Is Variation in Growth Trajectories genetically correlated with Meat quality Traits in Australian Terminal Lambs?

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ABSTRACT: This study used meat quality traits on 5164 crossbred terminal lambs and a total of 32061 weight records measured between the ages of 75 to 250 days to do a bivariate random regression model, to determine the genetic relationship between growth patterns and meat quality traits in lambs. The genetic correlations between both weight and growth at different ages and carcass eye muscle depth (CEMD), fat depth (FAT5), shear force (SHF5), pH of the M. Semitendinosus (pHST) and percentage of intramuscular fat (IMF) were calculated. We found that genetic correlations of early growth (100-150d) were higher compared to late growth (200-250d) for CEMD 0.43 vs. 0.14; FAT5 0.49 vs. 0.14; SHF5 -0.50 vs. -0.26; pHST -0.18 vs. 0.15 and IMF 0.27 vs. 0.12. This study showed the potential to influence meat quality when growth curves are changed by breeding.

Keywords: Random Regression Model; Genetic correlations; Meat quality

Introduction

Australian meat sheep breeders select mainly on lean meat (Fischer et al. 2006) and growth as these are the main traits affecting the farm's productivity and profitability (Pannier et al. 2014). Selection is mostly based on the Australian Sheep Breeding Values (ASBV) of post weaning weight (PWT), eye muscle depth and fat depth (Pannier et al. 2014). However, modern consumers are increasingly demanding healthy and high quality food (Fisher et al. 2000). Therefore, these existing breeding objectives should be expanded to incorporate meat quality traits. Important meat quality traits are intramuscular fat (IMF) and shear force as they both affect the flavour and tenderness of meat (Hopkins et al. 2010) and pH as this trait is important for visual appeal and shelf-life (Young et al. 1993; Ferguson et al. 2001). However, the genetic evaluation of these traits is problematic as they cannot be measured on live animals. Both carcass eye muscle depth (CEMD) and fat depth are important carcass traits as farmers' breeding objectives include selection on lambs that grow heavy, lean and muscular carcasses (Fischer et al. 2006). Therefore, it is of interest to know if there is an association between growth and meat quality traits. This is especially important for the traits that are affected by early life growth (growth up to PWT), as it has been suggested that selection on PWT can change the shape of the growth curve. To predict a possible impact of such a change on meat quality, we analysed the relationship of growth at different stages of the lambs' growth path with meat quality traits. We hypothesised that animals that reach the same final weight but via different growth paths (e.g. fast early growth vs fast late growth etc.) show differences in meat quality or carcass composition traits. Therefore, the aim of this study was to find genetic correlations between both weight and growth at different ages and carcass eye muscle depth (CEMD), fat depth on the 5th rib (FAT5), shear force after 5 days of aging (SHF5), pH of the *M. Semitendinosus* (pHST) and percentage of intramuscular fat (IMF) by the use of bivariate random regression models.

Material and methods

Data: Data was recorded from year 2007 to 2011 on crossbred progeny of terminal sire breeds. The data originated from the sheep information nucleus database (INF) established by the Australian Sheep CRC. This study used meat quality and carcass composition traits on 5164 crossbred terminal lambs and a total of 32061 weight records measured between the ages of 75 to 250 days. These lambs were progeny of 177 terminal sires (either Poll Dorset or White Suffolks) and 3203 dams (either Merino (M) or Border Leicester x Merino (BLxM)). As a result, terminal lambs are either terminal first cross (TxM) or terminal second cross (TxBLM). Details of the experimental design can be found in van der Werf et al. (2010).

Carcass and meat quality measurements: Lambs were slaughtered in collaborating commercial abattoirs of the CRC Meat program if the lambs reached an average target carcass weight of 22 kg. The slaughter age ranged between 134 to 431 days but was on average 241 days. After slaughter hot carcass weight (HCWT) was determined. Subsequently eye muscle depth of the *M longissimus lumborum*, (CEMD), fat depth on the fifth rib, 110 mm from the midline of the chilled carcass (FAT5), shear force after 5 days of aging (SHF5), pH of the *M. Semitendinosus* (pHST) and the percentage of intramuscular fat (IMF) were recorded.

