Evaluation of two muscling QTL in sheep using ultrasound (US), computer tomography (CT) and video image analysis (VIA)

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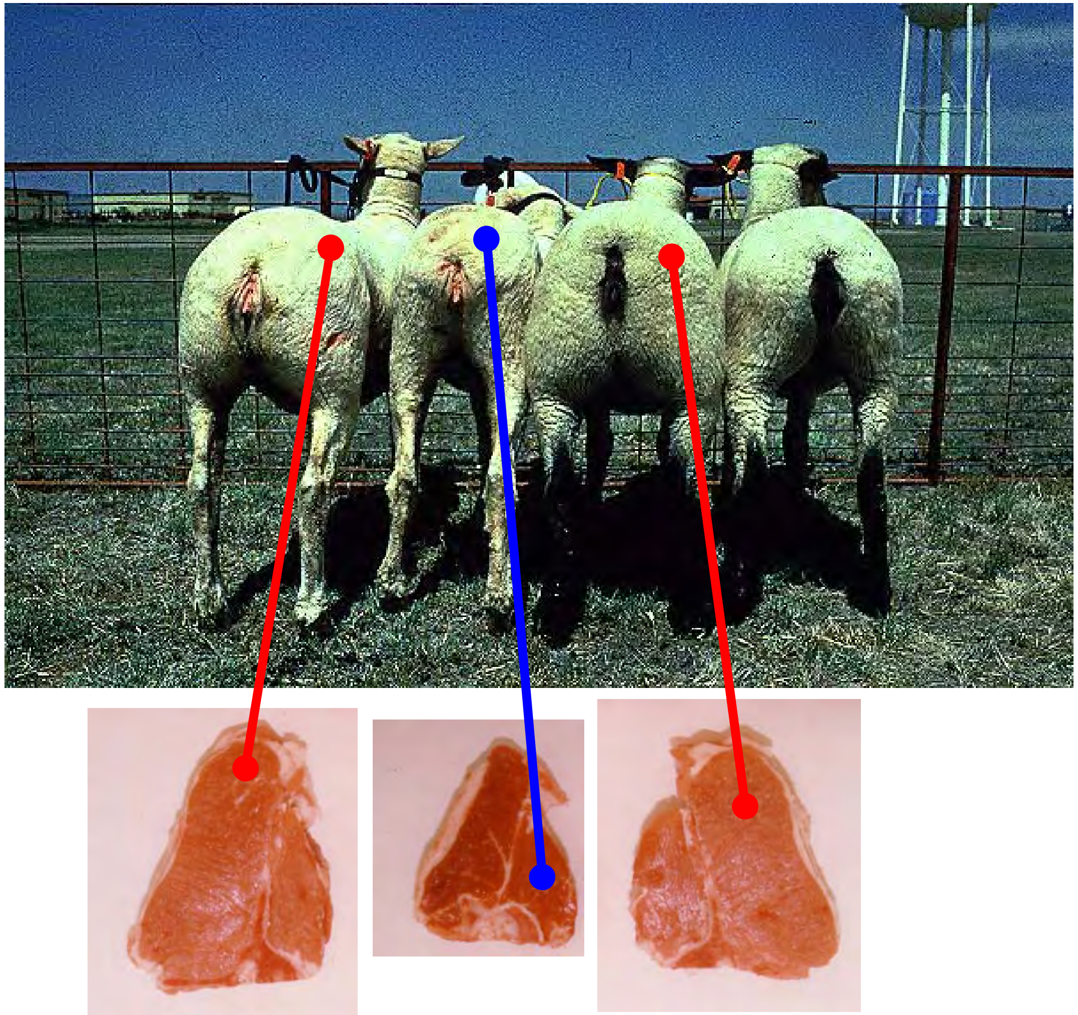
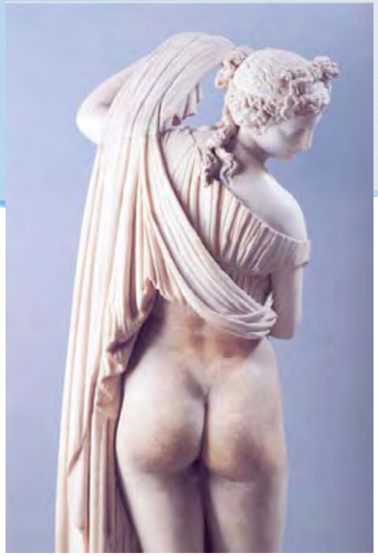
But there are lessons from Callipyge and other major genes/QTL



Photos on the left from Cockett et al. 2003
CT images from Gootwine et al. 2002



From: 'beautiful buttocks'

To: Butchers nightmare

A QTL needs to be validated and comprehensively evaluated!

