EVOLUTION OF GENETIC EVALUATION FOR EWE REPRODUCTIVE PERFORMANCE

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SUMMARY

This paper describes characteristics of the new analysis for reproductive traits of ewes, as applied to data from maternal breeds. Components of reproduction are treated as different traits for yearling and adult ewes. The new procedures produce breeding values for conception, litter size, rearing ability of ewes, maternal behaviour and condition scores from a multi-breed, multi-trait analysis, using industry and information nucleus phenotypes, genotypes and single-step methodology. Breeding values will be released as research (interim) breeding values by Sheep Genetics while further refinements are made. Future implementation is targeted for Merinos.

INTRODUCTION

Prior to 2007, the phenotype for reproductive performance of a ewe analysed by Sheep Genetics was a single record reflecting the number of lambs weaned per lambing opportunity. This phenotype was inferred from lamb pedigree. Only ewes joined to produce pedigreed lambs over their lifetime obtained an accurate record. In addition, the trait definition was imprecise, as it did not allow for important systematic and temporal effects influencing annual outcomes, it did not capture lamb losses, and contemporary comparisons were also limiting. Since 2007, reproductive performance of ewes has been evaluated using annual phenotypes for the number of lambs born (NLB) or weaned (NLW) (Brown *et al*. 2007). These are also composite traits which combine the components of conception (CON) and litter size (LS), along with the ability of the ewe to successfully rear lamb(s) (ERA). That is, NLB is a function of CON+LS, while NLW is a function of CON+(LS×ERA). Despite better trait definition and models, data for NLB and NLW were frequently censored due to incorrect recording for one or more of the above component traits. Information regarding dry ewes, lambs born dead and an update to individual lamb rearing outcomes were required to correctly identify all components contributing to NLB and NLW.

To improve identification of dry ewes and litter size when lambs were not individually recorded, pregnancy scan data became a secondary data source in 2017. However, inaccurate identification of lambs born dead, lamb survival outcomes and incorrect contemporary grouping across multiple data sources (e.g. lambs vs scans) and component traits (e.g. joining vs lambing contemporary groups) remained problematical. In this paper, we describe new procedures for genetic evaluation of the component traits contributing to ewe reproductive performance. These procedures provide better use of data recorded by breeders subject to both data limitations and opportunities and provide breeding values for the above component (and other) traits in a multi-breed, multi-trait format, using phenotypes, genotypes and single step methodology.

MATERIALS AND METHODS

Inventory-based recording commenced in 2009, giving breeders an opportunity to provide additional detail on joining dates, service sire(s), pregnancy scan outcomes, and management groups (mgp) specified for joining and lambing separately. Component traits were defined annually for joined ewes

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as CON: 0=failed to conceive, 1=conceived; while LS (1 to n lambs born) and ERA (lambs surviving/ lambs born) were defined for ewes which lambed. For ewes without lambs recorded, CON and LS could be assigned using pregnancy scan results (Bunter *et al*. 2016). After further consultation with breeders, values for CON were altered to 0 if conception occurred more than 60 days after joining commenced, to better reflect commercial targets.

For the reproductive traits, records with obvious data errors and in small contemporary groups were discarded. Additional data recorded for ewes included maternal behaviour score (MBS: from 1: good to 5: poor), as described by Brown *et al*. (2016), and pre-joining weight (WT) and condition score (CS) recorded within the 30 days prior to joining. Data further describing body composition and development, thought to be relevant to reproductive outcomes, include scanned post-weaning carcase fat (PFAT) and eye muscle depth (PEMD), along with post-weaning (PSC) or yearling (YSC) scrotal circumferences. Data for these four traits were extracted from the Sheep Genetics database only for those flocks included in analyses of reproductive performance for maternal breeds. Data from the information nucleus research flocks (van der Werf *et al*. 2010) was also used to commence a genomic reference population for reproductive traits, augmented by more recent genotyping of industry animals with phenotypes.

