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Post-weaning growth, ultrasound and skeletal measurements, muscularity scores and carcass traits and composition of progeny of five beef suckler cow genotypes

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Post-weaning growth, ultrasound and skeletal measurements, muscularity scores, and carcass traits and composition of the progeny of spring-calving Limousin (L), Charolais (C), Limousin × Holstein-Friesian (LF), Limousin × (Limousin × Holstein-Friesian) (LLF) and Simmental × (Limousin × Holstein-Friesian) (SLF) cow genotypes was determined over 3 years. Bull and heifer progeny were slaughtered at ~460 and ~610 days of age, respectively. Post-weaning growth did not differ significantly between the genotypes. Progeny from LF and SLF cows had the highest ($P < 0.001$) carcass gain per day of age, whereas progeny from L and C cows had the highest ($P < 0.01$) carcass conformation score and lowest ($P < 0.001$) fat score. The proportion of meat in the carcass was higher ($P < 0.001$) and bone lower ($P < 0.001$), and meat to bone ratio higher ($P < 0.001$) for the progeny of L cows than all other genotypes, which were similar. Carcass fat proportion was similar for progeny of L and C cows and lower ($P < 0.001$) than LLF and SLF, with LF being intermediate. The progeny from L cows tended to have the greatest proportion of hind-quarter in the carcass. Genotype effects were minimal when the proportion of high-value cuts was expressed relative to weight of meat in the carcass and hind-quarter. In conclusion, there was no effect of cow genotype on the performance of their progeny from weaning to slaughter. However, crossbred cows with good maternal (milk) traits produced progeny with a higher carcass weight per day of age, whereas the purebred continental cows produced progeny with superior carcass classification traits.

Keywords: carcass; genotype; growth; suckler cow

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Introduction

The proportion of Irish beef exports going to the higher-priced markets of the European Union, where the quality specifications require lean carcasses of good conformation, has increased dramatically from about 0.20 in 2001 to 0.43 in 2007 (Drennan, 2006; Bord Bia, 2007). High growth rate and efficient production of carcasses (or animals) suitable for the highest-priced markets are two important aims of suckler beef enterprises. Breed is one of the main determinants of growth rate, conformation score and carcass composition (Kempster, Cuthbertson and Harrington, 1982; Keane, 1993a and 1993b; Robelin and Tulloh, 1992).

Beef suckler cow numbers almost trebled in Ireland during the past 25 years and they now comprise approximately half of the national cow population of 2.2 m (CSO, 2006). Traditionally the heifers selected as replacement breeding stock for the national suckler cow herd were mainly the product of crosses of early-maturing British beef-breed bulls on Friesian dairy cows. The benefits of suckler cow replacements from the dairy herd having late-maturing "continental" breed than early-maturing British-beef breed ancestry was demonstrated in a comparison of Limousin \times Friesian and Hereford \times Friesian cows in a calf-to-beef production system (Drennan and McGee, 2004). Progressively, bulls of later-maturing "continental" breeds have predominated and 85% of beef suckler cows are now bred to such sires (CMMS, 2006). The increased size of the national herd of beef cows relative to the dairy cow herd has meant that proportionately fewer of the replacement breeding heifers in beef herds now come from the dairy herd. This process has been accelerated by the dominance of Holstein ancestry within the national dairy herd, since the progeny of these cows produce

carcasses of lower beef value (McGee *et al.*, 2005c; Drennan, 2006).

A breeding policy based on selecting replacement heifers from within the beef herd will inevitably result in the genotype of many beef cows being composed almost exclusively of continental beef breeds and in some cases, of a single breed. The reduced proportion of dairy genes in the suckler cow would result in decreased milk production and, therefore, a lower calf weaning weight (McGee, Drennan and Caffrey, 2005b). However, the increased proportion of continental breeding would lead to a major increase in meat yield (Drennan, McGee and Keane, 2005). There is limited information on the relative performance of the progeny produced by these recently produced cow genotypes under Irish conditions.

The objectives of this study were to determine the effect of cow genotype on post-weaning growth, ultrasound and skeletal measurements, muscularity scores, carcass traits and composition of their progeny. Data pertaining to cow performance, feed intake, milk yield and calf pre-weaning growth are presented by Murphy *et al.* (2008).