Part of a complex research project

(= also the acknowledgement slide)

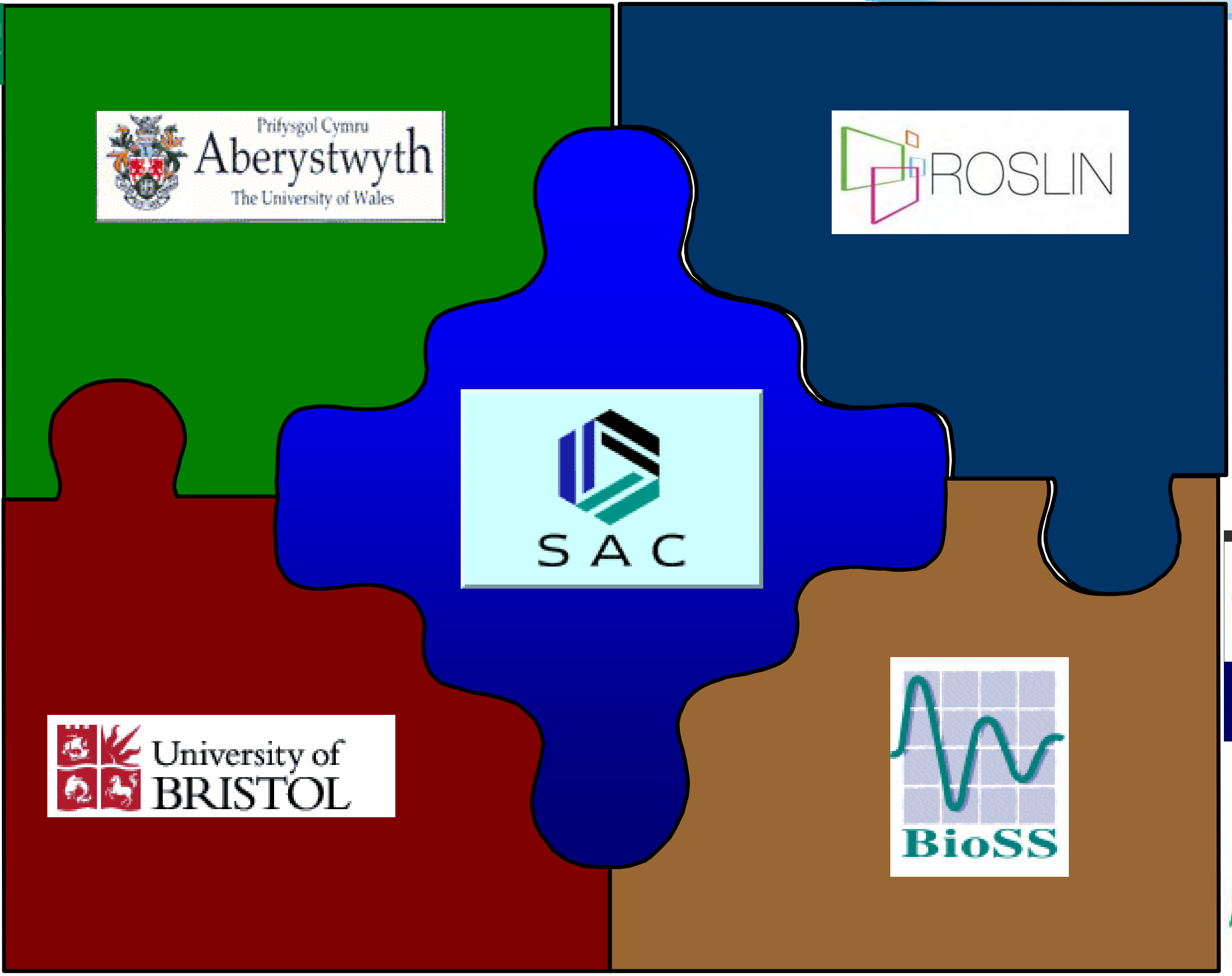
eBLEX English Beef and Lamb Executive

HYBU CIG CYMRU
MEAT PROMOTION WALES

QMS
QUALITY MEAT SCOTLAND
representing the Scottish red meat industry

TEXEL
SHEEP SOCIETY

SUFFOLK SIRE
Reference Scheme



