

# Genetic and non-genetic relationships between growth and carcass quality traits of crossbred cattle

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## Abstract

Hereford cows (581) were mated to 97 sires from Jersey, Wagyu, Angus, Hereford, South Devon, Limousin and Belgian Blue, resulting in 1144 calves born over four years to estimate the (co)variance components of the body weights and carcass quality traits. Data included 13 (for steers) and 8 (for heifers) body weight measurements at approximately every 50 days from birth until slaughter and four carcass quality traits: hot carcass weight (HCWt), fat depth (P8), eye muscle area (EMA) and intramuscular fat (IMF). The mixed model fitted 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 (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. Management correlations between carcass traits were high except between P8 and IMF (0.26). Phenotypic, sire and dam correlations between body weights with HSCW, EMA were positive and moderate to high from birth up to feedlot period. Permanent environmental correlations between live-weights and all carcass quality traits were low. Management correlations between body weight and carcass traits during the pre-weaning period were positive except for IMF.

## Introduction

Numerous studies have reported estimates of genetic or phenotypic parameters for growth (at specific ages), or carcass traits, but few have reported estimates of relationships among these groups of traits over the growth path. Hence, a major point of interest within this study was to answer a basic question. If growth traits and carcass quality traits were correlated, did that correlation change over time, and if so, then how did it vary? This paper expands on estimated (co)variances (Mirzaei et al., submitted) to develop a set of functions to visualize time-dependent correlations between growth path and carcass quality traits for different genetic and non-genetic effects.

## Material and methods

*Animal.* The animals and data used in this study were from the “Australian Southern Crossbreeding Project”. The design management and operations of the project as well the exploratory analysis of the data used in this paper described in the companion paper by Mirzaei et al. (submitted).

*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. Therefore, the use of the natural logs of the body weights rather than the original body weights seemed sensible. It also demonstrated that 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 consisted of hot carcass weight (HCWt), P8 fat depth, eye muscle area (EMA) and intramuscular fat (IMF). Carcass traits exhibited a skewed distribution (not shown) and so were transformed.

*Statistical analysis.* Estimated (co)variance components obtained from a joint growth-carcass sire model with random regression to investigate correlations among the body weights and carcass quality traits. The fixed effects are as for the individual analysis of growth and carcass traits reported by Mirzaei et al. (submitted). Random effects consist of constant, linear, quadratic and cubic terms for each of the four component random effects (Sire, Maternal, Management and Permanent environmental).

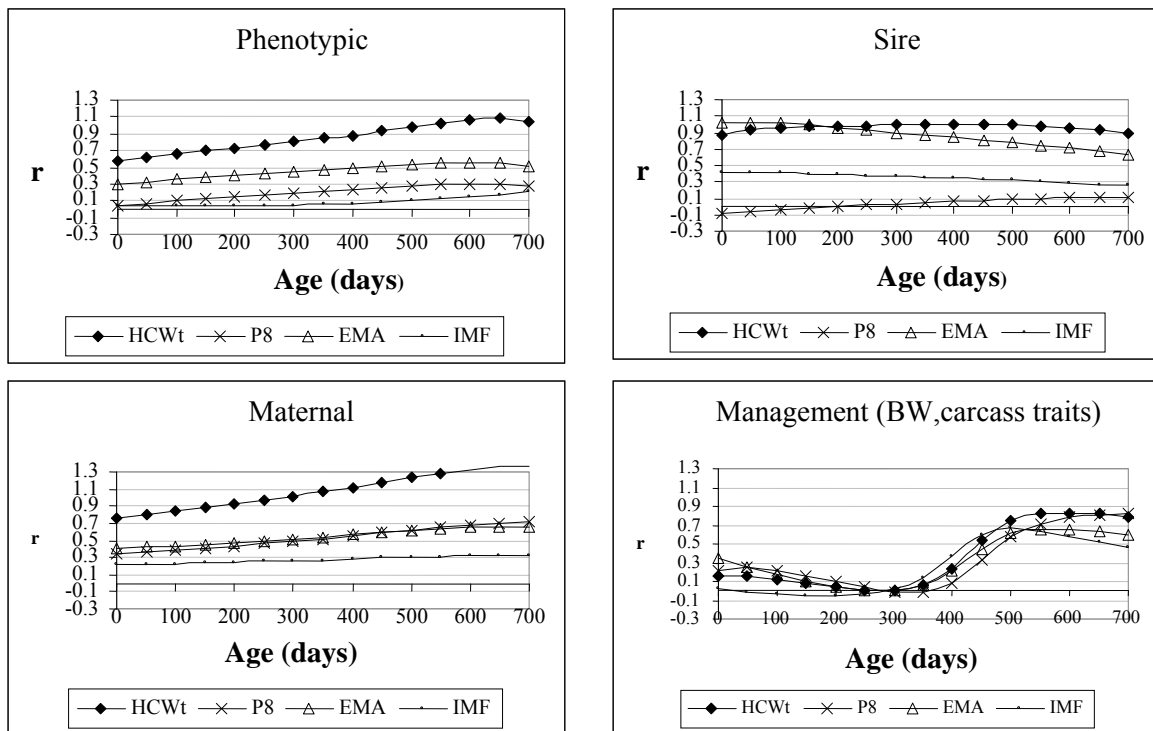
As stated earlier the main objective of this paper was to estimate corresponding correlations between growth path (longitudinal body weights and relative growth rate) and carcass quality traits.