Based on previous analyses (Bunter and Brown 2013), yearling and adult performances of CON, LS and ERA are treated as separate traits. The basic model for non-genetic effects influencing reproductive traits includes cgp + age, where cgp refers to joining (CON, LS) or lambing (ERA) contemporary groups (based on site-year-timegp-mgp details) and age represents the ewe's age in years (adult ewes). Timegp is assigned based on dates to accommodate evidence of gaps between separate but unspecified joining events. Contemporary groups were further refined (Bunter *et al*. 2017) to include: 1) month of birth and dam status (yearling or adult) in the cgp for yearling traits, and 2) previous status (no lamb, lambed and lost or weaned, unknown) in the cgp for 2yo traits, enabling flock specific effects with respect to these factors. Litter size group (1, 2, 3 or more, unknown) at birth was fitted as an additional model term for ERA, since litter size alters the rearing challenge for ewes (Bunter *et al*. 2017). Additional model terms included birth-rear type group for yearling but not adult reproductive traits. Regressions on age, but not weight, were applied to raw data for PFAT, PEMD, PSC and YSC where significant (p<0.05), modelled using contemporary groups previously defined for these traits (Brown *et al*. 2007).

Following a series of univariate and bivariate analyses to estimate genetic parameters for each trait and trait combination, covariance matrices were adjusted for consistency. After preliminary investigation, the genomic relationship matrix (G) was also partitioned into 15 breed sub-groups to improve consistency of genomic with pedigree-based relationships (described by the numerator relationship matrix, A), after correcting obvious anomalies (e.g. unidentified or incorrect pedigree parents) (Gurman *et al*. 2019). Single step procedures were implemented constructing the H-matrix according to Aguilar *et al*. (2010). The research breeding values (RBVs) were subsequently estimated using RACEMULE software (AGBU), which enables data to be analysed fitting desired model terms directly to the data, without pre-adjustment. The predictive capacity of the resulting RBVs was assessed by regressing adjusted phenotypes (post 2013) on sire breeding values estimated from data recorded before 2013. Estimates of variances due to genetic groups are described in Bunter *et al*. (2019). The reportable traits from these analyses are confined to RBVs for conception, litter size, rearing ability, maternal behaviour and condition scores, since ASBVs for all other traits are already reported for a larger sample of flocks through Sheep Genetics.

RESULTS AND DISCUSSION

The new procedures dramatically increase the number of animals with reproductive phenotypes,

most commonly litter size (N>700K), compared to a comparable export of data used for analyses of NLB and/or NLW (N<350K). The relative magnitude and direction of the estimated genetic and phenotypic correlations between traits for maternal breeds is shown in Figure 1. Traits correlated with ewe conception (PSC, YSC) and ERA (MBS) enhance the accuracy of prediction for these traits through low to moderate genetic correlations. Traits reflecting individual variation in post-weaning body composition (PFAT and PEMD) were moderately correlated with pre-joining weight and condition score for ewes, and their inclusion improves accuracy of breeding values for YCS/CS. However, after accounting for the model terms noted earlier (e.g. age, dam age, birth-rear type status, and previous status), all body composition traits showed modest to negligible genetic correlations with reproductive traits in this data. Therefore, body composition traits are not strongly predictive of genetic merit for component traits in maternal breeds and recording reproductive outcomes directly is important for improving accuracy of evaluation for reproductive performance.
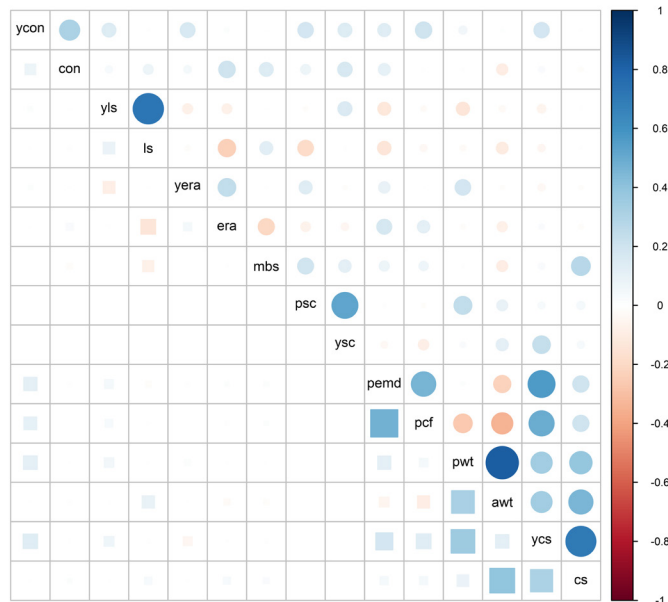