Statistical analysis: Univariate analysis was used to determine the best random regression model to fit variation in growth patterns. The fixed effects consisted of birth x rearing type (6 levels), age of dam (7 classes, 2 -8), flock x birth-year (8 flocks x 5 years), sex (wether or ewe) and dam breed (M and BLxM). We also fitted a regression on breed proportions determined by using a deep pedigree. Legendre polynomial of age

(days) of order k=4 was nested within all fixed effects except for breed proportion.

Orders of a *k*-order polynomial fit on age, up to k = 4 were considered for random effects of direct genetic, maternal, permanent environment and maternal permanent environment. An additional interaction between sire and flock was fitted as a fifth random effect. Model selection was guided by the AIC and BIC criteria. Residual effects were considered to be independently distributed and homogenous within 4 different classes depending on age (75-100, 101-150, 151-200 and 201-250). The statistical analyses were done using ASReml (Gilmour et al. 2009).

Estimates of genetic correlations between weight and growth at different ages with meat quality and carcass composition traits were obtained via bivariate analyses. All meat traits were corrected for the same fixed effects as the uni-variate analyses but an additional correction for slaughter age was included. No Legendre polynomial order was fitted for the meat traits. For the carcass traits CEMD and FAT5, HCWT was included as a linear covariate. (Co)variances for growth were calculated as a linear combination of (co)variances of weight at different ages. The growth periods were chosen to be early growth 100-150 days, mid growth 150-200 days and late growth 200-250 days.

Results

The best model fitted Legendre polynomials of order k=3 for additive genetic, maternal genetic, permanent environment and order k=2 for maternal environmental effect, with 4 classes of error variances.

Results in Table 1 show that CEMD and pHST have quite similar genetic correlations with weight at different ages. SHF5 has a low negative genetic correlation with early weight but the magnitude of this negative correlation increases towards d250. Both FAT5 and IMF showed an increasing positive genetic correlation from d100 onwards.

Table 1. Estimated genetic correlations between weight at different ages and meat quality traits.

Day	CEMD^1	FAT5 ²	SHF5 ³	pHST ⁴	IMF ⁵
100	0.55	0.30	-0.13	-0.30	0.12
150	0.55	0.40	-0.29	-0.29	0.19
200	0.58	0.46	-0.37	-0.26	0.23
250	0.62	0.49	-0.43	-0.22	0.27

¹Carcass eye muscle depth of the *M* longissimus lumborum 2 Fat depth on the fifth rib

³ Shear force after 5 days of aging

⁴ pH of the *M. Semitendinosus*

⁵ Percentage of intramuscular fat

In Table 2 the direct genetic correlations between growth at different time intervals and meat quality and carcass traits are shown. Early growth (100-150) and mid growth (150-200) are positively genetically correlated with CEMD, FAT5 and IMF but show a negative genetic correlation with pHST and SHF5. Late growth (200-250) was genetically less correlated with all meat quality and carcass composition traits except for pHST. pHST showed a shift from a low negative genetic correlation with early and mid growth to a low positive genetic correlation with late growth. CEMD, FAT5, SHF5 and IMF all had higher correlations with early and mid growth compared with late growth.

Table 2. Estimated genetic correlations betweengrowth and meat traits.

Day					
interval	CEMD ¹	FAT5 ²	SHF5 ³	pHST ⁴	IMF ⁵
100-150	0.43	0.49	-0.50	-0.18	0.27
150-200	0.43	0.47	-0.51	-0.03	0.29
200-250	0.14	0.14	-0.26	0.15	0.12
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¹Carcass eye muscle depth of the *M* longissimus lumborum 2 Fat depth on the fifth rib

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Discussion

This study describes estimation of genetic correlations between weights and growth patterns at different ages with five meat quality and carcass composition traits in Australian terminal lambs. Fogarty et al. (2003) found genetic correlations between live weight (532 days) and CEMD 0.01±0.10, pH -0.21±0.11 and FATGR (tissue depth on the 12^{th} rib at the GR site) of -0.12±0.11, these meat and carcass traits were also corrected for HCWT and slaughter day. In our study, estimated correlations with weight were high even for traits that had been adjusted phenotypically for variation in HCWT. Without the adjustment correlations were even higher. For example, correlation between weight at 100d, 150d, 200d, 250d and unadjusted CEMD were 0.74, 0.75, 0.77 and 0.80, respectively. Mortimer et al (2014) discuss some potential problems with adjusting for correlated traits by including them as covariates.

