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Estimation of autumn live weight breeding values in progeny test datasets when progeny are slaughtered to achieve a target carcass weight

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ABSTRACT

An analysis was undertaken to investigate how lamb autumn live weight breeding values could be calculated from fixed carcass weight progeny tests (*e.g.* lambs slaughtered at monthly intervals at a threshold carcass weight). Analysis of growth rate is problematic for this progeny test design as the slaughter groups may experience vastly different environmental conditions, both within and between years.

Variance components were estimated from an animal model using restricted maximum likelihood (REML) on data from 11,411 Coopworth progeny records and 126 Coopworth sires. The dataset contained records of weaning weight and live weight at four, five and six months of age (LW4, LW5 and LW6, respectively) collected from 1995 to 2004 in a flock run at Woodlands Research Station. The multivariate mixed linear model included lamb birth day deviation as a covariate, sex of lamb, birth rearing rank, age of dam and live weight contemporary group as fixed effects, and sire as a random effect. The WWT model also had dam fitted as a random effect to give WWT direct and maternal effects (WWT_d and WWT_m). The analysis was then repeated, but with animals records removed from the dataset once they achieved a threshold weight of 31 and 27kg for ram and ewe lambs, respectively, on data prior to or following linear scaling by contemporary group mean.

The heritabilities estimated from the full dataset for WWT_d, WWT_m, LW4, LW5 and LW6 were 0.30±0.03, 0.04±0.01, 0.49±0.02, 0.49±0.02 and 0.51±0.02, respectively. These traits were highly correlated with both phenotypic and genetic correlations between the direct traits ranging from 84 to 99%. The same analysis on the two culled datasets resulted in only minor changes the variance components. The correlation between sire breeding values for autumn live weight (LW6) estimated from the full and the two culled datasets were 98.8% for both models. Autumn live weight breeding values can be accurately estimated from datasets which include progressive culling if a multivariate live weight analysis is undertaken, and data from all animals measured at each date are used.

Keywords: Sheep; genetic parameters; progeny test.

INTRODUCTION

Progeny testing is a method of selection widely used in animal breeding, and is most useful for sex-limited traits, traits that have low heritabilities, or for traits in which the animal has to be slaughtered in order to collect the desired measurements. Meat quality traits fall into the last category, and the increase in the ratio of sheep farm income derived from meat relative to wool has seen the establishment of a number of progeny tests for meat traits in New Zealand (Johnson *et al.*, 2002; McLean *et al.*, 2006; Muir *et al.*, 2006). While individual progeny test designs for meat trait measurements can vary considerably, they fall into two general classes based on the slaughter endpoint, namely constant-age at slaughter or constant-live weight at slaughter.

Constant-age endpoints give results that can be applied over a range of carcass weights, but the design produces considerable variation in carcass weight caused by differences in growth rates. Carcass weight variation results in a loss of carcass

value in the larger and smaller carcasses, and as a result this design is more expensive than a constant-live weight design. Constant-live weight endpoints mean that the carcasses are all within a relatively narrow weight band, but differences in slaughter date make the definition of growth rate difficult because of selective culling of records over the extended drafting period. Days to slaughter is an alternative measure of growth rate that can be used, but animals that are slaughtered later will potentially experience different environmental conditions to those that were slaughtered earlier, and the differences are compounded over years making such evaluations fraught. The analysis of days to slaughter ignores intermediate measures of weight for animals with lower growth rates, and breeding values can be biased as a result. Arguably the most meaningful estimate of growth rate is weight at a constant date, with the date sufficiently removed from weaning so as to reduce maternal influences on growth. Autumn live weight (live weight at either 6 or 8 months of age) is an accepted industry measure of

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growth rate, but constant-carcass weight designs produce a biased subset of animals (*i.e.* the slowest growing animals) which have measurements collected at the appropriate time.

Multivariate best-linear unbiased prediction (BLUP) is very useful for the prediction of traits measured later in life based on measurements collected at an earlier stage, especially when the measurements are highly genetically correlated. The objective of this research was to investigate whether multivariate BLUP could be used to accurately predict breeding values for LW6 in a dataset in which a simulated progressive culling of the heaviest animals had occurred.

MATERIALS AND METHODS

Animals

Monthly liveweight data from weaning until six months of age were available for 11,411 Coopworth lambs from 126 Coopworth rams. The lambs were born between 1995 and 2004 and run together in a single flock per year on AgResearch's Woodlands Research Station in Southland. The flock was a fully recorded Coopworth stud.

Lambing season began in the first week of September each year and continued until the second week of October. Lambs were identified to dams within 14 h of birth, and sex, birth rank, rearing rank and age of dam recorded. Lambs were weaned at an average weight of 23.7 kg and an average age of 75.9 days. They were weighed at monthly intervals from weaning until six months of age, such that the dataset included weaning weight and liveweights at four, five and six months of age (WWT, LW4, LW5 and LW6, respectively). There was minimal culling of lambs in the dataset prior to measurement of LW6. The raw means, standard deviations and coefficients of variation for the four traits are shown in Table 1.

