

INFLUENCE OF ENVIRONMENTAL FACTORS AND TRAIT REPRESENTATION ON THE GENETIC EVALUATION OF REPRODUCTIVE TRAITS IN SHEEP

D. J. Brown, A. Reverter and B. Tier

Animal Genetics and Breeding Unit*, University of New England, Armidale, NSW 2351

SUMMARY

Reproductive traits have a large influence on profitability in all sheep production systems. It is important to obtain the best estimate possible of the animal's genetic merit for these traits. However analysis of reproductive traits is complicated by low heritability, time taken to express the trait and repeated measurements. Data were simulated to investigate nine different traits based on reproductive records. The level of fertility and registration (probability of being recorded) reduced the phenotypic variance and heritability for two ratio based number of lambs born traits, but increased the phenotypic variance and decreased the heritability for parity and accumulated parity based traits. The effect of registration was greater than that of fertility. As the proportion of dams that skipped a mating season increased, the phenotypic variance generally increased and the heritability decreased. Recovery rate after skipping a mating season did not influence the phenotypic variance or the heritability of any trait. Accuracy of selection and ease of interpretation of EBVs could be increased by utilising the accumulated total number of lambs born after each parity as a new trait.

Keywords: Reproductive traits, LAMBPLAN, simulation, analysis

INTRODUCTION

The profitability of most grazing animal enterprises is significantly influenced by the reproductive rate of the breeding stock. Therefore, it is important to obtain an accurate estimate of genetic merit for these traits. Given their low heritability, and the time taken for expression, reproductive traits are more difficult for genetic analysis. Reproductive traits are expressed repeatedly during the life of a female. This improves the accuracy of selection, but makes analysis more complicated. The distribution of the number of lambs born within each parity is also discrete and non-normal. The number of lambs weaned in a ewe's reproductive life is influenced by several components including ovulation rate, embryonic survival, litter size, post-natal survival and inter-lambing interval. OVIS (Brown *et al.* 2000), the analytical software for LAMBPLAN genetic evaluation, utilises two traits to assess reproductive performance, number of lambs born and number of lambs weaned, both being expressed as a ratio of lambing opportunities of the ewe. As the data for these traits are generated from the pedigree, missing information in the pedigree makes accurate calculation of these traits difficult. Missing records or incomplete information complicates the analysis of these traits and as a result the actual reproductive record of a dam may be different to that recorded.

This paper examines several traits and methods for their analysis through simulation. The influences of fertility, missing records and recovery rates on the genetic parameters for these traits are examined.

MATERIAL AND METHODS

The PARITIES (Reverter *et al.* 2001) program was used to simulate data for this study. PARITIES is

* AGBU is a joint institute of NSW Agriculture and The University of New England

a FORTRAN 95 program that stochastically simulates number of individuals born at a sequence of parities. Genetic parameters, circumstances such as fertility rate, parity distributions, registration or recording patterns, inbreeding depression, replacement rates, sex ratios, recovery rate and number of generations can be easily adjusted at each run.

A base population of 1000 ewes and 50 rams were simulated and mated for 10 consecutive mating seasons with an interval of 12 months between lambings. The number of lambs born at each parity was assumed to have a phenotypic variance of 0.8 and heritability of 0.10, which are in line with the current parameters used by LAMBPLAN. While successive lambings were assumed to be perfectly correlated at the genetic level, the residual correlation was set at 0.85. Inbreeding depression was modelled with a linear component of -0.0001 and quadratic component of -0.0003 for each 1% of inbreeding. Minimum dam age at first lambing was set at 12 months at which the dam was at 85% of production capacity. Standard dam age was 54 months (100% of production capacity) and maximum dam age was 120 months (90% of production capacity). At the end of each mating season 25% of the ewes and rams were randomly replaced. If a ewe failed to have a lamb after 2 mating seasons she was replaced. Using the simulated data, nine traits were created; R1 = number of lambs born (nlb) / lambing opportunity (nlop), $R2 = \text{nlb} / (\text{nlop})^{0.5}$, P1, P2, P3 and P4 = nlb in the ewes first, second, third and fourth lambing opportunities respectively, and T2, T3 and T4 = total nlb after 2, 3 and 4 lambing opportunities respectively.