SCOTTISH ASSOCIATION
SAMW
OF MEAT WHOLESALERS

GRAMPIAN COUNTRY FOOD GROUP
Traditional Goodness

e+v

Pfizer Pfizer Animal Health
Animal Genetics

Innovis™

ASDA

CHAROLLAIS SIRES

The Livestock & Meat Commission
for Northern Ireland

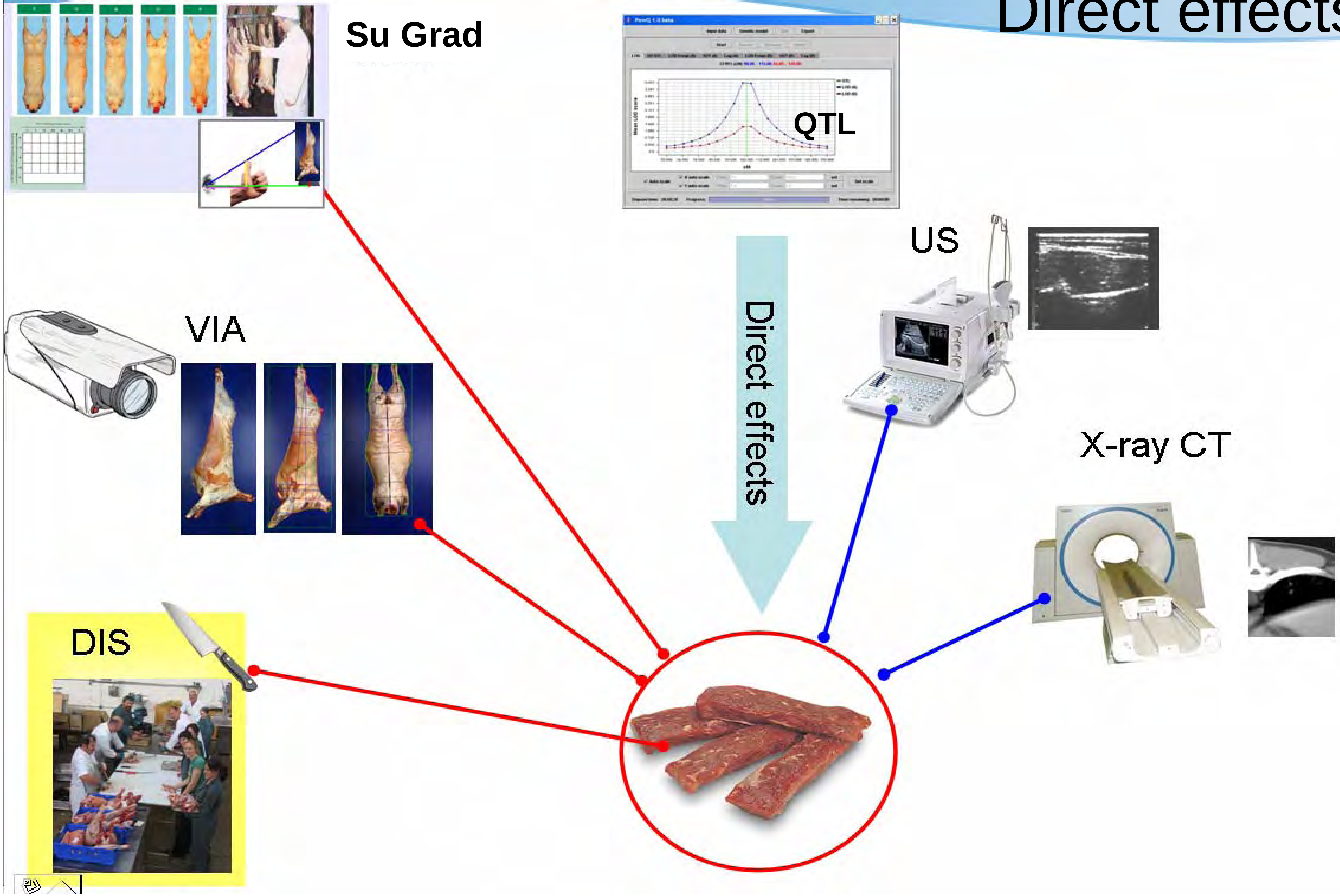
DEFRA
Department for
Environment,
Food & Rural Affairs