Table 1: Means, standard deviations and coefficients of variation for live weight traits.

Trait	Mean	SD	CV%
Weaning weight (kg)	23.8	4.5	18.9
Liveweight at:			
4 months (kg)	30.6	5.1	16.7
5 months (kg)	35.6	5.4	15.1
6 months (kg)	39.0	5.5	14.1

Variance component estimation

Variances and covariances were estimated simultaneously from an animal model using Restricted Maximum Likelihood (AsREML; Gilmour *et al.*, 1999). The multivariate mixed linear model included terms for lamb birth day deviation as a covariate, sex of lamb, birth rearing

rank, age of dam and live weight contemporary group (year of birth and sex) as fixed effects, and sire as a random effect. The model for WWT also included dam as a random effect to give both WWT direct and maternal effects (WWT_d and WWT_m, respectively).

Liveweight data were linearly scaled by the mean of the contemporary group to ensure uniformity of variance between contemporary groups. WWT, LW4, LW5 and LW6 were scaled to a mean of 23.0, 31.0, 35.5 and 39.0 kg, respectively, within contemporary group.

The analysis was run with the full dataset, and then repeated after applying a culling routine to the dataset. The aim of the culling routine was to simulate drafting for slaughter at monthly intervals using a live weight threshold at each weighing. The threshold weight was set to 31 and 27kg for ram and ewe lambs, respectively. If a lamb achieved the live weight threshold at a weighing, then all subsequent live weights were set to missing. At that threshold level, approximately one quarter of the animals were 'culled' from the dataset at each of the weighings. The culling routine was used to create datasets for analysis either before scaling or after scaling.

The genetic parameter estimates were compared between the three models to quantify the effects of biased culling in the dataset. The sire breeding values estimated from the three models were also compared between models to quantify the effects of biased culling on LW6 breeding value estimates. Breeding values for sires with less than 20 progeny in the dataset were not considered, which left 107 sires for the comparison.

RESULTS

Table 2 presents the estimates of heritabilities, and the genetic and phenotypic correlations, among juvenile live weight traits. The heritabilities estimated for WWT_d, WWT_m, LW4, LW5 and LW6 were 0.30 ± 0.03 , 0.04 ± 0.01 , 0.49 ± 0.02 , 0.49 ± 0.02 and 0.51 ± 0.02 , respectively (mean \pm se). All of the live weight measurements were highly positively correlated with each other

Phenotypic correlations for the four direct live weight measurements were 84% or higher, and genetic correlations amongst the direct traits were 89% or better. The genetic correlations between WWT_m and the four direct live weight traits were somewhat lower, ranging between 54 and 72%.

The simulated culling of the heaviest animals at monthly intervals had a relatively minor effect on the genetic parameters (Table 2). The heritabilities decreased slightly for WWT_d and LW6, and increased for WWT_m, LW4 and LW5, but the

Table 2: Genetic and phenotypic parameters^a of live weight traits using the full dataset, for pre- or post scaling selective culling to a threshold live weight.

Trait	WWT _d	LW4	LW5	LW6	WWT _m
Full dataset					
WWT _d	0.30	0.90	0.90	0.84	
LW4	0.93	0.49	0.92	0.86	
LW5	0.91	0.96	0.49	0.92	
LW6	0.89	0.91	0.99	0.51	
WWT _m	0.54	0.72	0.63	0.54	0.04
Monthly culling to threshold liveweight post-scaling					
WWT _d	0.29	0.90	0.92	0.85	
LW4	0.93	0.51	0.91	0.87	
LW5	0.92	0.96	0.52	0.91	
LW6	0.89	0.89	0.99	0.48	
WWT _m	0.55	0.74	0.65	0.60	0.05
Monthly culling to threshold liveweight pre-scaling					
WWT _d	0.29	0.90	0.91	0.85	
LW4	0.93	0.51	0.90	0.86	
LW5	0.92	0.95	0.52	0.90	
LW6	0.89	0.88	0.98	0.47	
WWT _m	0.56	0.74	0.64	0.60	0.05

^aHeritabilities are on the diagonal, phenotypic correlations are above and genetic correlations are below the diagonal.

Table 3: Correlations between LW6 sire breeding values (kg) in the three models and breeding values from the full dataset, and summary statistics for breeding values for the three models.

Model	Correlation	Mean (kg)	SD	Minimum	Maximum
Full dataset	1	-0.11	1.53	-5.43	4.81
Culling post-scaling	0.99	-0.11	1.45	-5.37	4.53
Culling pre-scaling	0.99	-0.11	1.46	-5.44	4.62

changes were minor. The estimates changed by a maximum of 3% for both the pre-and post scale culling models. Similarly, there were very small differences in both the genetic and phenotypic correlations between the three statistical models. Genetic correlations changed by a maximum of 3% between the direct traits, while phenotypic correlation changed by a maximum of 2% between models. The greatest change was in the genetic correlation between WWT_m and LW6, which increased from 54% in the full model to 60% in the two culled models. Differences between the pre- and post-scaling culling models were minimal.

