufficiently high to record this trait in isolation of PJWT or PCOND, which are much easier to record on farm. However, individual variation in weight and condition provided very little information on whether ewes had attained puberty or not. Therefore, preliminary estimates suggest that when combined together, these three traits will be synergistic with respect to information content and should provide some improvement in accuracy of EBVs for yearling lambing performance, at least in flocks where fertility rates are relatively low. However, more accurate parameters to apply in index calculations are required to confirm this.

A lack of suitable software for data collection and collation, and accompanying pipeline development to get data into Sheep Genetics databases, currently remains the most limiting factor to improving reproductive performance within the Sheep Industry generally.

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