META-ANALYSIS OF CROSS-BRED PROGENY DATA FOR AUSTRALIAN TERMINAL SIRE SHEEP

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SUMMARY

Meta-analysis of data from a number of progeny tests, involving crossbred progeny of terminal sire rams with known ASBVs, shows that in general LAMBPLAN ASBVs predict progeny performance as expected. There is however a considerable range around the mean regressions for all traits examined, and in the case of the regression of cross-bred progeny carcase weight on sire post-weaning weight ASBV, some anomalous results requiring further investigation. IN general, lamb producers can be confident in use of LAMBPLAN information in sourcing flock rams.

INTRODUCTION

LAMBPLAN has been providing genetic evaluation services to the Australian lamb industry since 1988 (Banks 1990), and now analyses include data on approximately 105,000 new animals per year from 415 terminal sire breed flocks. The core traits analysed in LAMBPLAN remain growth rate, ultrasound fat depth and eye muscle depth measured on animals in the ram breeding sector, although there has been significant development in terms of stages of growth that can be analysed, as well as in the models for evaluation. In addition, there has been substantial genetic change in all 3 traits over the period 1989-present (Swan *et al.* 2009). The primary aim of LAMBPLAN remains to assist industry identify animals with superior merit for breeding fast-growing slaughter lambs with valuable carcases. This paper examines the relationship between the core LAMBPLAN genetic evaluation traits and traits expressed in cross-bred commercial progeny, by analysing sire-progeny regressions in a number of progeny tests conducted since 1990.

MATERIALS AND METHODS

Data. Data from 45 separate progeny tests were available, comprising 25,134 progeny of 257 sires. These data were from a) Terminal Sire Central Progeny Test trials, conducted during the early 1990s, b) a small number of PIRD (MLA producer initiated research and development) projects and datasets collected by individual stud breeders during the period 1995-present, and c) Information Nucleus sites of the Sheep CRC. Progeny number per progeny test group ranged from 29 to 856, and data recorded varied but always included live and carcase weight at slaughter, a measure of fat or tissue depth on the carcase and eye muscle depth. Traits examined in the cross-bred progeny were birth weight (bwt), post-weaning weight (pwt), carcase weight (cwt), carcase fat depth (cfat) and carcase eye muscle depth (cemd). Breeding values of sires used in analysis were for birth weight (bwt), post-weaning weight (pwt), post-weaning fat (pfat) and post-weaning eye muscle depth (pemd). The fat and muscle depth traits of both sires and progeny were adjusted for body/carcase weight, and procedures for estimating breeding values have been described (Brown *et al.* 2007). Carcase fat measures were the GR Tissue Depth (tissue depth at the 12/13th rib, 110 mm out from the backbone).

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Model of analysis. Individual progeny deviations from contemporary group mean were calculated, fitting age, birth and rearing status, sex, dam age and for the fat and muscle measures, carcase weight fitted as a covariate. Contemporary groups were defined by breed, flock, year of birth, date of measurement and management group. Regressions of progeny deviation on sire breeding value were estimated for each site, year and trait combination, using sire ASBVs from the most recent LAMBPLAN analysis (March 2009). In addition, a combined analysis was conducted across all years and sites, fitting the same fixed effects.

RESULTS AND DISCUSSION

Regression Coefficients. Table 1 summarises the regression coefficients calculated from the combined dataset and the ranges of values obtained within individual datasets.

Table 1. Summary of the regression coefficients (se) across and within datasets

Sire Breeding Value	Progeny Trait	Regression Coefficients			
		All data, all sires	All data, only sires > 50% accuracy	Minimum value across datasets*	Maximum value across datasets*
Birth weight	Birth weight	0.45 (0.04)	0.52 (0.04)	0.06 (0.30)	0.99 (0.15)
Post-weaning live weight	Post-weaning live weight	0.37 (0.01)	0.36 (0.01)	- 0.24 (0.31)	1.09 (0.14)
Post-weaning live weight	Carcase weight	0.05 (0.01)	0.03 (0.01)	- 0.19 (0.18)	0.70 (0.09)
Post-weaning C fat**	Carcase GR Tissue depth**	1.96 (0.09)	1.94 (0.10)	- 0.96 (0.76)	3.22 (0.51)
Post-weaning eye muscle depth**	Carcase eye muscle depth	0.35 (0.02)	0.35 (0.03)	0.00 (0.21)	0.77 (0.11)

*only coefficients estimated from datasets with at least 15 progeny measured are included in this range
**trait is adjusted for constant weight (either live or carcase as appropriate)

With one exception, these sets of regression coefficients are broadly in agreement with expectations;

- Birth weight: cross-bred progeny birth weight increases by 0.45kg for each 1 kg increase in sire breeding value for birth weight. This is very close to expectation.
- Post-weaning live weight: cross-bred progeny post-weaning weight increases by 0.37 kg for each 1 kg increase in sire breeding value for post-weaning weight. This is slightly lower than expectation, and may reflect increased variance in dam contribution to cross-bred progeny weight, or that this contribution is less accurately accounted for in cross-bred progeny, where often little is known about the dams. This may also indicate that the direct genetic effects are larger in the crosbred progeny than observed in the purebred ram breeding flocks, which if coupled with a lower variance in the cross-bred progeny could generate a lower b value.
- Carcase weight: cross-bred progeny carcase weight increases by 0.05 kg for each 1 kg increase in sire breeding value for post-weaning weight. A simple expectation for this relationship would be an 0.25 kg increase, reflecting half for the sire contribution to progeny and half reflecting the approximately 50% dressing weight. This result is also surprising in view of the stronger relationship for post-weaning weight, which is expected to be well correlated with carcase weight.