The estimated breeding values were highly correlated between the three analyses (Table 3). Breeding values from the two analyses of simulated culling data were 96% correlated with breeding values from the full dataset and 99% correlated for sire breeding values.

The summary statistics for the three analyses reveal that the average for the sire breeding values estimated in two culled dataset were exactly the same as found for the full dataset at -0.11kg. The standard deviation of the sire breeding values was reduced in both culling models compared to the full dataset, although the reduction in variation was marginally greater in the post-scaling culling model. The minimum and maximum breeding

values for each analysis reflected the differences in means and standard deviations between models. Culling post scaling had the smallest range, whereas the Culling pre-scaling had a similar minimum but a lower maximum compared to the full dataset.

DISCUSSION

The heritabilities obtained from the current analysis are similar to or higher than other published estimates of liveweights, with the exception of weaning weight (McEwan *et al.*, 1993; Morris *et al.*, 1996; Clarke *et al.*, 2000). The heritability for WWT_d was found to be considerably higher in the current study at 0.30 compared with a range of 0.11 to 0.15 in the papers above. The heritability of the maternal component of weaning weight (WWT_m) at 0.05 in the current study, was markedly lower than the heritability of 0.15 reported by Clarke *et al.* (2000). The average carcass weight at slaughter in New Zealand has undergone pronounced change, having increased from around 13.0kg twenty years ago to an average of 17.5kg at present. While some of the differences in heritability when compared to the above Romney datasets may be due to the change in slaughter endpoint, the high heritabilities for

growth traits are expected given that the Coopworth breed is effectively an interbreed composite and as such has higher genetic variation (Safari & Fogarty, 2003).

Biased culling is a problem in any dataset used for estimation of breeding values. Only a minor subset of animals will be present for the final liveweight measurement in the case of a progeny test where progeny are selected for slaughter at monthly intervals based on a liveweight threshold. This subset of animals will all be the progeny of the slower growth rate sires rather than a random sampling of progeny from each sire. There may well be no progeny alive for sires with a high growth rate at the final liveweight measurement, meaning breeding values for these animals are predicted entirely from correlated traits.

The results have demonstrated that breeding values for autumn liveweight can be estimated accurately from a dataset where there has been heavy selective culling if intermediate liveweights are included in the analysis. These intermediate liveweights give additional information on the growth pathway for each animal and have the potential to improve the estimation of a liveweight at a constant age, *e.g.* LW6, even after heavy selective culling.

Two models were tested, one in which the culling occurred prior to scaling of the data, and the second after scaling. The two scenarios reflect different potential progeny test designs. The pre-scaling model is analogous to a design where the drafting threshold is rigid and animals are drafted to that threshold liveweight regardless of how this affects the proportions of animals slaughtered at each kill. The post scaling model simulates a design where the threshold liveweight is flexible, and is moved up or down as required so that a given proportion of animals are slaughtered at each kill. While these two models have marked differences in the animals that are selected for slaughter at any given kill, there were effectively no differences in the genetic parameter estimates from the two analyses.

In addition to the consideration of differences in genetic parameter estimates, it is also important to consider the estimates of the breeding values themselves. A feature of BLUP used in breeding value estimation is that the estimates are reduced towards the mean as accuracy of estimation falls (van Houwelingen, 2001). Both the pre-scaling and post-scaling models had some shrinkage of the breeding values as evidenced by a lower standard deviation for LW6 breeding value when compared with the full model. The shrinkage indicates a modest loss of accuracy in the sire breeding values due to biased culling, but the effects are minimal,

and the ranking of sires is effectively unchanged.

To conclude, it is possible to accurately estimate LW6 breeding values from progeny test data which has had selective culling based on liveweights. Multivariate BLUP using weaning weight for all animals, and any intermediate liveweight measurements (*i.e.* LW4 and LW5) produced genetic parameters and breeding values that correlated highly in a culled dataset when compared with the results from the same dataset without any culling of records. Some shrinkage of breeding values did occur, with the shrinkage being greater when the threshold is flexible so as to ensure a set proportion of animals are drafted for each slaughter. If possible, the liveweight threshold should be rigid so as to minimise the shrinkage effect. Although, these results may not be surprising based on theoretical calculations, it is important that their robustness using actual multi-year scaled and unscaled data was checked to provide a practical demonstration of the reliability of live weight breeding value estimates from fixed carcass weight progeny tests.

ACKNOWLEDGEMENTS

The authors acknowledge the support of Meat & Wool New Zealand who funded this project.

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