

Effect of the Texel muscling quantitative trait locus (TM-QTL) on fore quarter, hind quarter and saddle weights, weight distribution and carcass composition in purebred Texel lambs

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Introduction TM-QTL is a QTL which increases loin muscling by 4 to 11% in Texel lambs (e.g. Macfarlane *et al.*, 2010a) and Texel-sired crossbred lambs (e.g. Macfarlane *et al.*, 2009) with a polar overdominant action (phenotype is expressed only if one copy inherited from sire) and has an additive effect on carcass weight (Macfarlane *et al.*, 2010b). This study examines TM-QTL effects on carcass composition and weight distribution in Texel lambs.

Material and Methods Purebred Texel lambs (n = 209) born in 2009 on two farms were reared with their dams on pasture until slaughter at ~20 weeks of age, except for 12 artificially-reared lambs, which were reared indoors until ~8 weeks then grazed and creep-fed until slaughter. After slaughter, carcasses were chilled for 7, 8 or 9 days, weighed, split and each side cut into fore-quarter (FORE ¼), saddle (SADDLE) and hind-quarter (HIND ¼). These were weighed and butchered into lean meat (LMY), fat trim and bone. Proportion of total carcass weight contained in each region and proportion of LMY (LMY/CWT), fat trim (FAT/CWT) and bone (BONE/CWT) in the carcass were calculated. Lambs were blood-sampled and TM-QTL genotypes assigned (described by Macfarlane *et al.*, 2010a). There were 40 non-carriers (+/+), 17 heterozygote carriers inheriting TM-QTL from the dam (+/TM), 53 heterozygote carriers inheriting TM-QTL from the sire (TM/+), 34 homozygote carriers (TM/TM) and 65 with unknown genotype. Data on lambs with unknown genotype were included in analyses to give more robust estimations of fixed effects, but only results for the 4 known genotypes are presented. General linear mixed models (REML) for the variables described above were run in Genstat (GenStat 11, 2008) including TM-QTL genotype, sex (entire male or female), rearing rank (single, twin or artificial), farm (SAC or IBERS) and dam age (2, 3, 4 years or older) as fixed effects, sire as a random effect (7 sires, 3 common across farms) and CWT as a linear covariate for all variables other than itself. CWT was included as a linear covariate for the proportion variables due to a strong relationship between these variables and CWT, probably due to the wide range of CWT present in the data (8 – 25kg, mean 15.2 kg).

Results TM-QTL effects on *M. longissimus lumborum* weight adjusted for CWT (+/+ vs. TM/+, difference = 4%, P = 0.046) and CWT (+/+ vs. TM/TM difference = 10%, P = 0.036) were verified. When not adjusted for CWT, FORE ¼, SADDLE and HIND ¼ weights were heavier for TM/TM than +/+ (by 8.7 to 13.5%) with no significant differences between other groups. When adjusted for CWT, there were no significant differences between genotypes for weights in each area or the proportion of total CWT contained in each carcass area (Table 1). LMY/CWT was 1.36 to 2.37% higher in TM/TM compared to the other groups although the difference was significant only for TM/TM vs. +/TM. FAT/CWT and BONE/CWT were not significantly different between genotypes.

Table 1 Least squares means[†] for area weights (g), weight distribution and carcass composition for the 4 TM-QTL genotype groups

	HIND ¼ wt	SADDLE wt	FORE ¼ wt	HIND ¼ wt/CWT	SADDLE wt/CWT	FORE ¼ wt/CWT	LMY /CWT	FAT /CWT	BONE /CWT
+/+	2650	1678	2804	0.183	0.115	0.194	0.586 ^{ab}	0.043	0.304
+/TM	2637	1705	2768	0.182	0.116	0.192	0.581 ^b	0.042	0.306
TM/+	2666	1678	2791	0.184	0.115	0.193	0.587 ^{ab}	0.039	0.308
TM/TM	2645	1708	2808	0.183	0.117	0.194	0.595 ^a	0.042	0.301
ave s.e.d.	21.4	31.3	28.7	0.0016	0.0019	0.0019	0.0053	0.0034	0.0055

[†]Within column, means with a common superscript character are not significantly different when tested with pair-wise s.e.d. (P>0.05); average s.e.d. (ave s.e.d.) shown for reference only. Least square means in table are those with CWT fitted in the model

Conclusions The previously reported effect of TM-QTL on carcass weight has been shown here to be reflected in increased weight of all carcass areas, with no effect of TM-QTL on weight distribution. Carcass composition was affected by TM-QTL; homozygote TM-QTL carriers had a greater proportion of LMY compared to other groups. In addition to previously reported benefits, if TM-QTL were included in breeding programmes to produce homozygote carrier lambs, meat yield could be increased in carcasses of equal weight.

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