FIRST ESTIMATES OF COVARIANCE FUNCTIONS FOR LIFETIME GROWTH OF ANGUS CATTLE

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SUMMARY

Estimates of covariance functions for weights of Angus cattle from birth to 3000 days of age were obtained using Bayesian analysis. Data consisted of records in 69 herds with at least 50 mature cow weights, and records in 6 additional herds with 60% or more animals having at least four weights, $551,259$ records on $197,915$ animals in total. The model of analysis fitted contemporary groups and cubic regressions on orthogonal polynomials of age nested within sex, birth type, dam age class and lactation status as fixed effects. Random effects fitted were cubic and quartic regressions on orthogonal polynomials of age for animals' direct genetic and permanent environmental effects, and quadratic regressions, restricted to 0 to 600 days of age, for maternal genetic and environmental effects. Measurement error variances were modelled through a step function with 32 classes, yielding 69 covariance components to be estimated.

Keywords : Beef cattle, growth, covariance function, genetic parameters

INTRODUCTION

Random regression (RR) analyses have been used to model growth of beef cattle from birth to about two years of age (Albuquerque and Meyer, 2001; Meyer, 2002a). Genetic evaluation systems for beef cattle, such as BREEDPLAN however, consider weights of mature cows in addition. Ideally, weights of animals at all ages are to be treated as 'repeated' records of the same trait, and modelled as a single curve. Analogously, covariances for lifetime growth are summarised by one covariance function for each source of variation. This paper presents a first attempt at estimating such covariance functions for growth of Australian Angus cattle.

MATERIAL AND METHODS

Data. Raw data comprised more than 1.6 million weights until 2 years of age, and pedigree information for 0.9 million animals, but only $34,302$ records for weights of mature cows. After initial edits, means and standard deviations (SD) for ages at recording, grouped in 7-day intervals were calculated. Weights up to 3000 days of age were extracted for all animals in 69 herds, which had at least 50 mature cow weight records, and 6 additional herds with more than 50 animals in which at least 60% of animals had 4 or more observations. Observations more than 2.5 SD from the respective, weekly mean and records clearly 'out of sequence', i.e. records taken more than 45 days apart and corresponding to a daily growth rate less than -1 or greater than 2.5 kg/day since the previous weighing were disregarded. Only mature cow weight (MCW) records for which a matching weaning weight of the calf was found were retained.

Data structure, This yielded a total of $551,259$ records on $197,915$ animals in total, with a mean weight of 269.0 kg and mean age of 323.2 days. Birth weight was recorded for $126,045$ animals.

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[1] AGBU is a joint venture of NSW Agriculture and UNE

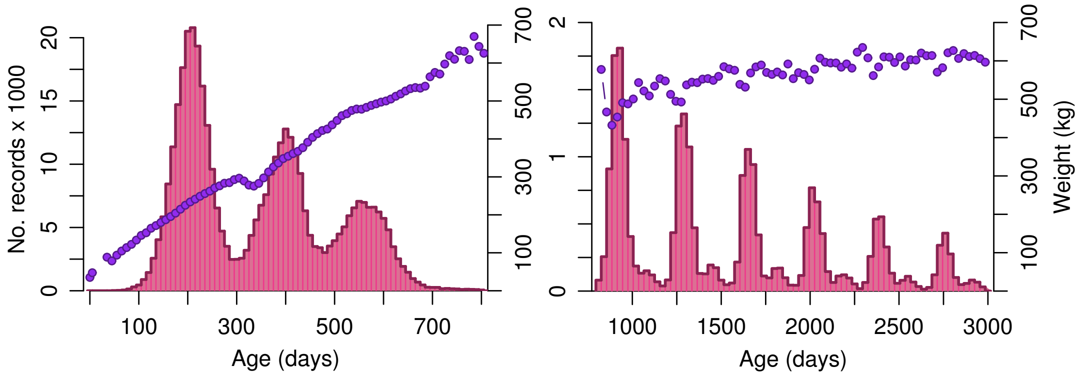

Figure 1. Numbers of records (■) and means weights(●) for ages at recording in 10 day intervals up to 2 years of age (left), and 30 day intervals for mature cow weights (right).

Figure 1 shows the distribution of weights over other ages at recording, together with corresponding means. There were 34,216, 58,957, 46,044, 40,506 and 12,733 animals with 1, 2, 3, 4 and 5 records, respectively, and 5,459 animals had 6 or more weights recorded, up to a maximum of 11. Animals with records were progeny of 5,722 sires and 71,675 dams. Pedigree information for parents not in the data was obtained for up to 4 generations backwards, resulting in 232,779 animals in the analysis. Whilst only 30% of animals in the data had 4 or more records themselves, 30,239 and 113,519 of the remainder had a parent or a sib, respectively, with at least 4 records, i.e. at least 85% of animals in the data had sufficient information available to allow a cubic polynomial to be fitted.

