# DESCRIPTION OF LAMB GROWTH USING RANDOM REGRESSION ON FIELD DATA

**T.M. Fischer[1], J.H.J. van der Werf[1], R.G. Banks[2] and A.J. Ball[2]**
[1]Department of Animal Science, University of New England, Armidale, NSW, 2351
[2]LAMBPLAN, MLA, c/- Department of Animal Science, UNE, Armidale, NSW, 2351

## SUMMARY
Random regression (RR) has been proposed as an accurate method for evaluation of growth data, however this method has seldom been applied to data from an extensive industry where few records per animal exist. Consequently, field data containing weight records of Poll Dorset sheep from 50 to 500 days of age were analysed fitting a RR model. This model included quadratic polynomials for direct genetic and environmental and maternal environmental effects, a linear polynomial for maternal genetic effects and heterogeneous error variances. Direct heritability estimates increased steadily throughout time and were in agreement with literature estimates taken at specific ages. Some estimates for the highest ages with the least records were considered too high, in particular direct heritability beyond 450 days. Variances due to maternal effects were low throughout the trajectory. Results show that covariances between weights of sheep for a considerable range of ages can be modelled adequately through random regressions.
**Keywords:** sheep, growth, random regression, heritability

## INTRODUCTION
A flexible method for growth performance evaluation recently advocated by animal breeders is random regression (RR), which facilitates the estimation of genetic parameters for traits that change continuously over a trajectory (e.g. weight over time) without the limitations of discrete multi-trait (MT) methods. Under the infinite-dimensional framework proposed by Kirkpatrick *et al.* (1990), the continuous nature of the trait is accommodated throughout time and the correlation among successive measures is implicitly modelled by the random regressions. RR models have been applied to sheep data from research flocks (Lewis and Brotherstone 2002), which typically contain many repeated records per animal. However, weight data are generally less comprehensively measured by sheep producers, hence it is of interest to investigate whether sufficient field data are collected to estimate covariance functions for sheep growth. Consequently, this study involves the estimation of genetic parameters for growth using RR, and in doing so, attempts to quantify the variation that exists in growth curves in an Australian sheep population.

## MATERIALS AND METHODS
**Data.** Data originated from the LAMBPLAN database and consisted of weight records for Australian and New Zealand Poll Dorset sheep. Standard data edits for LAMBPLAN are detailed in Brown *et al.*, (2000). Following this, only animals with a recorded Poll Dorset sire and dam and birth date post 1990 were extracted. In addition, only contemporary groups possessing a minimum of 10 animals were considered and only animals that possessed 3 or more records within the specified age range (50 to 500 days) were extracted. Animals that possessed weights more than 4 standard deviations from the closest 10-day mean were eliminated.

*Data Structure.* Following data edits this yielded a total of 16,826 records on 5,420 animals, with a mean weight of 50.6 kg and a mean age of 236 days. Figure 1 shows the distribution of weights over ages of recording, together with corresponding mean weights for ages in 10-day intervals. There were 4,854 and 566 animals with 3 and 4 records respectively. Animals with records were progeny of 291 sires, 3,192 dams and 406 maternal grand-sires. Each dam possessed an average of 1.7 progeny allowing maternal permanent environmental effects to be distinguished from maternal genetic effects. Pedigree for parents not in the data was obtained for up to 3 generations, resulting in 11,462 animals in the analysis.
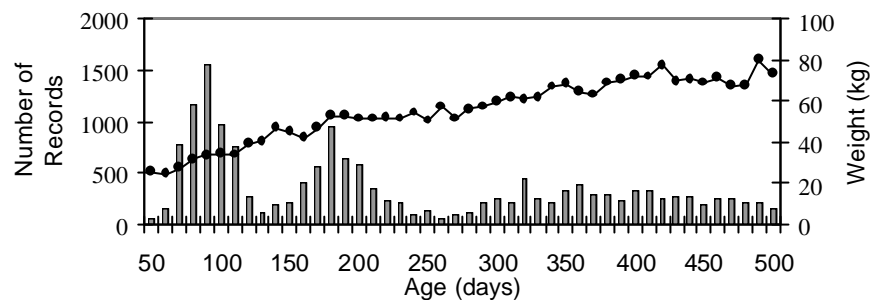


**Figure 1. Numbers of records (bars) and mean weights (points) for ages in 10-day intervals.**

**Analyses.** All estimates were obtained using ASREML (Gilmour, 2002), which employs the average information algorithm to locate the maximum of the likelihood.

