Using variation in cattle growth to develop a predictive model of carcass quality

By

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Abstract

This thesis utilised body weights at various ages, hot carcass weight (HCWt), fat depth (PD), eye muscle area (EMA) and intramuscular fat percentage (IMF) data for heifers and steers from the "Southern Crossbreeding Project" where 581 purebred Hereford cows 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; 'Straan' near Naracoorte and 'Wandis' near Mount Gambier in the south-east of South Australia (S.A.). Calves stayed with their dams on pasture until weaning and calves were grown until 12 to 18 mo of age and then transported to a commercial feedlot. The mixed model for growth traits 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. For carcass analysis fixed effects were sex, sire breed, slaughter age nested within sex and random effects were sire, dam, management and environmental effects. The objective of the work described in this thesis was to model relationships between continuous growth traits and carcass quality traits for steers and heifers. The model is being used to predict the effect of growth path on carcass quality. The analyses were based on the following steps:

*Step 1. Describing variation in growth using principal component analysis (PCA) and random regression models of growth*
Applying PCA indicated that the first two principal components (interpreted as the overall size and feedlot growth) accounted for 85% of total variation. Sire effect was significant for overall size and feedlot growth traits and management had a big impact on both components.

A cubic polynomial with sire as a random effect was the simplest and most stable model. Twenty two (co)variances were able to be estimated, using random regression analysis. Variance components for genetic variation within breeds were generally low. In contrast, management group accounted for the large proportion (79%) of the total variation.

**Step 2. Describing variation in carcass quality using principal component analysis (PCA) and multi-trait mixed models**

A large proportion (76%) of variation in the carcass traits were explained by two principal components which were interpreted as market suitability and muscling and were similar for both heifer and steers.

A multi-trait mixed sire model was used to estimate 40 (co)variance components of the four carcass traits. Similar to body weights, non-genetic, in particular management group variation contributed to a large proportion of total carcass variations, up to 50% of total variation.

**Step 3. Joint modeling of growth and carcass quality**

With perseverance, 99 (co)variance components estimated by the joint model to answer the basic questions of how the correlations between growth traits and carcass quality traits change over time. The magnitudes of the coefficient for management correlations were significantly higher than genetic, dam and permanent environmental correlations. Management correlations between live weight and carcass traits during the pre-weaning period were positive except for IMF. The magnitude of those
correlations decreased from birth to weaning, then increased dramatically up for the feedlot period, where they plateaued except IMF which decreased from 500-700 days. Genetic correlations between live weight with HCWI and EMA were moderate to high and positive. In contrast, genetic correlations between live weight and fat traits were low. The pattern of phenotypic correlations between live weight and IMF as the animal grew indicated that the intramuscular fat is later developing than subcutaneous fat.

**Step 1. Predicting carcass quality**

The strength of the model developed lies in its simplicity and the capability to give answers to "what if" questions. However, due to using random regression with a polynomial, the model was subject to over estimations at the end of the trajectory. In addition, because of large residual between animal variances and very small covariances between carcass fat traits and body weights, predictions were of lower accuracy than would be desirable for commercial application of the model. The model was tested against an independent data set and gave predictions that were reasonable although not great. The model could be improved by including other growth traits and other data sets with greater variation in pre-weaning growth.

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