- Carcase fat depth: the regression here is close to 2mm additional tissue depth in the cross-bred progeny carcase for every 1mm increase in sire's breeding value for C fat depth. There is an approximately 3:1 relationship between GR tissue depth and C site fat depth in the animal itself. This suggests that there is a scale difference between cross-bred progeny and their sires' measures, since otherwise the expected value of the regression would be 1.5:1.
- Carcase eye muscle depth: cross-bred progeny eye muscle depth increases by 0.33mm for each 1 mm increase in sires' breeding value for post-weaning eye muscle depth. Thus the observation is lower than expectation (0.5:1), with unaccounted variation in dam muscling being a possible contributory factor.

In broad terms, these results provide a basis for confidence that sires' breeding values predict crossbred progeny outcomes. However, two questions remain: why is the regression for carcase weight lower than expected, and how much variation is observed in these regressions, or in other words, how confident can a user be in the predictions?

Regression of carcase weight on sire post-weaning weight. Assuming a high genetic correlation between post-weaning weight and carcase weight (these are measured at similar ages), we would expect the sire:offspring regression between these two traits to be around 0.25. Here we find an estimate across all data sets of 0.05, with a range from -0.19 to 0.70. At the same time, the sire:progeny regressions for post-weaning weight, the live trait, is 0.37, slightly lower than expected.

Two possible explanations for this anomaly are:

- changes in the data recorded and/or the model for analysis of post-weaning weight mean that there has been a change in what is being predicted over time
- the genetic correlation between live weight and carcase weight is lower than anticipated.

The first hypothesis reflects the following changes: when LAMBPLAN began the main weight trait recorded in pure-bred studs as at around 10-12 months, rather than the 7-10 months now predominant, and closer to the age at which cross-bred lambs are slaughtered; and the analytical model for weight traits now separates the direct, maternal and common environment contributions. Together, these effects would lead to a time trend in the regression coefficients. Figure 1 shows the pattern of regression estimates against the year of observation.

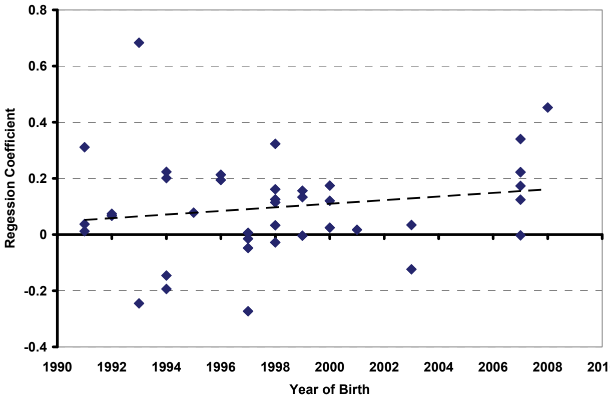

Figure. 1 Estimated carcase weight regression coefficient vs Year of Birth of lambs in each dataset

The regression has a positive slope, but is not significant. This does not suggest any clear change in the regression due to changes in the data. Trends in the regression coefficients across time were small but not significantly positive for carcase fat and carcase eye muscle depth.

The second hypothesis is that the correlation between live and carcase weight in cross-bred lambs is lower than might be expected. This could either be due to a biological relationship, such as there being considerable variation in skin weight and/or gut fill within datasets, or possibly statistical artefacts due to constrained slaughter groups. This latter possibility warrants further investigation.

A further aspect of these results with significance for extension messages is the large variation amongst estimates across sites and years. This is apparent for both the weight and composition traits, and can be seen clearly in Figure 1 for instance for year 2007. The data points in this year are all from Information Nucleus sites, with the same set of sires in each case, yet the regression coefficients for carcase weight on sire post-weaning weight range from 0 to 0.35. Similar patterns (not shown) are apparent for carcase fat depth and carcase eye muscle depth. In the case of Information Nucleus sites, the regression estimates are based on 100-200 progeny of at least 20 sires. This range in the observed regressions estimates again points to the need for further investigation of the carcase data.

CONCLUSIONS

This meta-analysis has shown that;

- for live weight and for carcase composition traits, regressions of cross-bred progeny performance on the corresponding sire trait LAMBPLAN breeding values are similar to expectations across a range of datasets collected between 1990 and 2008
- the regression for carcase weight on sire post-weaning weight in these data is lower than anticipated, and as yet unexplained
- there is considerable variation amongst the estimates across sites and years for all traits, which may be partly due simply to sampling effects, but also suggests that more detailed examination of factors affecting carcase weight is warranted.

Taken as a whole, these results suggest that lamb producers can confidently use LAMBPLAN breeding values to choose sires that will breed lambs with superior growth and carcase characteristics. The regression of progeny carcase weight on sire post-weaning weight predicts the impact of that selection on processor and retailer returns, and the values for that regression estimated here suggest that further investigation of both the data and the analytical model should be conducted.

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