LINK
COLLABORATIVE RESEARCH

bbsrc
biotechnology and biological
sciences research council

Comprehensive evaluation of muscling "QTL"s

Direct effects



Su Grad

QTL

US

VIA

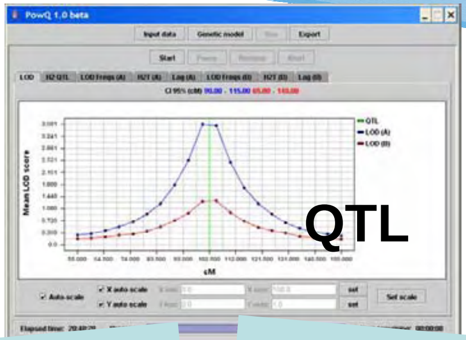
Direct effects

X-ray CT

DIS

Comprehensive evaluation of muscling “QTL”s

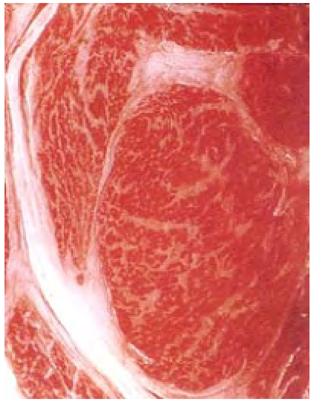
Indirect effects



QTL

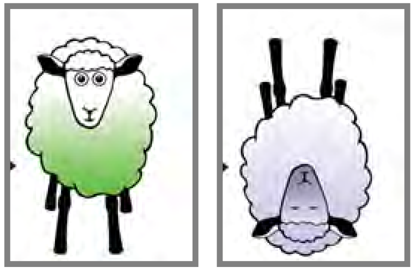
Indirect effects

Lambing ease



Intra-muscular fat

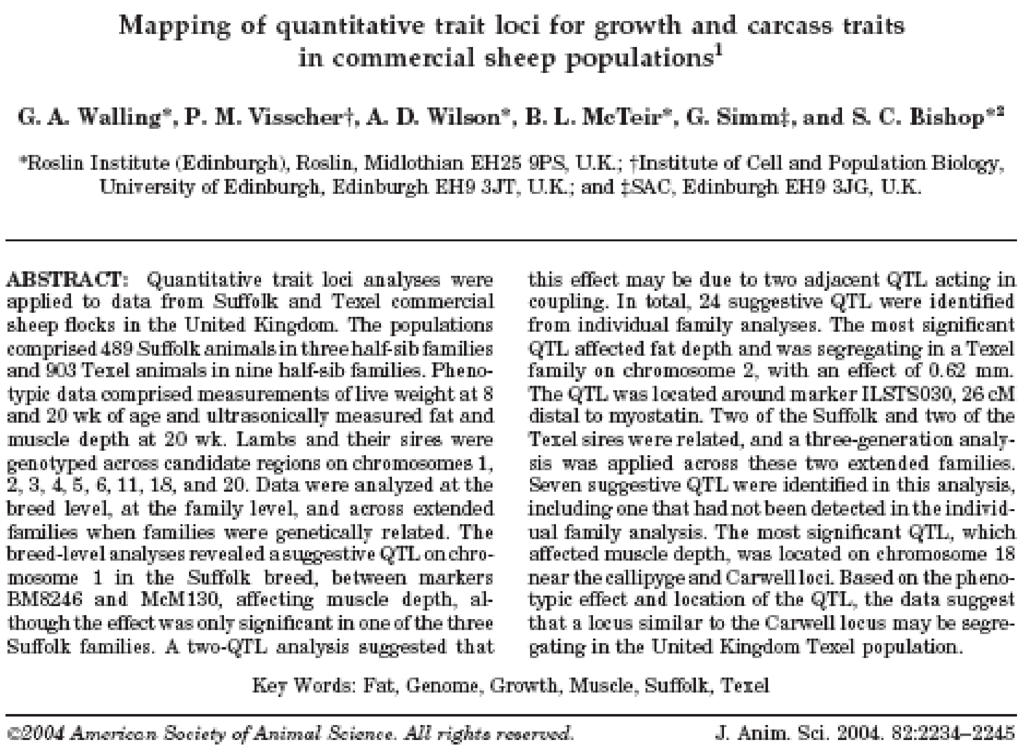
Vigour/survival



Disease resistance

Tenderness

Prior Knowledge: TM-QTL



Mapping of quantitative trait loci for growth and carcass traits in commercial sheep populations[1]

