Using CT scanning to simultaneously breed UK slaughter lambs for improved carcass and meat quality

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Summary

X-ray computed tomography (CT) scanning can provide non-invasive predictions of intramuscular fat (IMF) in live lambs and meat cuts, providing potential to select for meat quality within a sheep breeding programme. The genetic control and relationships of these traits with carcass quality must be determined across relevant breeds and within the context of the new UK combined breed analysis (CBA), before recommending incorporation into existing breeding programmes. UK national data were analysed within-breed from several thousand commercial, CT scanned ram lambs of 3 terminal sire breeds, and using a snapshot of CBA data, across 7 terminal sire breeds and crosses. In most cases, IMF levels were moderately heritable (0.23-0.4), highly positively genetically correlated with total carcass fat and moderately negatively correlated with total carcass muscle and muscularity, although there were some marked breed differences. In a separate trial, genetic parameters estimated for IMF in meat from crossbred progeny (n=1204) of Suffolk sires (n=28), predicted by CT post-mortem, gave a similar heritability (0.21), with moderate positive genetic correlations with carcass EUROP grades for fat and conformation. Results suggest scope to use CT within a breeding programme to select for more taste and less waste in commercial slaughter lambs.

Keywords: lamb, meat quality, intramuscular fat, CT scanning

Introduction

Meat quality traits are difficult and expensive to measure routinely in lamb, as in other species. There is also a perception that meat quality in lamb has not suffered due to genetic selection for reduced carcass fat and increased lean yield, as in beef or pork. Consequently, practical examples of breeding for lamb meat quality traits are not common. Intramuscular Fat (IMF) is known to positively affect consumer perceptions of eating quality (Hopkins et al., 2006). However, research in different UK breeds (Lambe et al., 2008, 2017) suggests IMF levels in slaughter lambs are suboptimal for consumer acceptance (Savell & Cross, 1988; Hopkins et al., 2006).

CT scanning data on live animals have been incorporated into UK terminal sire sheep breeding programmes for 20 years, accelerating genetic gains in carcass composition (Bunger et al., 2014) when the top 15-20% of ram lambs, based on growth and ultrasound data, are CT scanned. Tissue densities measured during CT scanning provide good in vivo estimates of IMF in the loin of different breeds (Clelland et al., 2015a; Karamichou et al., 2006; Lambe et al., 2008) and prediction equations are transferable across breeds and crosses (Clelland, 2015), providing an objective prediction of eating quality in live animals. In vivo CT-
predicted IMF was reported to be moderately heritable in Texel sheep (Clelland et al., 2015b). As CT is non-invasive and non-destructive, it can also be used on meat destined for human consumption. Scanning of primal cuts could reduce costs and practical barriers compared to scanning live lambs. Recent research (Lambe et al., 2017) shows that CT scanning can predict IMF with moderate accuracy in loin cuts from crossbred lambs.

Around 66% of UK slaughter lambs are commercial crossbreds (Pollott, 2014), although genetic selection is performed in pure breeds and crossbred lambs are rarely performance recorded. This could be resulting in suboptimal genetic gains for crossbred slaughter lambs, as evidence suggests low genetic correlations between purebred and crossbred performance (Dekkers, 2007). UK terminal sire breeding programmes provided by the Agriculture and Horticulture Development Board (AHDB), will produce EBVs from a combined breed analysis (CBA; Moore et al., 2016) from 2018 onwards, incorporating data from pure- and cross-bred performance-recorded sheep.

The aims of this paper were: 1) to use previously-derived CT prediction equations to assess IMF levels in lambs of different terminal sire breeds; 2) to estimate genetic parameters for in vivo CT-predicted IMF in different terminal sire breeds, or using a combined breed analysis; 3) to estimate genetic parameters for levels of IMF in meat from crossbred progeny predicted by CT post-mortem.

Material and methods

In vivo CT predictions of IMF

Archived CT data were used from male terminal sire lambs, scanned live at an average of 21 weeks, across 20 years. For Texel, Suffolk and Charollais lambs, respectively, 2640, 1534 and 1465 records were available for CT-predicted IMF % in M. longissimus lumborum (CTIMF; Clelland et al., 2015a), and 3525, 2353 and 2012 records were available for current CT traits for which EBVs are available: total carcass fat weight (CTFWT), total carcass muscle weight (CTMWT) and gigot musculature (ratio of depth to width of the hind leg muscle; CTMusc) (Bunger et al., 2014). Uni- and bi-variate genetic analyses were performed using ASReml v3 (Gilmour et al., 2009), to estimate heritabilities ($h^2$) and genetic correlations ($r_g$) amongst the CT traits. Pedigree files contained sires and dams for 137,774 Charollais, 32,168 Texel, and 19,247 Suffolk animals (full pedigree files for Texel and Suffolk were pruned to reduce computational time). Current animal models used in UK genetic evaluations for CT traits were fitted, including age at CT, litter size, dam age, contemporary group (describing flock, year, season, management group) and dam breed at weaning (Texel only). The covariate age at CT was replaced by live weight at CT in additional analyses.

