BRIEF COMMUNICATION: Effect of MyoMAX® on carcass lean and fat

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Keywords: MyoMAX®; GDF8; sheep; meat yield; computed tomography; Viascan.

INTRODUCTION

Previous research has identified quantitative trait loci (QTL) for increased lean meat yield and decreased fat in similar regions of sheep chromosome 2, in New Zealand and Belgian Texels (Broad *et al.*, 2000; Johnson *et al.*, 2005; Laville *et al.*, 2004; Marcq *et al.*, 2002). In the case of the Belgian Texels it has been demonstrated that a single G to A transition (*g+6723G-A*) in the 3' untranslated region of the growth and differentiation factor 8 (GDF8) gene is responsible for the QTL effect (Clop *et al.*, 2006). Recently, the presence of the *A* allele was confirmed in Australian Texels (Kijas *et al.*, 2007). However, the presence and effect of the *A* allele in New Zealand Texels has not been confirmed. In addition, previous studies have only reported the size of the QTL effect in animals inheriting a single copy of the *A* allele. The purpose of this study was to determine the effects of zero, one, or two copies of the *A* allele in New Zealand Texel cross animals at varying lamb ages and carcass weights, using both computer tomography (CT) and Viascan (a two dimensional imaging system that estimates lean content of the carcass (Hopkins *et al.,* 2004)) to estimate lean and fat content in primal cuts.

MATERIALS AND METHODS

Two Texel cross rams, known to be carrying one copy of the *A* allele were each joined with 100 Texel cross ewes with primarily one copy of the *A* allele to generate 187 weaned progeny that carried either zero, one or two copies of the *A* allele. Mating groups were balanced for source of origin and ewe age. The progeny were genotyped for the *A* allele and randomly assigned to one of four slaughter groups balanced for animals carrying zero, one or two copies of the *A* allele, sex and sire. The average live-weight for the four slaughter groups was 33, 40, 43 and 48 kg respectively, with their ages ranging from 4 to 8 months. Carcass weight, GR (fat depth), and Viascan carcass estimates of leg, loin, shoulder and total lean yield expressed as a percentage of carcass weight were recorded at slaughter.. Animals in the fourth slaughter group, were CT scanned as live animals using the Cavelleri procedure on four occasions, at similar times to the first three slaughters and prior to their own slaughter. The CT scan weights corresponded to the slaughter weights. CT images were analysed using the protocol of Kvame *et al.* (2004). CT provides accurate carcass composition estimates (Afonso, 1992).

Slaughter data were analysed using the general linear model procedure in SAS (2004). The models fitted included fixed effects of sex (ram or ewe), slaughter group (1, 2, 3 or 4), sire (1 or 2), and *A* allele status (0, 1 or 2 copies), with carcass weight fitted as a covariate where appropriate. Computed tomography data were analysed using the mixed model procedure in SAS (2004), which allowed for the fitting of repeated measures as each animal was CT scanned on four separate occasions. The model fitted included fixed effects of sex (ram or ewe), scan number (1, 2, 3 or 4), sire (1 or 2), and *A* allele status (0, 1 or 2 copies), repeated measure of lamb as a random effect, and a covariate of carcass weight fitted for all traits except carcass weight. Interactions between all fixed effects and covariates were tested for all models, but were not significant and were excluded from the final models.

RESULTS AND DISCUSSION

The presence of the *A* allele was confirmed in the New Zealand Texel. The slaughter data results are summarized in Table 1 and the CT results are summarized in Table 2.

This study supports findings of Johnson *et al.* (2005) that the *A* allele does not affect measures of live weight and carcass weight, hence growth rate. The results, are also consistent with findings of Johnson *et al.* (2005), Laville *et al.* (2004), and Kijas *et al.* (2007) that the *A* allele increases carcass lean and decreases carcass fat. However, this study goes further than previous studies by investigating differences between the three genotypes (0, 1 or 2 copies of the *A* allele) and their magnitude across different carcass weight end points.

The results suggest that the effect of the *A* allele was largely additive for most carcass composition traits, although in this study the difference between animals carrying one and two copies of the *A* allele was not always statistically significant.

TABLE 1: Least squares means for the effect of zero, one, or two copies of the *g+6723G-A* transition in the GDF8 gene on carcass traits measured at slaughter. All non-weight measurements were adjusted to a common carcass weight. RSD = Residual standard deviation. Viascan is a two dimensional imaging system

Carcass trait	*A* allele status			RSD
	0	1	2	
Number of animals	47	80	60	
Pre-slaughter weight (kg)	42.0	40.5	41.9	6.14
Carcass weight (kg)	17.6	16.6	17.7	2.23
GR (mm)	5.1[a]	4.7[a]	4.0[b]	1.82
Viascan lean yield (%)				
Leg	21.2[a]	21.5[a]	22.3[b]	0.98
Loin	13.8[a]	14.0[a]	14.5[b]	0.84
Shoulder	16.7[a]	17.1[b]	17.8[c]	0.94
Total	51.7[a]	52.6[b]	54.7[c]	2.29

Means not sharing a common superscript within a row were statistically different (P <0.05).

TABLE 2: Least squares means for the effects of zero, one, or two copies of the *g+6723G-A* transition in the GDF8 gene on weight-adjusted carcass traits measured using a computed tomography scanner, from repeated scanning of the same animals. SEM = Standard error of mean.

Carcass trait	*A* allele status			Average SEM
	0	1	2	
Number of animals	14	15	15	
Liveweight at scanning (kg)	39.9	39.0	41.9	1.71
Carcass				
Weight (kg)	19.5	18.9	19.9	0.65
Total lean (kg)	12.4[a]	12.9[b]	13.3[c]	0.11
Total fat (kg)	3.6[a]	3.2[b]	2.8[c]	0.12
Intermuscular fat (kg)	2.1[a]	2.0[a]	1.8[b]	0.08
Total bone (kg)	2.7	2.7	2.7	0.03

Means not sharing a common superscript within a row were statistically different (P <0.05).

The interaction between slaughter group, scan group or carcass weight and *A* allele status (0, 1 or 2 copies) was not significant for any trait examined, suggesting the size of the *A* allele effect changes little over the carcass weight end points examined here.

This research suggests that there are advantages to be had from having the *A* allele present in both maternal and paternal lines as the results are largely consistent with an additive mode of inheritance. The *A* allele effect can also be detected commercially via Viascan and CT scanning at New Zealand commercial carcass weights. A test for the *A* allele is now commercially available as the MyoMAX® test (www.catapultsystems.co.nz).

ACKNOWLEDGEMENTS

This work was funded by Ovita Ltd. We thank staff at Alliance Ltd. who processed the lambs and provided Viascan results and the ongoing support for this work by Murray Behrent. Staff from Woodlands Research station helped with the processing of the carcasses. Neville Jopson was instumental with the CT programs and Helga Gunnarsdottir analysed most of the CT images.

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