*Random effects.* RR analyses fitted a set of *k* regression coefficients for each random effect. All models fitted Legendre polynomials (LP) of age (in days) at recording for direct and maternal genetic effects, and direct and maternal permanent environmental effects. Analyses were carried out considering different orders of fit for the four random effects, with the choice of model determined using the Bayesian Information Criterion (BIC), and by examining variance and correlation estimates for ages in the data. The aim was to determine the minimum order of fit required for each random factor, and thus determine the most parsimonious model describing the data. Results are not shown for these criteria, for further details see Fischer *et al.* (2003). Residual effects were considered independently distributed with heterogeneous measurement error variances ($s^2_e$). Changes in $s^2_e$ with age were modelled as a step function with 9 classes (50-100,…,450-500).

*Fixed Effects.* Mean age trends were taken into account by a fixed cubic regression on LP of age in days. Other fixed effects fitted included contemporary group (CG), defined as flock-year-paddock-sex subclasses (607 levels), rearing type (1, 2 or 3) and dam age as a covariate (linear and quadratic).

**RESULTS**

A model fitting quadratic LP for direct genetic and permanent environmental and maternal permanent environmental effects and linear LP for maternal genetic effects was chosen as 'best' on the basis of BIC. In addition, parameter estimates obtained from this model were in excellent agreement with other models that ranked closely on BIC but required more parameters to be estimated, hence only results from this model are presented.

*Heritability.* Estimates of heritability for ages in the data are shown in Figure 2. Direct heritability increased steadily until 350 days, where it increased sharply to very high values beyond 450 days. The heritability estimates proposed by Fogarty (1995), of 0.20, 0.23 and 0.25 for weaning, post-weaning and yearling weights (mean age of 100, 200 and 350 days respectively) were consistent with the results found in this study. Estimates at older ages were significantly inflated in this study due to declining variance for the other effects at later ages. Similar erratic behaviour of covariance function estimates for ages with the least data has been reported (Meyer 2002a), and this remains an unresolved problem for this type of modelling. Maternal heritability was relatively low (<0.10) at all ages. Maternal permanent environmental effects as a proportion of phenotypic variance declined with age to very low values beyond 150 days. A general paucity of literature estimates for maternal effects in sheep over a range of ages make comparison with this study difficult, however, most studies report similar results in that maternal effects decrease as time lapses beyond post-weaning (>200 days).
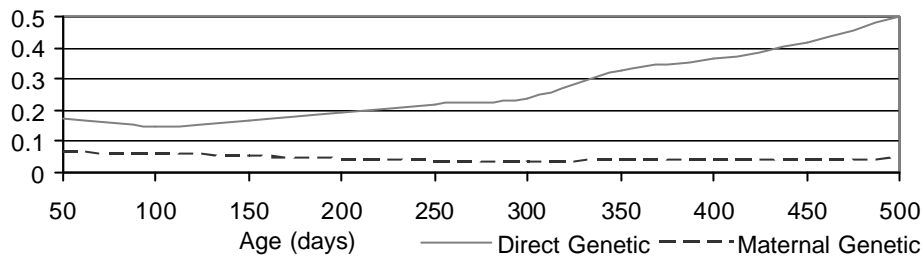


**Figure 2. Estimates of direct and maternal heritability from random regression analyses.**

*Correlations.* Table 1 shows how phenotypic and genetic correlations decline as the time between weights increases. The genetic correlation between subsequent ages approaches unity, however, the genetic correlation between early (day 50) and late (day 500) weights is moderate (0.34) suggesting that early weights are not under the same genetic control as weights taken at an older age. This has implications for selection on the shape of the growth curve as an animal can be above average weight at younger ages, but below average weight at older ages. In addition, genetic correlations between weights at younger ages (50 v. 200 days) are lower (0.44) than correlations between weights taken at older ages (300 v. 500 days) with the similar time lag (0.87). This is largely attributable to the influence of maternal effects at younger ages (<150 days). Maternal genetic correlations (not shown) were very high (>0.75) for all ages and decreased as the time between weights increased.