Four non-genetic factors were varied to investigate their effects on the phenotypic variance, heritability and correlation between true breeding value (TBV) and estimated breeding value (EBV) for each trait. The four factors were;

1. Registration rate (REG – the probability of being recorded eg. animals may not be recorded because they die before recording, they are missed in the paddock or the breeder chooses not to record all animals.) – 100 and 85%
2. Fertility rate (FERT – the probability of animals being fertile or having the physical ability to rear a lamb) – 100 and 85%
3. Skipping rate (SKIP – the probability of fertile animals skipping a mating season due to reasons other than fertility eg. Missing ram or artificial insemination) – 0 and 15%
4. Within Skip – (REC – two levels of recovery (nutritionally based increase in phenotype for fertile animals that skipped a season)) – 0 and 50%

All combinations of levels were examined. 10 replicates were simulated at each combination. Some important assumptions when simulating the data included: 1) All females had the opportunity to bear a lamb in their first mating season, 2) A ewe's last recorded lamb was her last lambing opportunity, and 3) A ewe had the opportunity to lamb in all years between 1) and 2) and if a lamb was not recorded the observation was included as $\text{nlb} = 0$.

Genetic Analysis. The phenotypic variance, heritability and genetic value were estimated for each trait in each replicate using ASREML (Gilmour *et al.* 1999). R1 and R2 were analysed using univariate analyses with trait mean fitted as a fixed effect, dam age as a covariate and animal fitted as a random effect. P1 to P4 and T2 to T4 were run as two separate multivariate analyses with trait mean and dam age fitted as fixed effects and animal included as a random effect. The EBVs were then correlated against the simulated TBV from the simulated data to gauge the accuracy of the trait in

estimating true genetic merit.

RESULTS AND DISCUSSION

Although all possible combinations were explored, for clarity only the five combinations that illustrate the main effects are presented. The results were generally very similar between the 10 replicates performed. At the base scenario (Table 1) an average of 2 lambs were born and recorded in each parity. Reducing fertility and registration and increasing skipping generally reduced the number of records available for the parity traits (P1 to T4), but less so for the ratio traits (R1 and R2). As expected the number of records declined for the parity traits as parity number increased. Reducing the rate of registration resulted in a large reduction in the mean for all traits examined. Recovery, while having no clear effect on the number of observations present, increased the mean value for all traits. Increasing skipping rate did not effect the mean for all traits.

Table 1. Number of records (N) and mean for each trait for the 10 replicates at each level of fertility, registration, skipping and recovery

Trait	Control ¹		FERT ²		REG ³		SKIP ⁴		REC ⁵	
	N	Mean	N	Mean	N	Mean	N	Mean	N	Mean
R1	3296	2.00	3376	2.02	3252	1.79	3382	2.01	3399	2.02
R2	3296	3.32	3376	3.13	3252	2.93	3382	3.04	3399	3.04
P1	3296	2.00	3376	2.01	3252	1.78	3382	2.01	3399	2.02
P2	2530	2.00	2301	2.03	2432	1.81	2246	2.01	2240	2.03
P3	1666	2.00	1414	2.03	1565	1.83	1318	2.01	1302	2.02
P4	1078	1.99	861	2.02	984	1.85	756	2.00	752	2.01
T2	2530	4.00	2301	4.03	2432	3.60	2246	4.01	2240	4.04
T3	1666	6.00	1414	6.06	1565	5.46	1318	5.99	1302	6.08
T4	1078	8.01	861	8.07	984	7.36	756	7.99	752	8.09

¹=FERT 100%, REG 100% SKIP 0% REC 0%, ²=FERT 85%, REG 100% SKIP 0% REC 0%, ³=FERT 100% REG 85% SKIP 0% REC 0%, ⁴=FERT 100% REG 100% SKIP 15% REC 0% and, ⁵=FERT 100%, REG 100% SKIP 15% REC 50%.

