GENETICS OF SEAM FAT IN CATTLE

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INTRODUCTION

As far as most consumers are concerned, a good steak is a steak with visibly desirable colour (doneness), a large portion of muscle and a small amount of fat, especially the seam fat located between the muscles. During the intensive growth to commercial slaughter weights in feedlots, there is a distinct change in the composition of the body with the amount of fat increasing and the musculature remaining reasonably constant (Pitchford and Bottema, 2000). Cattle breeds deposit fat at different rates and in different locations (subcutaneous, intermuscular or intramuscular). For example, early maturing Jersey cattle deposit more fat intramuscularly than late maturing Limousin cattle (Pitchford and Bottema, 2000). These differences suggest that there is a genetic basis for fat distribution. The aim of this study was to investigate the genetic variation in seam fat distribution within loin muscles of Jersey and Limousin cross cattle, independent from carcass size and fatness.

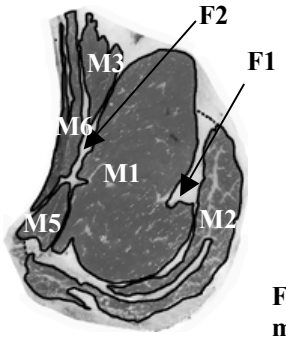
MATERIALS AND METHODS

Animals and management. The animals used in this study were part of the Davies Cattle Gene Mapping Herd, ¾ Jersey (XJ) and ¾ Limousin (XL) (Kruk *et al.*, 1997). They were born between April/May, 1997. The animals comprised 50 XJ and 31 XL steers, progeny of pure Jersey and Limousin dams crossed to the three F1 (Jersey/Limousin) sires (# 361, 368, 398). The steers were raised on pastures under the same management conditions, weaned at 250 days of age, fed a grain based ration for 170 days and then slaughtered.

Slaughter, measurements and data collection. All steers were slaughtered and after standard processing, the carcasses were stored in the chiller (0-4°C). Approximately 18 hours later, carcasses were quartered between 10^{th}-11^{th} rib and chiller assessment was performed by accredited AUS-MEAT and MSA graders. Parameters such as meat colour, fat colour, eye muscle area, loin temperature, ossification, pH and marbling score were assessed. Additionally, photographs of each eye muscle area cross-section were taken using a Pentax P30N camera. Every image contained a small ruler used for calibration.

Image processing and analysis. After the photographs were developed, a computer program (PV32) was used to measure the total (steak) area as trimmed according to retailer specifications (3-5 mm of fat). Also various muscle areas and fat depots between the muscles were measured. Each image was individually calibrated and the area of interest assessed manually. The following areas of the image were calculated: *M. longissimus dorsi (M1), M. spinalis dorsi (M2), M. longissimus costarum (M3), M. trapezius thoracis (M4*-not present on the diagram*), M. multifidi dorsi (M5), Mm. intercostals externus and internus (M6),* fat area F1

(between M1, M2, M5), fat area F2 (between M1, M3, M5, M6), and fat area F3 which was the remaining fat in the image (Figure 1).



TSA – total steak area (trimmed to 4 mm of fat)
M1÷M6 – muscle areas as describe in the text
F1, F2, F3 - fat areas as described in the text
TMA – total muscle area = Sum (M1÷M6)
TFA – total fat area = Sum (F1÷F3)
All areas expressed in cm^2
All symbols followed by "%" are expressed as percentage of TSA

Figure 1. Diagrammatic representation and description of areas measured

Statistical analyses. The measurement of areas was expressed in square centimeters (cm^2) as well as a percentage of the total steak area. Least squares analysis of variance was carried out using Proc GLM (SAS 1989). The model for analysis of percentage areas (Model 1) included fixed effects of breed, sire and the interactions between breed and sire. To test that the fat areas expressed in cm^2 were purely due to the fat distribution and not due to the total fatness or animal size, another model (Model 2) was utilized that included hot standard carcass weight (HSCW) and rump (P8) fat depth fitted as covariates as well as breed, sire and their interaction. Breed by sire interactions were not significant for all traits and removed from the models. Residual correlations between variables were computed using Proc CORR (SAS, 1989).

RESULTS

Breed effect on fatness and muscularity. As expected, Jersey and Limousin cross cattle differed significantly in most of the fat and musculature areas. Carcasses of Limousin crosses were 28% heavier, had 7% more muscle in trimmed steak area and the steaks from this breed were 19% larger (Table 1). *M. longissimus dorsi* (M1) and *M. spinalis dorsi* (M2) had the largest influence on total muscle area (42-48% of TMA and 14-15% of TMA, respectively). The variation in musculature traits was low and for total steak area (TSA), hot standard carcass weight (HSCW) and total percentage of muscle within steaks (TMA%) was 11, 10 and 6, respectively. The variation for M1% was also low (8%). The highest variation of musculature was observed with the area of M2% (16%). There was a breed by muscle interaction with Limousin having larger M1 (48.0 vs 42.3%) and Jersey having larger M2 (15.7 vs. 14.4%).

More variation was observed with fatness traits. P8 fat depth had a CV of 31% and there was no difference between Jersey and Limousin crosses. A similar amount of variation was observed with F2 and F3 (39% and 35%, respectively) with Jersey crosses having significantly more F3%. F1% and total fat percentage (TFA%) had less variation (23% and 19%, respectively). These two areas were significantly different between the breeds. Limousin cattle had significantly higher values for the majority of musculature traits, while Jersey crosses were higher in almost all fatness traits.