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ABSTRACT: Quantitative trait loci analyses were applied to data from Suffolk and Texel commercial sheep flocks in the United Kingdom. The populations comprised 489 Suffolk animals in three half-sib families and 903 Texel animals in nine half-sib families. Phenotypic data comprised measurements of live weight at 8 and 20 wk of age and ultrasonically measured fat and muscle depth at 20 wk. Lambs and their sires were genotyped across candidate regions on chromosomes 1, 2, 3, 4, 5, 6, 11, 18, and 20. Data were analyzed at the breed level, at the family level, and across extended families when families were genetically related. The breed-level analyses revealed a suggestive QTL on chromosome 1 in the Suffolk breed, between markers BM8246 and McM130, affecting muscle depth, although the effect was only significant in one of the three Suffolk families. A two-QTL analysis suggested that this effect may be due to two adjacent QTL acting in coupling. In total, 24 suggestive QTL were identified from individual family analyses. The most significant QTL affected fat depth and was segregating in a Texel family on chromosome 2, with an effect of 0.62 mm. The QTL was located around marker ILSTS030, 26 cM distal to myostatin. Two of the Suffolk and two of the Texel sires were related, and a three-generation analysis was applied across these two extended families. Seven suggestive QTL were identified in this analysis, including one that had not been detected in the individual family analysis. The most significant QTL, which affected muscle depth, was located on chromosome 18 near the callipyge and Carwell loci. Based on the phenotypic effect and location of the QTL, the data suggest that a locus similar to the Carwell locus may be segregating in the United Kingdom Texel population.

Key Words: Fat, Genome, Growth, Muscle, Suffolk, Texel

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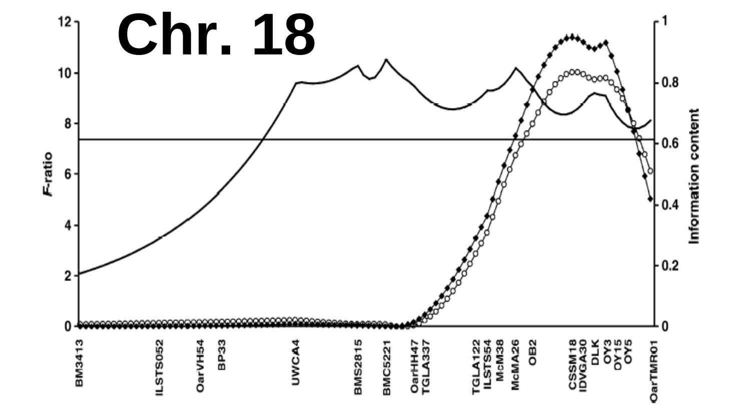


Walling,G.A., Visscher,P.M., Wilson,A.D., McTeir,B.L., Simm,G. & Bishop,S.C. (2004)

Mapping of quantitative trait loci for growth and carcass traits in commercial sheep populations

Journal of Animal Science **82**, 2234-2245

Increase of 1.2 - 2 mm in loin muscle depth in Texel lambs

Prior Knowledge:

LM-QTL

a.k.a. Carwell, REM, LoinMax^{TM}

- LM-QTL identified in Australian Poll Dorset sheep (Nicoll *et al*., 1998)
  - – on chromosome 18
  - – discrete from Callipyge locus (McLaren *et al*., 2003)
- Increases area and weight of loin muscle by 11% and 8% respectively (Poll Dorset × Romney lambs) (McEwan *et al*., 2000)
- Minor negative impact on tenderness (Jopson *et al*., 2001)

