(Co)Variance components of growth and carcass quality traits of crossbred cattle

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Abstract

Hereford cows (581) were mated to 97 sires from Angus, Belgian Blue, Hereford, Jersey, Limousin, South Devon and Wagyu, resulting in 1144 steers and heifers born over 4 years to estimate the (co)variance components of the body weights and carcass quality traits. Data included thirteen (for steers) and eight (for heifers) body weight measurements at approximately every 50 days from birth until slaughter and four carcass quality traits: hot carcass weight, P8 fat depth, eye muscle area and intramuscular fat. The mixed model included fixed effects of sex, sire breed, age (linear, quadratic and cubic), and their interactions between sex and sire breed with age. Random effects were sire, dam, management (location-year-post-weaning groups) and permanent environmental effects. Management variation accounted for the large proportions of total variations in two growth and carcass traits. The management variances increased rapidly from 500-700 days. Sire variances increased steadily over time, though with a small amount. The maternal (co)variance component was low for all carcass traits.

Introduction

A successful prediction of the economically important carcass quality of cattle following specific growth path depends as much on a correct estimation of (co)variance components of its genotype parameters as on a detailed description of its environment. In much of the published work, covariances between growth and carcass traits at specific (discrete) ages are provided (Marshall, 1994; Bertrand et al., 2001) and essential information regarding estimation of covariances between longitudinal growth data and carcass quality traits is often lacking. Therefore, the main objective of this paper was to estimate genetic and non-genetic covariances between longitudinal body weights and carcass quality traits using the joint growth-carcass sire model with random regression.

Materials and methods

Animal. Purebred Hereford cows (581) were mated to semen of sire breeds Angus (11 sires), Belgian Blue (16 sires), Hereford (10 sires), Jersey (12 sires), Limousin (16 sires), South Devon (15 sires) and Wagyu (17 sires). There were generally 12-15 progeny per sire, with an average of 13 calves per sire and 14 sires per breed. The project comprised 1141 of the heifers (female) and steers (castrated male) born in autumn (average birth date 3rd April) at two locations; 'Struan' near Naracoorte and 'Wandilo' near Mount Gambier in the south east of South Australia (Pitchford et al., 2002).

Data. Live body weights (unfasted) consisted of thirteen measurement for steers and eight measurements for heifers at approximately every 50 days from birth until slaughter. The standard deviation for live weight of both heifers and steers increased from the first to the last weighings. To overcome this variance heterogenous, the use of the natural logs of the body weights rather than the original body weights seemed sensible. It also demonstrated that growth has an approximately cubic pattern. Hence, the cubic polynomial in the time forms the basis of the joint model, but at various levels, considered in the current study.

Carcass quality traits. Carcass quality traits consisted of hot carcass weight (HCWt), P8 fat depth (P8), eye muscle area (EMA) and intramuscular fat (IMF). HCWt was assessed based on a standard trim (AUSMEAT, 1995). Most carcass traits exhibited a skewed distribution (not shown) and so were transformed.

Statistical analysis. A joint growth-carcass sire model with random regression was conducted using ASREML (Gilmour, 2000). The mixed model fitted was of the form $y = X\tau + Zu + e$, where X is the incidence matrix of fixed effects; τ is the vector of fixed effects, Z is the incidence matrix for random effects; u is the vector of random effects e is the vector of random errors (temporary environmental effect or measurement error), NID $(0, \sigma^2)$. The vector y contains both the growth and carcass measurements. The fixed

effects fitted were sex, sire breed, age (linear, quadratic and cubic), and their interactions between sex and sire breed with age. Random effects were sire, dam, management (birth location, year, post-weaning groups) and permanent environmental effects and for each of these when possible, their interactions with linear, quadratic and cubic growth.