Sire effect on size, fatness and muscularity. Sire influence was evident only in some fatness traits. A significant difference was observed for P8 fat, F1% and F2%. The progeny of sire 361 had the thickest subcutaneous fat layer (9.7 mm) and the largest proportion of fat in areas F1 and F2 (7.5% and 5.8%, respectively). The progeny of the remaining two sires did not differ except in F1% where the sire 398 had significantly less fat than sires 361 and 368 (Table 1).

Table 1. Least square means for carcass traits and meat and fat distribution

Trait	XJ	XL	Sire 361	Sire 368	Sire 398
HSCW (kg)	310.9±4.8^{B}	399.7±6.2^{A}	362.2±6.3	353.1±6.2	350.6±7.6
P8 fat (mm)	8.4±0.4	8.7±0.5	9.7±0.5^{A}	7.8±0.5^{B}	8.1±0.6^{B}
TSA (cm^2)	166.1±2.7^{B}	197.7±3.5^{A}	181.0±3.6	182.6±3.5	182.1±4.3
M1%	42.3±0.5^{B}	48.0±0.7^{A}	44.8±0.7	46.9±0.7	45.3±0.8
M2%	15.7±0.3^{A}	14.4±0.5^{B}	15.4±0.5	14.3±0.4	15.5±0.5
TMA%	74.9±0.6^{B}	80.4±0.8^{A}	76.6±0.8	77.6±0.8	78.7±1.0
F1%	7.2±0.2^{A}	5.6±0.3^{B}	7.5±0.3^{A}	6.6±0.3^{B}	5.2±0.4^{C}
F2%	5.2±0.3	4.7±0.4	5.8±0.4^{A}	4.6±0.4^{B}	4.6±0.4^{B}
F3%	12.7±0.6^{A}	9.3±0.7^{B}	10.1±0.7	11.2±0.7	11.6±0.9
TFA%	25.1±0.6^{A}	19.6±0.8^{B}	23.4±0.8	22.4±0.8	21.3±1.0

$^{A-C}$ within rows means of the same class followed by the same letter are not significantly different (P>0.05)

Table 2. Correlations between musculature and fatness traits

	TSA	M1	M2	TMA	F1	F2	F3	TFA
TSA		0.77	0.49	0.85	0.24	0.06	0.26	0.32
M1	***		0.25	0.91	-0.01	-0.20	-0.15	-0.21
M2	***	*		0.56	0.14	0.12	-0.21	-0.08
TMA	***	***	***		0.0	-0.15	-0.19	-0.22
F1	*	ns	ns	ns		0.23	0.05	0.45
F2	ns	ns	ns	ns	*		0.09	0.39
F3	*	ns	ns	ns	ns	ns		0.83
TFA	**	ns	ns	*	***	***	***	

ns = not significant (P>0.05), *** = P<0.001, ** = P<0.01, * = P<0.05

Fatness and muscularity based on the statistical model 2. Model 2 was designed to test the significance of measured steak areas (expressed in cm^2) which would not be affected by animal size (HSCW) or fatness (P8). With HSCW and P8 fat as covariates, all breed differences in musculature traits were no longer statistically significant except the size of M1 (data not presented). In terms of fatness, however, TFA and F1 were influenced by breed and sire as in model 1. Although F2% was affected by sire in the model 1, its counterpart F2 (area) was less significant in the model 2 (P=0.08). F3%, previously affected by breed in model 1, was not significant when expressed as area (F3).

Correlations between fatness and muscularity. The total area of steak was highly correlated with total muscle area, as well as with the area of the two major muscles, M1 and M2 (Table 2). The correlations between musculature and fat areas were low and not significant. Between

different fat areas, there was a moderate correlation between F1 and F2. Total fat area was highly correlated with F3 and moderately correlated with F2 and F1. Total fat was also correlated with total meat area and the correlation was negative. The total area of steaks was highly associated with total meat area and moderately with total fat area.

DISCUSSION

A proverb "size does not matter" may not apply to the size of a steak on a consumer's plate as larger steaks are always more appreciated if purchased for a reasonable price. The size of a steak and its composition (muscle and fat content and distribution) can be influenced by the breed of cattle, size of the animal and feeding regime (Ewers *et al*., 1999). This was evident in the Jersey and Limousin crossbred steers, which differed significantly in body size and consequently, had larger steak areas. When HSCW and P8 fat were fitted as covariates, the breed effect was no longer significant, demonstrating that all variation related to the steak area was due to the carcass size.

However, the composition of steaks (muscling) was breed specific and, even after accounting for carcass size and fatness, was still significant. Thus, there could be breed specificity in the shape and size of muscles at a particular point of quartering. Rutley *et al*. (2002) did not find breed differences in the size of eye muscle between different quartering sites. However, other muscles were not measured in that study and these greatly contribute to the total steak area and possess a larger variation. Moreover, total steak area is more correlated with total muscle area than with M1 alone.

Fat distribution within steaks was also breed dependent and remained so in most cases, even when P8 fat was fitted as the covariate. The breed influence on total fat percentage and F1 was highly significant. F1 is important from a retailer perspective because if F1 and M2 are trimmed, then ~20% of the total steak area is lost. The F1 and F2 as well as P8 fat depth differed between sires. Sire 361 produced fatter progeny with more fat deposited within steaks. These results clearly demonstrate that fat deposition within the muscles of loin in cattle has a genetic basis.

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