This study showed that the genetic correlations of most meat traits with growth periods or weights are age sensitive as they vary between different time points. Gregory et al. (1995) also showed in cattle that correlations between weight and meat traits are highly influenced by age. Furthermore, this study found that overall early and mid growth are more influential than late growth. Although we did not present formal estimates of standard errors on these correlations, the magnitude of data would suggest that these should be well below 0.10. Therefore the differences shown could well be significant for some traits, but this needs to be more formally tested.

FAT5 composition showed a high positive genetic correlation with early growth (0.49) but reduces to a moderate correlation (0.14) with late growth. The positive correlations do correspond with multiple studies that found that carcass fatness was lower in slower growing lambs (Murphy et al. 1994). Selection on early or mid growth would have a favourable effect on shear force (-0.50; -0.51 resp.). This is underpinned by Hopkins et al. (2005) as they found slower growing lambs to have elevated shear force. The genetic correlations of pHST should be interpreted with care since pH is a very acute and variable trait which is highly responsive to pre-slaughter nutrition and stress (Ferguson et al. 2001), therefore it is of no surprise that the genetic correlations between both early and late growth and pHST are relatively low (-0.18; 0.15 resp.). Lastly, this study found a favourable positive genetic correlation between IMF and early (0.27), mid (0.29) and late growth (0.12). This is substantiated by Murphy et al. (1994), who found that slower growth resulted in an unfavourable decrease in IMF content.

Conclusion

This study found that different growth periods (early vs. mid vs. late) show different genetic correlations with meat quality and carcass composition traits in Australian Terminal lambs. These results imply that changing growth curves by selection can simultaneously influence meat quality and carcass traits. This provides new information to be used in the design of breeding objectives and selection indexes for the Australian meat sheep industry.

Literature cited

- Ferguson, D. M., Bruce, H. L., Thompson, et al. (2001). Aust. J. Exp. Agric, 41(7), 879-891.
- Fischer T.M., Werf J.H.J.v.d., Banks R.G. et al. (2006). *Anim. Sci.* 82, 13-22.
- Fisher A.V., Enser M., Richardson R.I. et al. (2000). *Meat Sci.* 55, 141-7.
- Fogarty N.M., Safari E., Taylor P.J. et al. (2003) *Aust. J. Agri. Res.* 54, 715-22.
- Gilmour A.R., Gogel B., Cullis B. et al. (2009) *ASReml user* guide. Release 3.0. VSN International Ltd, Hemel Hempstead, UK.
- Gregory K.E., Cundiff L.V. & Koch R.M. (1995). J. Anim. Sci. 73, 1920-6.
- Hopkins D., Toohey E., Warner R. et al. (2010). Anim. Prod. Sci. 50, 382-5.
- Hopkins D.L., Hegarty R.S. & Farrell T.C. (2005). Aust. J. Exp. Agric. 45, 525-33.
- Mortimer S.I., Swan A.A., Brown D.J. et al. (2014). Proc.10th World Congress Genet. App. to Livest. Prod.
- Murphy T.A., Loerch S.C., McClure K.E. et al. (1994). J. Anim. Sci. 72, 3131-7.
- Pannier L., Pethick D.W., Geesink G.H. et al. (2014). *Meat Sci.* 96, 1068-75
- van der Werf J.H.J., Kinghorn B.P. & Banks R.G. (2010) Anim. Prod. Sci. 50, 998-1003.
- Young O.A., Reid D.H. & Scales G.H. (1993) N. Z. J. Agric. Res. 36, 363-70.