Analyses. Estimates of (co)variance components were obtained by Bayesian analysis, employing a Gibbs sampling algorithm via program RRGIBBS (Meyer, 2002b). Two Markov chains with 160,000 and 170,000 samples, respectively, were drawn, assuming flat priors. Variances and genetic parameters for ages in 10 day intervals were calculated for each sample. Estimates were obtained as posterior means, disregarding the first 30,000 samples in each chain as "burn-in" period.

Random effects. The model of analysis fitted a RR on Legendre polynomials (LP) of age at recording for each random effect. A cubic (4 coefficients) and quartic (5 coefficients) polynomial was fitted for direct genetic (A) and permanent environmental (R) effects, respectively. Maternal genetic (M) and permanent environmental (C) effects were modelled through quadratic regressions, restricting their effect to ages from 0 to 600 days. Pedigrees for direct and maternal effects were "pruned" separately, treating any animals without a direct expression and pedigree links to only one other animal as if they were unknown. This left 221,757 direct and 75,853 maternal genetic effects. Residuals were considered independently distributed with heterogeneous measurement error variances (σ_i^2). Changes in σ_i^2 with age were modelled as a step function with 32 classes (0, 1–30, ..., 271–300, 301–360, ..., 721–780 and 781–820 days). This gave a total of 69 covariance components to be estimated.

Fixed effects. Changes in mean with age were modelled through fixed, cubic regressions on LP of age, nested within sex, dam age class (in years, treating ages $>$ 9 years as one class), birth type (single *vs.* twin) and calf number × age subclass (7 classes). In addition, contemporary groups (CG) were fitted as cross-classified fixed effects (43,548 levels). CG were defined as herd-sex-management

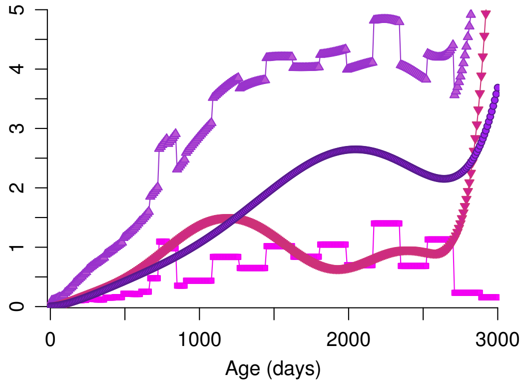

Figure 2. Estimates of variance components (▲ phenotypic, ● direct genetic, ▼ direct permanent environmental, and ■ measurement error; in 1000 kg^2)

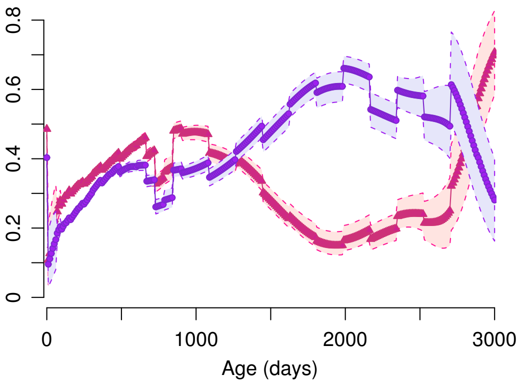

Figure 3. Direct heritability (●) and proportion of permanent environmental effects (▼) together with 95% highest posterior density regions (shaded areas)

group-year/month of weighing subclasses for birth weights, and herd-sex-management group-date of weighing subclasses for other weights till 2 years. To reduce the range of ages compared directly, CG classes were further subdivided applying an "age slicing" of 45 days up to 300 days, and 60 days for higher ages. CG for MCW records were defined as herd of origin-herd-lactation status-management group-date of weighing subclasses.

RESULTS AND DISCUSSION

Figure 2 shows estimates of phenotypic (σ^2_P), direct genetic (σ^2_A), direct permanent environmental (σ^2_R) and measurement error σ^2_i variances. As observed in other studies, estimates for the highest ages with least observations, from about 2800 days in this case, were implausible. In particular, the variance function for σ^2_R showed a drastic increase. Estimates of σ^2_i fluctuated between age classes, with a peak between 720 and 840 days of age, i.e. ages in the transition period between late final weights and early MCW and very few records, and an erratic decline at the highest ages, compensating for the excessive variation 'taken up' by the covariance function for σ^2_R. Alternatively, seasonal differences as observed for MCW in Western Australian data (Meyer, 2000) cannot be ruled out - whilst most MCW records corresponded to spring calvings, there was a proportion of records for autumn calvers. Phenotypic variances for MCW of 3500 to 4000 kg^2 were higher than values reported for Angus (Johnston *et al.*, 1996), but in line with estimates of 3189 kg^2 and 4354 kg^2 for Polled Hereford and Wokalup cows in the Wokalup selection experiment (Meyer, 1995).