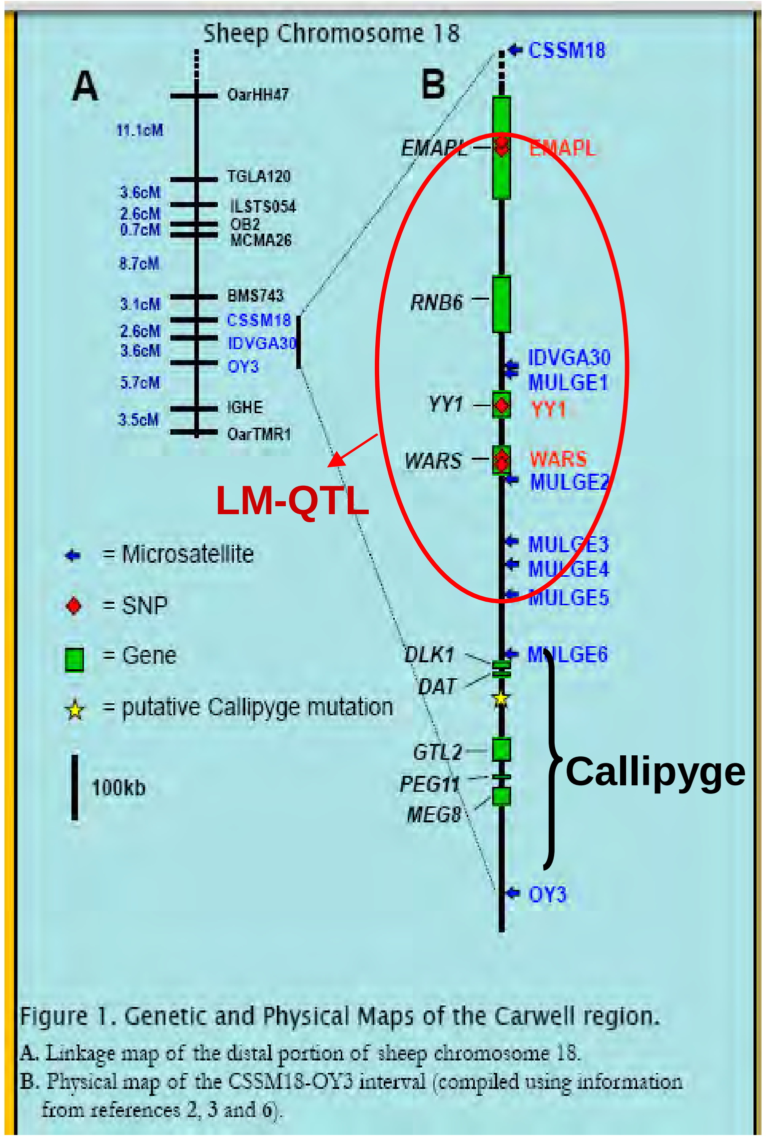
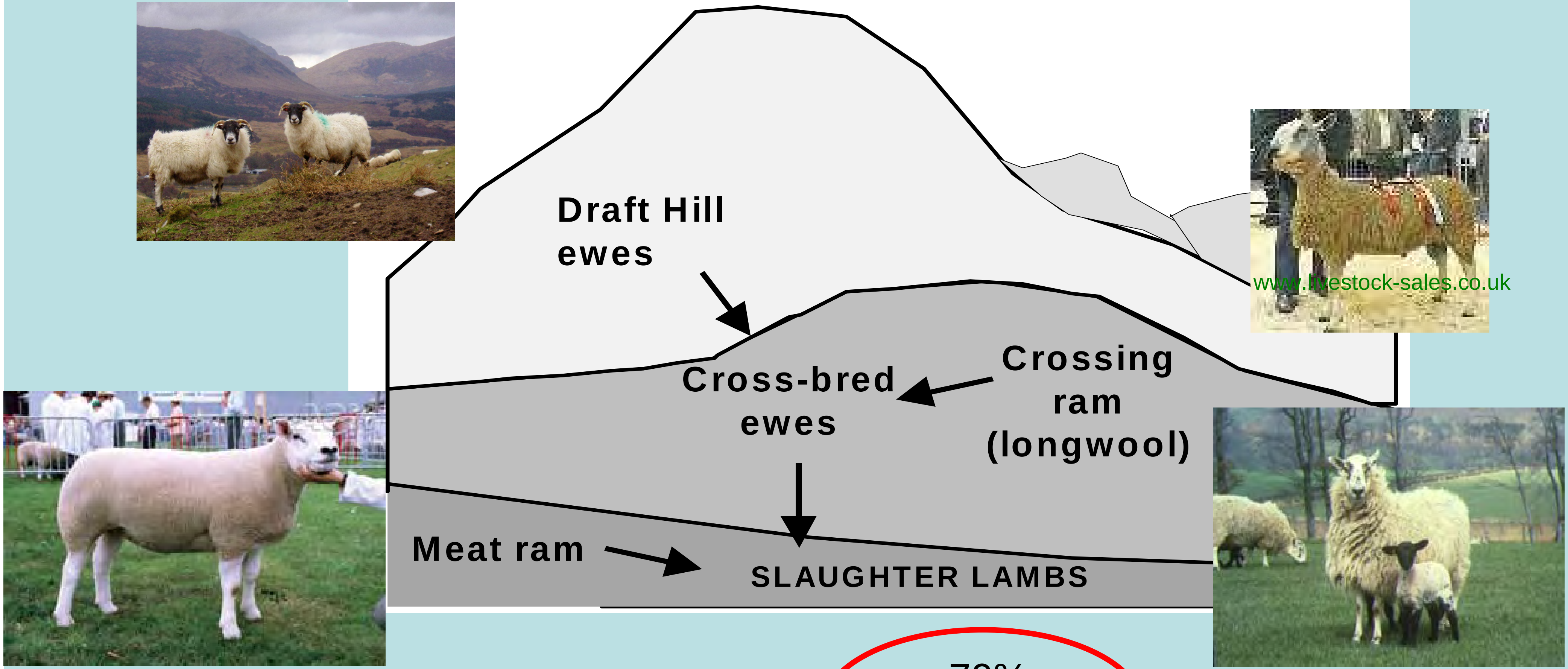