Results and discussion

*Growth components.*The remarkable changes occurred where management variances increased rapidly from 500-700 days, so all driven by steer feedlot phase (Figure 1). Genetic variances increased steadily over time, though with a small amount. Maternal variancesis are shown to be low and tend to be constant throughout the trajectory (Figure 1). Maternal varianceses were consistent with Fischer et al. (2004) who reported constant maternal variances over growth path (500 days) for sheep. Other studies have shown that maternal variance declines with age (Meyer, 2002). The shape of the permanent environmental variance was generally similar to dam variance. However, it should be noted that all of those components were pretty small. This result was consistent with Meyer (2002) who observed that data points at the beginning and end of the lactation trajectory for which an animal has records have a relatively large impact on the regression coefficient estimates, when polynomials are used as the covariance function.
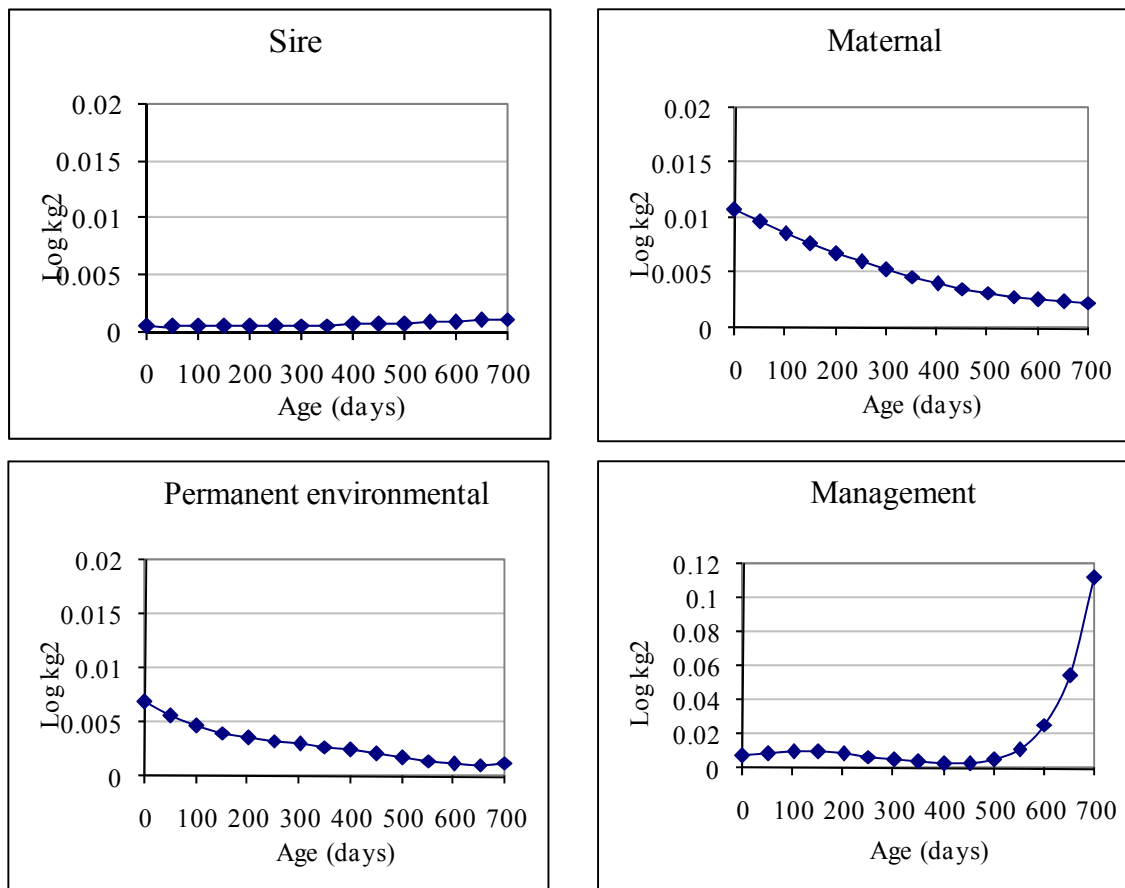

Figure 1. Variance components for sire, dam, permanent environmental and management effects at different ages.

Carcass quality components. The relative contribution of variance components of the carcass quality to the total phenotypic variance is shown in Figure 2. Generally 83% to 90% of the variability in carcass quality were non-genetic. Management variation was considerable and accounted for 48%, 33%, 41% and 44% of total variation for HCWt, P8, EMA and IMF, respectively. The environmental variance (PE+TE) contribution of HCWt, P8 fat, EMA and IMF were of 0, 56, 29 and 50 %. The sire variation was about 12%, 6%, 6% and 3% for HCWt, P8, EMA and IMF, respectively. It should be noted that the sire component describes one quarter of the additive genetic variance.
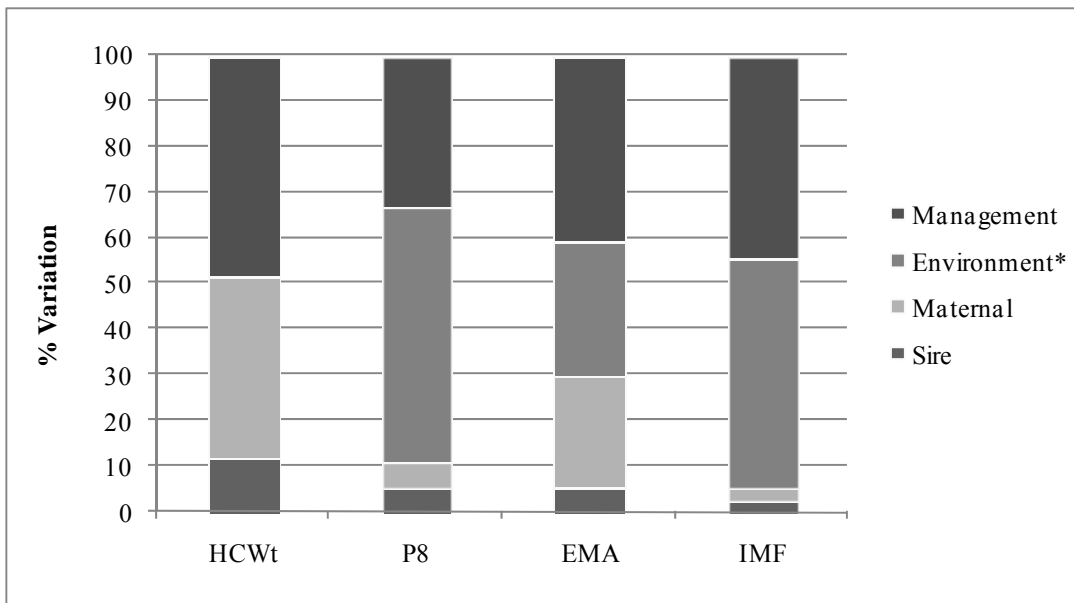
Figure 2. Variance components of carcass quality traits (*For carcass traits Environment includes PE +TE).

Implications

  Growth traits determine more by the environmental conditions than by the genetic characteristics of the calf. In both growth and carcass traits, the management (co)variances were more important that other components; genetic, maternal and permanent environmental. For obtaining "better" estimates of (co)variance components suggest using larger and more carefully selected data set and mathematical functions other than polynomials as the alternatives. High growth will lead to heavier carcasses with more fat depth and will likely change IMF in breeding animals. Increasing HCWt would increase the genetic potential for EMA but may reduce marbling and tend to slightly increase P8. The estimates of (co)variance components will lead to establish the carcass correlation curves over time and development of a predictive model.

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