$$\text{Thus } \rho(\text{Inc}_{ij}, \text{Ing}_{ijt}) = \frac{\text{cov}(\text{Inc}_{ij}, \text{Ing}_{ijt})}{\sqrt{(\text{var}(\text{Inc}_{ij})\text{var}(\text{Ing}_{ijt}))}}$$

where  $\ln c_{ij}$  is log of  $i$ th carcass trait of  $j$ th calve,  $\ln g_{ijt}$  is log of  $i$ th body weight of  $j$ th calve at time  $t$ ,  $\text{var}(\ln g_{ijt})$  is the variance of growth components,  $\text{var} \ln c_{ij}$  is the variance of growth components and  $\text{cov} \ln c_{ij}, \ln g_{ijt}$  is the covariance between growth and carcass quality traits. In fact, the model is in term of log-weights and log-carcass trait. Using properties of the log-normal distribution (Limpert et al., 2001).

## Results and discussion

The very low environmental correlations between birth weight and HCWt implied that environments affecting HCWt was independent of that influencing birth weight (Figure 1). High genetic correlation between birth weight and HCWt was in general agreement with other works (AAABG, 2004).



**Figure 1.** Correlations between body weight and carcass traits over time

The very low phenotypic and genetic correlations between birth weight and fat depth, indicated that very few genes may affect both traits and that there will be little correlated change in one trait as a result of selection for the other trait, consistent with values reported by AAABG, (2004).

As the birth weight, the environmental estimates of correlation between weaning weight and HCWt was low, indicating independency of the environments that affect both traits. Favorable phenotypic and genetic correlations between weaning weight and HCWt may represent opportunities for increased productivity. This is in strong agreement with other literature (AAABG, 2004).

The pre-weaning body weights were negatively related genetically with P8 fat depth (Figure 1), in general agreement with Crews and Kemp (1999). The negative relationship between weaning weight and P8 fat depth could be related to maturing rate. Animals that are heavier at weaning may mature slowly and consequently could have increased amounts of lean muscle tissue relative to external fat. Those animals that had higher pre-weaning growth had heavier carcasses although they also tended to be fatter than carcasses from animals that had low pre-weaning growth rates.

The estimates of phenotypic and maternal correlations between weaning weight and EMA were in agreement with Splan et al. (2002) who reported that correlations between weaning weight and EMA were moderate and positive at age, marbling, and fat-thickness end points (Figure 1). The estimate of genetic correlation for pre-weaning and weaning weight was consistent with Splan et al. (2002) who reported a positive genetic correlation between weaning weight and marbling (0.12 and 0.21, respectively). Estimates of

correlations for phenotypic and maternal effects of pre-weaning and weaning weight with IMF were low (Figure 1), in agreement with Splan et al. (2002). Arnold and Bennett (1991) found that marbling was uncorrelated with weaning weight. The subjective nature of marbling score may account for the inconsistent estimates.

High phenotypic, genetic and maternal correlations between post-weaning body weights with HCWt was in agreement with other reports by AAABG (2004). Shackelford et al. (1994) observed the values of 1.26 and 1.10 for genetic correlations between post-weaning growth rate with carcass weight. The low phenotypic correlations between yearling weight and P8 fat depth was in agreement with Arnold and Bennett. (1991). The moderate to high positive genetic correlation between post-weaning growth and EMA (Figure 1) indicated that selection for higher growth should also lead to more total muscle mass as reflected in the size of the EMA. On a theoretical basis, faster-gaining animals will be fatter if they have capacity to dispose of more calories by fat accretion. This, in turn, should reduce mature size.

### **Implications**

To meet demand for quality beef, seed stock and commercial producers need to consider not only growth but also carcass traits in selection decisions. Knowledge of growth-carcass curve shape, in particular its non-genetic determination would be of interest for optimising breeding goals and management practices to meet market specifications. It seems that selection for increased direct genetic value for pre-weaning and weaning body weights would be expected to increase HCWt, EMA, IMF (to some extent). Maternal correlations between body weight and HCWt were high, but they were lower for other traits. So, emphasis on maternal milk or maternal effects on pre-weaning and weaning and post-weaning body weights may lead to positive correlated responses in HCWt and EMA. However, because most of the correlations between maternal genetic effects for weaning weight are not large in magnitude, selection for carcass fat traits would not be expected to result in important changes in maternal ability.

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