Figure 1. Genetic and Physical Maps of the Carwell region.
A. Linkage map of the distal portion of sheep chromosome 18.
B. Physical map of the CSSM18-OY3 interval (compiled using information from references 2, 3 and 6).

(McLaren *et al*., 2003)

Stratified system - UK sheep production



Draft Hill ewes

Cross-bred ewes

Crossing ram (longwool)

Meat ram

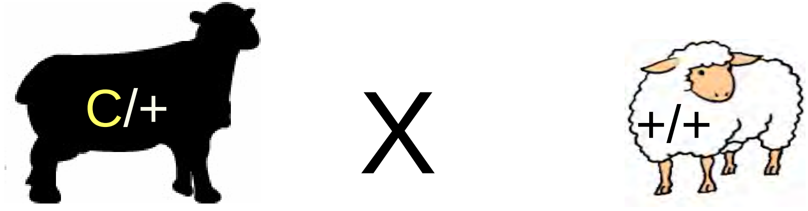
SLAUGHTER LAMBS

www.livestock-sales.co.uk

~70%
of all slaughter
lambs

Material and methods

TM-QTL

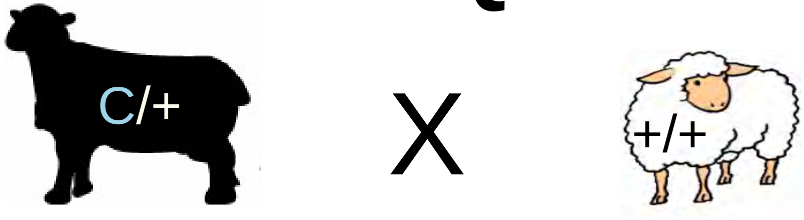


TEXEL **MULE**

C/+	+/+
62	49

Method	16 weeks	20 weeks
US		X
CT		X
Su grad		X
VIA		X
DIS		X

LM-QTL



POLL DORSET **MULE**

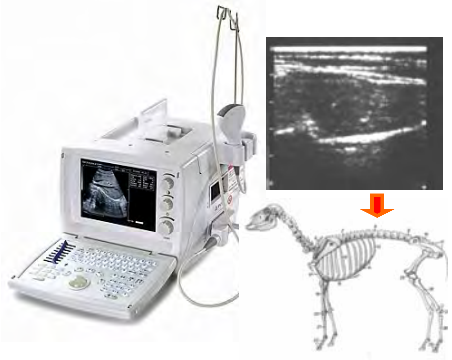
C/+	+/+
73	94

Method	16 weeks	20 weeks
US		X
CT	X!	
Su grad		X
VIA		X
DIS		

Results: ultrasound

TM-QTL

C/+	+/+
62	49



LM-QTL

C/+	+/+
73	94

trait	**C/+**	**+/+**	**Diff(%)**
UFD (mm)	**4.21**	**4.11**	**-2.5**
UMD (mm)	**23.4**	**24.4**	**4.5 ***

trait	**C/+**	**+/+**	**Diff (%)**
UFD (mm)	**3.27**	**3.31**	**-1.3**
UMD (mm)	**25.2**	**24.2**	**3.7 ***

UFD = ultrasound fat depth
UMD = ultrasound muscle depth

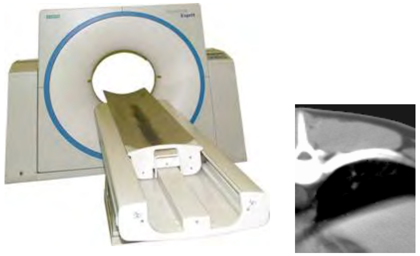
Results: CT (MLL =loin)

TM-QTL

C/+	+/+
62	49

LM-QTL

C/+	+/+
73	94



20 weeks

trait	C/+	+/+	Diff (%)
MLL_A (cm^2)	**19.6**	**18.7**	**5.1 ***
MLL_W (mm)	**73.2**	**71.0**	**3.0 ***
MLL_D (mm)	**30.8**	**28.9**	**6.7 ***