The combined breed data included 5887 CTIMF records and 5952 records for CTFWT, CTMWT and CTMusc, from male lambs of 7 terminal sire breeds and crossbreds. The CBA pedigree file contained sires and dams for 165,004 animals. Similar uni- and bi-variate genetic analyses were performed, fitting the same model, but including effects for heterosis and recombination (Moore et al., 2016).

Post-mortem CT predictions of IMF

Research data were available from 1204 female and castrated male crossbred lambs, from 28 Suffolk sires and 777 mixed-age Scotch Mule dams, collected across 2 farms. Lambs were slaughtered across 17 batches (target live weight 42kg, condition score 3). Cold carcass
weights (CCWT) averaged 19.6kg (14.6-29.7kg). EUROP fatness (FAT) and conformation (CONF) grades were converted to numeric scales (Kempster et al., 1986). The chilled left side loin cut, bone-in, was collected, vacuum-packed, and CT scanned 7-8d post-mortem. IMF in the longissimus muscle was estimated from CT data (CTIMFpm; Lambe et al., 2017).

Uni- and bi-variate genetic analyses were performed for CTIMFpm, FAT and CONF. The pedigree files contained sires and dams for 16650 Suffolk animals. Sire models were fitted, including CCWT, farm, sex, slaughter batch and dam age (8 levels, 2-9y old), and a random effect of dam (for univariate models only, due to bivariate convergence issues).

**Results and Discussion**

Predicted CTIMF levels within each breed, and in the CBA data (Table 1), were within published ranges for chemical IMF at similar ages in UK breeds (e.g. Lambe et al., 2008; Clelland, 2015). Even though these lambs were CT scanned heavier than commercial pre-slaughter weights, average predicted IMF % was below recommended levels for consumer acceptance (Savell & Cross, 1988; Hopkins et al., 2006). The crossbreed lamb loins, CT scanned post-slaughter, had similar predicted IMF % (Table 1).

**Table 1. Raw averages (and standard deviations) for traits of interest**

<table>
<thead>
<tr>
<th>Breed</th>
<th>CT age (d)</th>
<th>CT LWT (kg)</th>
<th>CTIMF (%)</th>
<th>CTFWT (kg)</th>
<th>CTMWT (kg)</th>
<th>CTMusc[^1]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Texel</td>
<td>150 (19)</td>
<td>54.8 (8.3)</td>
<td>1.79 (0.47)</td>
<td>5.09 (1.83)</td>
<td>16.9 (2.9)</td>
<td>67.2 (7.0)</td>
</tr>
<tr>
<td>Suffolk</td>
<td>149 (21)</td>
<td>59.7 (9.3)</td>
<td>2.54 (0.46)</td>
<td>6.70 (2.27)</td>
<td>15.7 (2.8)</td>
<td>61.0 (6.6)</td>
</tr>
<tr>
<td>Charollais</td>
<td>155 (12)</td>
<td>63.4 (7.7)</td>
<td>2.59 (0.47)</td>
<td>7.63 (2.12)</td>
<td>17.5 (2.3)</td>
<td>66.6 (6.2)</td>
</tr>
<tr>
<td>CBA</td>
<td>152 (18)</td>
<td>55.9 (9.9)</td>
<td>2.15 (0.64)</td>
<td>5.71 (2.29)</td>
<td>16.7 (3.0)</td>
<td>65.5 (7.6)</td>
</tr>
<tr>
<td>Suffolk x Mule</td>
<td>165 (30)</td>
<td>19.6 (2.1)</td>
<td>2.76 (0.40)</td>
<td>11.5 (1.4)</td>
<td>3.4 (0.5)</td>
<td></td>
</tr>
</tbody>
</table>

[^1]Ratio of depth to width of gigot muscle *10 (Jones et al., 2002)

Moderate h² estimates for CTIMF in Texel and Suffolk lambs, and from the CBA (Table 2), agree with previous estimates in Texels (Clelland et al., 2015b) and published h² for chemically-extracted IMF in lambs (e.g. Karamichou et al., 2006; Mortimer et al., 2014). Unexpectedly high h² were estimated for CTIMF in Charollais lambs, requiring further investigation. Within-breed, h² was similar when adjusted for age or live weight (Table 2).