Figure 1. Depiction of genetic (circles) and phenotypic (squares) correlations between traits for MATL analyses. Size and colour of icons reflects the magnitude and direction of correlations (white=negligible correlation)

The distribution of RBVs for reportable traits from a recent analysis for 2017 drop animals is illustrated in Table 1. Even though reproductive traits tend to have low heritability, genetic variation is quite large and there were some useful differences amongst young selection candidates with respect to reproductive component traits. This demonstrates that opportunities exist to select amongst recent candidates for different components of reproduction. Regression coefficients for daughter performance on sire EBVs (Table 1) were generally positive, as expected, and approaching the expected value of 0.5 when backed by significant data contributing to both the sire RBVs and post-2013 validation data (e.g. YLS). Regression coefficients for binary (YCON, CON) traits analysed with linear models are frequently under-predicted (Zhao *et al*. 2001).

Table 1. The distribution of RBVs for animals born in 2017 for reportable traits (with units below) from the MATL analyses, along with the coefficient for the regression of daughter performance (N) on sire RBVs

Percentile	Trait RBVs at percentile thresholds								
	YCS Score	CS score	YCON %	CON %	YLS lambs	LS lambs	YERA %	ERA %	MBS score
Top	0.85	0.69	30.8	10.1	0.39	0.40	11.8	8.91	-0.45
1%	0.33	0.16	14.3	3.9	0.16	0.18	4.87	3.30	-0.11
5%	0.26	0.11	11.0	3.1	0.13	0.14	3.83	2.58	-0.06
10%	0.20	0.09	8.3	2.5	0.10	0.12	2.95	2.08	-0.04
20%	0.14	0.07	6.0	2.0	0.08	0.09	2.09	1.67	0.00
40%	0.05	0.04	2.1	0.9	0.03	0.03	0.64	0.78	0.04
50%	0.02	0.02	0.5	0.3	0.01	0.00	-0.09	0.27	0.06
60%	-0.03	0.00	-1.0	-0.4	0.00	-0.03	-1.08	-0.24	0.09
80%	-0.12	-0.08	-4.6	-2.0	-0.04	-0.10	-2.90	-1.51	0.15
90%	-0.21	-0.16	-10.4	-3.1	-0.07	-0.14	-3.98	-2.61	0.20
Bottom	-0.51	-0.39	-17.8	-6.5	-0.16	-0.24	-7.36	-4.74	0.46
N	1586	7399	5776	3900	16678	51603	12524	29337	7533
Coefficient	-0.01	0.38	0.07	0.38	0.54	0.37	0.26	0.29	0.16

CONCLUSIONS

The data pipeline and software have been developed to improve evaluation of genetic merit for reproductive outcomes of ewes, allowing a substantially larger proportion of the maternal sheep population to receive more accurate breeding values for reproductive performance. Moreover, the new breeding values for component traits will enable breeders to make more precise selection decisions (e.g. litter size versus lambs surviving). Where data were sufficient, regressions of offspring performance on sire EBVs for reproductive traits generally supported predictive capacity for reportable traits from the new analyses. Accurate recording of reproductive data will underpin the procedures for genetic evaluation of reproductive performance. Similar improvements will be implemented for other breeds (e.g. Merinos) in the near future.

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