**Table 1 Genetic (below diagonal) and phenotypic correlations between weights at selected ages**

| Age (days) | 50 | 100 | 200 | 300 | 400 | 500 |
|------------|------|------|------|------|------|------|
| 50 | 1 | 0.80 | 0.49 | 0.30 | 0.22 | 0.14 |
| 100 | 0.87 | 1 | 0.68 | 0.53 | 0.46 | 0.32 |
| 200 | 0.44 | 0.82 | 1 | 0.72 | 0.69 | 0.52 |
| 300 | 0.29 | 0.70 | 0.97 | 1 | 0.72 | 0.59 |
| 400 | 0.28 | 0.65 | 0.91 | 0.97 | 1 | 0.72 |
| 500 | 0.34 | 0.60 | 0.78 | 0.87 | 0.96 | 1 |

**DISCUSSION**

Whilst there have been a plethora of studies that have applied RR models to experimental data, few have considered its application to field data, in particular, that arising from an extensive industry with limited collection of records. For example, in the Australian sheep industry, typically only 2-3 weight records are collected per animal. In addition, no study has estimated genetic parameters for weight in sheep under a RR framework covering the trajectory considered in this study (50-500 days).

The genetic parameter estimates obtained in this study using a RR model were in agreement with estimates at the specific ages proposed in the literature, hence this technique appears to be a reliable and accurate method for genetic evaluation. Furthermore, its inclusion into routine genetic evaluations as an alternative to current MT methods is of interest, however a series of issues need to be addressed before this recommendation can be made. The vast majority of studies involving RR have been on relatively complete data, hence the effect of using field data structures with few records per animal for genetic parameter estimates using RR models is largely unknown. This is an area requiring further study pending data availability. Meyer (2002b) showed that the inclusion of additional records (from 4 to 8 weight records) in beef cattle RR analyses yielded a 5% increase in accuracy over MT methods. This study also demonstrated that considerable genetic variation exists in the growth curves of sheep. It was shown that weight early in life is under different genetic control to weight later in life (Figure 2 and Table 1). This has implications for potential to select on the shape of the growth curve to suit specific objectives, hence, further study is recommended.

**CONCLUSIONS**

This study involved estimation of covariance functions for direct and maternal effects on growth over a 450-day trajectory of a sheep population using a field data set. The results presented in this study were in agreement with literature estimates suggesting that RR is a promising method for analysis of sheep data in the future. Implementing a RR model would not only remove the current limits on the number of records per animal that can be utilised and eliminate the need for age correction, but also provide estimates of genetic merit for any age of recording which is of immense interest to industry.

**ACKNOWLEDGEMENTS**

**REFERENCES**

Brown, D.J., Tier, B., Reverter, A., Banks, R., Graser, H.U. (2000) *Wool Tech. Sheep Breed.* **48**: 285
Fischer, T.M., van der Werf, J.H.J., Banks, R.G. and Ball, A.J. (2003) *Livest. Prod. Sci.* **Submitted**.
Fogarty, N.M. (1995) *Animal Breeding Abstracts* **63**: 101.
Gilmour, A.R., Cullis, B.R., Welham, S.J. and Thompson, R. (2002) 'ASREML Reference Manual.'
Kirkpatrick, M. Lovsfold, D. and Bulmer, M. (1990) *Genetics* **124**: 979
Lewis, R.M. and Brotherstone, S. (2002) *Anim. Sci.* **74**: 63
Meyer, K. (2002a) *Proc. 7th World Congr. Genetics Appl. Livest. Prod.* Montpellier, France. Communication No. 11-01.
Meyer, K. (2002b) *Livest. Prod. Sci.* **Submitted**.