Strong, positive rg estimates were estimated between CTIMF and CTFWT, with live weight adjusted values higher than age adjusted. These rg were significantly different from 1, except for Suffolk (age or live weight adjusted) and Charollais (live weight adjusted). For all except Suffolk, rg between CTIMF and CTMWT were moderate and negative when age adjusted, and strongly negative when live weight adjusted. CTIMF and CTMWT were not significantly genetically correlated in Suffolk lambs. CTMusc had a negative rg (weak-moderate) with CTIMF, except in Suffolks, where this rg was low and positive (with large standard errors).

True breed differences in the genetic control of these traits is likely to occur due to differing selection histories. For example, Texels are relatively leaner and more muscular at a given proportion of mature size than other breeds (Wolf et al., 2006). However, there may also be differences due to the selection of ram lambs for CT scanning. Sufficiently large data...
sets are not yet available from lambs of mixed sex and genetic merit to test this robustly.

The genetic parameters estimated from the crossbred slaughter lambs (Table 2) suggest a similar $h^2$ for CTIMFpm as for CTIMF in the live sires. Positive $r_g$ with carcass grades suggest increased FAT or CONF at a fixed CCWT would increase IMF in the loin, although large standard errors limit interpretation. A similar $r_g$ with CTIMFpm was found for ultrasound fat depth measured at weaning (0.49, s.e. 0.22), as was found for FAT, but no significant $r_g$ with muscle depth (-0.04, s.e. 0.27) at a fixed live weight, implying that the positive $r_g$ between CONF and CTIMFpm may be due to fat influencing CONF grades.

Table 2. Genetic parameters (with s.e.) for CTIMF or CTIMFpm and correlations with current CT traits or carcass grades

<table>
<thead>
<tr>
<th>Model adjusted for:</th>
<th>Breed</th>
<th>$V_A$</th>
<th>$h^2$</th>
<th>Genetic correlations of CTIMF(pm) with:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>CTFWT</td>
</tr>
<tr>
<td>Age</td>
<td>Texel</td>
<td>0.036</td>
<td>0.28 (0.07)</td>
<td>0.66 (0.08)</td>
</tr>
<tr>
<td></td>
<td>Suffolk</td>
<td>0.031</td>
<td>0.23 (0.09)</td>
<td>0.90 (0.10)</td>
</tr>
<tr>
<td></td>
<td>Charollais</td>
<td>0.112</td>
<td>0.88 (0.08)</td>
<td>0.89 (0.04)</td>
</tr>
<tr>
<td></td>
<td>CBA</td>
<td>0.050</td>
<td>0.38 (0.05)</td>
<td>0.79 (0.04)</td>
</tr>
<tr>
<td>Live weight</td>
<td>Texel</td>
<td>0.044</td>
<td>0.40 (0.07)</td>
<td>0.85 (0.04)</td>
</tr>
<tr>
<td></td>
<td>Suffolk</td>
<td>0.026</td>
<td>0.21 (0.08)</td>
<td>0.95 (0.06)</td>
</tr>
<tr>
<td></td>
<td>Charollais</td>
<td>0.098</td>
<td>0.87 (0.08)</td>
<td>0.96 (0.02)</td>
</tr>
<tr>
<td></td>
<td>CBA</td>
<td>0.045</td>
<td>0.40 (0.05)</td>
<td>0.82 (0.03)</td>
</tr>
<tr>
<td>CCWT</td>
<td>Suffolk x Mule</td>
<td>0.024</td>
<td>0.21 (0.09)</td>
<td>FAT</td>
</tr>
</tbody>
</table>

Conclusions and recommendations

CT scanning can predict IMF in live sires and in meat cuts. These predictions are under moderate genetic control. Genetic relationships with carcass composition traits generally suggest scope to use CT within a selection index to maintain IMF, for improved eating quality, while increasing lean and decreasing total fat, to improve carcass quality and reduce waste in commercial slaughter lambs. Marked breed differences suggest caution should be used when considering how to select for these traits across breeds.

Further work will produce sufficient data on crossbred lambs, sired by recorded, CT scanned, terminal (Texel) sires, to investigate relationships between purebred performance and the production of crossbred slaughter lambs superior for carcass and meat quality.
Acknowledgements

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List of References