Estimates from the ASREML analyses were averaged from all replicates that converged (98%) within each combination of effects. The average phenotypic variance and heritability for each trait is shown in Table 2. The correlation between EBV and TBV ranged between 0.20 and 0.45 across traits and combination of effects. The correlations are not presented as they exhibited similar trends to the estimates of heritability. Reducing the fertility of the ewes resulted in reduction in both phenotypic variance and heritability of R1 and to a lesser extent for R2. Reductions in registration rate had a similar but larger effect on the ratio traits than fertility. Both fertility and registration increased phenotypic variance and decreased the heritability of the parity (P1 to P4) based traits. Increasing the proportion of ewes skipping a mating season decreased the phenotypic variance for R1 and increased the phenotypic variance for the remaining traits. Skipping reduced the heritability for all traits. Both registration and skipping had a larger impact on the parity based traits than the accumulated total traits. When animals skipped a mating season their increased in phenotype the following season did not influence the phenotypic variance or heritability of any of the traits investigated.

While the reductions in registration and fertility rate were both set at 15%, registration affected both

sexes, while fertility only influenced dams. Therefore fertility effectively had a greater impact on the reproductive data being analysed. However registration had a larger impact on phenotypic variance and heritability estimates. This is a desirable result since fertility is not in the breeder's control whereas breeders can improve registration rates through better recording. These results highlight that it is important to record all lambs and pedigree to gain the most accurate estimate of the genetic merit of the dam.

Table 2. Mean phenotypic variance and heritability for each trait at each level of the effects

FERT	REG	SKIP	REC	R1	R2	P1	P2	P3	P4	T2	T3	T4
<i>Phenotypic Variance</i>												
1	1	0	0	1.85	0.65	0.75	0.75	0.75	0.73	2.67	5.55	9.21
0.85	1	0	0	1.67	0.67	0.76	0.75	0.76	0.79	2.70	5.68	9.57
1	0.85	0	0	1.49	0.55	0.78	0.76	0.76	0.74	2.34	4.56	7.30
1	1	0.15	0	1.65	0.67	1.05	1.01	1.01	1.01	2.81	5.38	8.66
1	1	0.15	50	1.66	0.68	1.04	1.00	1.02	1.00	2.80	5.39	8.64
<i>Heritability</i>												
1	1	0	0	0.10	0.10	0.08	0.08	0.10	0.11	0.10	0.11	0.12
0.85	1	0	0	0.08	0.09	0.11	0.12	0.09	0.06	0.10	0.10	0.11
1	0.85	0	0	0.08	0.08	0.06	0.05	0.05	0.06	0.07	0.07	0.08
1	1	0.15	0	0.07	0.07	0.06	0.05	0.03	0.07	0.08	0.08	0.09
1	1	0.15	50	0.07	0.08	0.05	0.06	0.04	0.05	0.08	0.08	0.09

The P traits were also examined using a repeatability model (data not shown). The phenotypic variance, heritability and correlation of breeding values showed similar trends as observed with the multivariate analyses. The repeatability however significantly decreased with reductions in registration and increases in the number of ewes skipping mating seasons. Results from this study have suggested that the current method used by LAMBPLAN to analyse reproductive traits is relatively accurate and only slightly affected by fertility, registration and skipping patterns. However the use of the accumulated totals as reproductive traits offers some additional benefits. It is apparent that using these traits in an analysis and reporting the EBVs from T3 or T4 would increase the phenotypic variance, improve the distribution of the observations, increase the heritability and accuracy of the evaluation. This would also result in a larger spread in the EBVs and larger numbers that would be easier for the breeders to interpret. For example, EBVs from the T3 trait could read as +1.2 lambs born after three parities rather than +0.4 lambs per lambing opportunity. Future research will examine these traits using multi-trait categorical analyses, which may improve the estimation of breeding values for these traits. As some breeders record more males than females, the effect of different levels of recording for each sex will also be investigated.

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