Direct heritabilities (h^2), shown in Figure 3, decreased sharply from 0.40 at birth to 0.10, and then increased gradually with age, to 0.25 at 200, 0.35 at 400 and 0.38 at 600 days, and values above 0.50 for MCW. Similarly low h^2 for early weights have been reported by Albuquerque and Meyer (2001); Meyer (2001, 2002a). Estimates for MCW from 1500 to 2800 days ranged from 0.48–0.66 with a mean of 0.57, higher than estimates of 0.43–0.47 for Australian Angus from a repeatability model analysis (Johnston *et al.*, 1996), but comparable with a h^2 of 0.59 from an analysis of mature weight of Angus estimated as the parameter of Brody's curve, when including weaning weight and repeated

MCW records (Kaps *et al.*, 1999). The importance of direct, permanent environmental effects declined as h^2 increased, leading to an almost constant repeatability from about 900 to 2800 days (mean 0.79).

Estimates of maternal heritabilities (m^2) and permanent environmental effects (c^2) are shown in Figure 4. Both peak around 200 days, with values of 0.06 for m^2 and 0.15 for c^2 in good agreement with previous weaning weight estimates for Angus, and a gradual decline to almost zero at 600 days. Fitting a quadratic rather than a cubic polynomial for maternal effects and restricting their influence to 600 days yielded more plausible estimates for postweaning weights than a previous, unrestricted analysis (Meyer, 2002a).

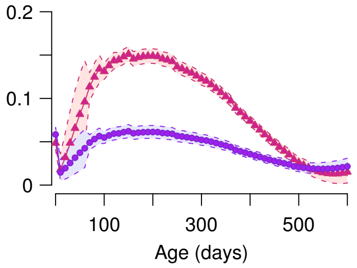

Figure 4. Estimates of maternal heritability (●) and permanent environmental effects (▲)

Figure 5 shows contour lines for direct genetic (r_A) and phenotypic (r_P) correlations, in steps of 0.05. Estimates of r_A declined gradually with differences in age, with an extended area of $r_A > 0.8$ between ages up to 800 and above 2500 days presumably spurious. Except for early ages, estimates of r_A between records 500 to 600 days apart were 0.9 or higher. Estimates of r_P were considerably lower, with few values 10 days apart above 0.8, but showed a similar pattern of decline. Angularity in contour lines was due to the step function used to model temporary environmental variances.

CONCLUSIONS

Overall estimates showed reasonable agreement with literature results, suggesting that changes in covariances between weights of beef cattle over a large range of ages can be modelled adequately by lifetime covariance functions. There were relatively few records for mature cow weights, resulting in large confidence regions for estimates for ages greater than 1200 days.

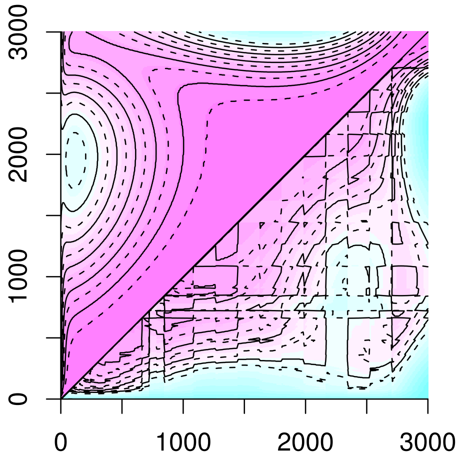

Figure 5. Estimates of direct genetic (upper triangle) and phenotypic (lower triangle) correlations

REFERENCES

Albuquerque, L. G. and Meyer, K. (2001) *J. Anim. Sci.* **79**:2776–2789.

Johnston, D. J., Chandler, H. and Graser, H.-U. (1996) *Aust. J. Agric. Res.* **47**:1251–1260.

Kaps, M., Herring, W. O. and Lamberson, W. R. (1999) *J. Anim. Sci.* **77**:569–574.

Meyer, K. (1995) *Livest. Prod. Sci.* **44**:125–137.

Meyer, K. (2000) *Livest. Prod. Sci.* **65**:19–38.

Meyer, K. (2001) *Genet. Select. Evol.* **33**:487–514.

Meyer, K. (2002a) *CD-ROM 7th World Congr. Genet. Appl. Livest. Prod.* Comm. No. 11–01.

Meyer, K. (2002b) *CD-ROM 7th World Congr. Genet. Appl. Livest. Prod.* Comm. No. 28–27.

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