16 weeks

trait	C/+	+/+	Diff (%)
MLL_A (cm^2)	**16.77**	**16.04**	**4.5 ***
MLL_W (mm)	**70.4**	**69.4**	**1.4 ***
MLL_D (mm)	**27.4**	**26.5**	**3.4 ***

MLL_A = loin muscle area; MLL_W = loin muscle width; MLL_D = loin muscle depth

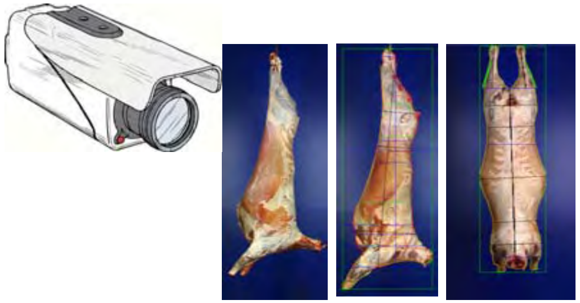
Results: VIA

TM-QTL

C/+	+/+
62	49

LM-QTL

C/+	+/+
73	94



trait	C/+	+/+	Diff (%)
P_loin (kg)	3.45	3.47	-0.6
P_chump (kg)	1.52	1.52	0
P_leg (kg)	5.19	5.18	0.2
P_breast (kg)	1.69	1.67	1.2
P_shoulder (kg)	6.64	6.65	-0.2

Trait	C/+	+/+	Diff (%)
TP_loin (kg)	1.426	1.395	2.2 *
TP_chump (kg)	0.809	0.813	-0.5
TP_leg (kg)	3.282	3.272	0.3
TP_breast (kg)	1.502	1.520	-1.2
TP_shoulder	3.79	3.81	-0.5

P, TP = weight of (trimmed) primal cut, predicted using VIA

Results: dissection

TM-QTL

C/+	+/+
62	49

LM-QTL

C/+	+/+
73	94

Trait	C/+	+/+	Diff (%)
MLL wt (kg)	0.526	0.492	7.1 *
chump (kg)	0.751	0.773	-2.9
leg - chump (kg)	2.381	2.407	-1.1
breast (kg)	0.857	0.878	-2.4
shoulder (kg)	3.326	3.330	-0.1

Trait	C/+	+/+	Diff (%)
MLL wt (kg)			
chump (kg)			
leg - chump (kg)			
breast (kg)			
shoulder (kg)			

No dissection

MLL wt = loin muscle weight

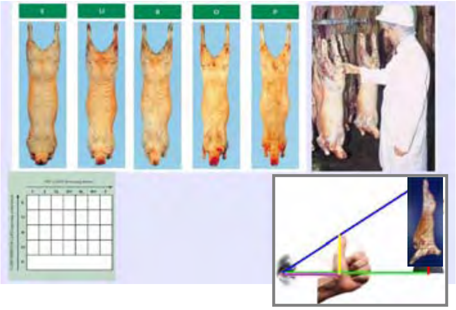
Results: Carcass traits

TM-QTL

C/+	+/+
62	49

LM-QTL

C/+	+/+
73	94



Trait	C/+	+/+	Diff (%)
CCW (kg)	17.60	17.47	0.8
CONF	2.45	2.53	-3.2
FAT	10.83	10.65	1.7

Trait	C/+	+/+	Diff (%)
CCW (kg)	18.77	19.25	-2.6
CONF	3.06	2.97	2.9
FAT	10.57	11.03	-1.7

CCW = cold carcass weight
CONF = conformation grade on numeric scale
FAT = fat grade converted to estimated subcutaneous fat %

Conclusions (**TM-QTL** & **LM-QTL**) (1)

- **TM-QTL** and LM-QTL cause significantly greater muscling in the loin region
- No evidence that either QTL affects other carcass traits
- Both QTL are located on chromosome 18 and have very similar phenotypic effects
- The phenotypic effect of the **TM-QTL** was not detected by the current carcass grading system, nor by the VIA-system
- The phenotypic effect of the **LM-QTL** was not detected by the current carcass grading system, but the VIA-system detected loin differences

Conclusions (TM-QTL & LM-QTL) (2)

- **TM-QTL** and LM-QTL could potentially provide the sheep industry with a method to increase carcass value through increased weight in the loin, a high value region.
- Still to be considered - the effects of TM-QTL on meat quality and animal health and welfare traits (also for the **LM-QTL**). The mode of inheritance is not fully understood.
- Further studies of the **TM-QTL** are underway in purebred lambs with all 3 genotypes.