Materials and Methods

Suckler cow herd management

The details of the cow breeding and management were described by Murphy *et al.* (2008). Briefly, a spring-calving suckler herd was used in this 3 year study. The five cow genotypes examined were Limousin (L), Charolais (C), Limousin \times Holstein-Friesian (LF), Limousin \times (Limousin \times Holstein-Friesian) (LLF) and Simmental \times (Limousin \times Holstein-Friesian) (SLF). In Year 1 the herd comprised of first parity cows only, while in year 2 first parity animals were present for all cow genotypes except C. In year 3 first parity cows were

present for the crossbred genotypes only. One easy-calving Limousin sire was used on all first parity animals and they were bred by artificial insemination (AI) to calve at 2 years of age. Two Charolais sires (AI) of similar growth merit, one of high and one of average conformation, were used on the mature cows in years 2 and 3. Mature cows were offered grass silage only during the indoor winter period, whereas first parity animals received an additional 1.5 kg of concentrates from parturition until turnout to grass at the start of the grazing season. Mean birth date was 31 March and the progeny spent from April at pasture with their dams until weaning in October/November on both Semi-intensive and Extensive grassland management systems.

Male progeny management

The male progeny were left intact in all 3 years. They were housed post-weaning (at 238, 210 and 212 days of age in years 1, 2 and 3, respectively) in a slatted-floor shed for the duration of the finishing period (217, 254, 239 days in years 1, 2 and 3, respectively). They were offered a diet of grass silage *ad libitum* and supplementary concentrates. The concentrate offered was barley-based and mean daily allowances during the finishing period were 4.0, 4.5 and 5.5 kg per head in years 1, 2 and 3, respectively. In years 1 and 2 the silage and concentrates were fed separately. In year 3 the silage and concentrates were fed separately for the first 61 days and subsequently as a total mixed ration (2:1 silage to concentrate ratio). The chemical composition and nutritive value of the feeds offered are given in Table 1. In Year 1 the male progeny were penned by cow genotype in groups of 5 or 6. In Year 2 the bulls were tied-up at random during the final 105 days prior to slaughter in order to measure individual silage intake. In

year 3 the progeny were grouped by cow genotype in pens of 3.

Female progeny management

The heifer progeny were housed post-weaning as per males. They were offered grass silage *ad libitum* plus 1 kg per head daily of barley-based concentrate until turnout to pasture (15 April 2002, 4 April 2003, and 1 April 2004 in years 1, 2 and 3, respectively). The genotypes remained within the grassland management system allocated pre-weaning. The duration at pasture was 192, 214 and 205 days in years 1, 2 and 3, respectively, following which they were accommodated on wood chip out-wintering pads in years 1 (for 36 days) and 2 (for 27 days), and in a slatted-floor shed in year 3 (for 47 days). During this final finishing period they were offered grass silage *ad libitum* and a barley-based concentrate, which was initially offered at pasture. The average daily intake of concentrate during the finishing period was 3.3 (84 days), 3.5 (111 days) and 4.0 (96 days) kg per head in years 1, 2 and 3, respectively. The composition and nutritive value of the feeds offered are given in Table 1.

Feed intake and efficiency

In years 2 and 3 the grass silage offered was weighed on 3 or 4 consecutive days per week for 54 and 42 days, respectively. Feed refusals were weighed daily and discarded at least once weekly. Silage (year 2) or total diet (year 3) was offered to at least 0.1 (proportionately) in excess of intake. Representative samples of the grass silage and juice extracts, and concentrates were obtained. Sample storage, dry matter determination chemical analyses (pH, ammonia-N, crude protein and ash) and *in vitro* dry matter digestibility were carried out using methods described by McGee, Drennan and Caffrey (2005a).

Table 1. Chemical composition, *in vitro* dry matter (DM) digestibility and estimated net energy value of grass silage, mixed diet and concentrates offered to progeny during the finishing period in years 1, 2 and 3

Year	Gender ¹	Dry matter (g/kg)	pH	NH ₃ -N (µg/mL)	Crude protein (g/ kg DM)	Ash (g/kg DM)	<i>In vitro</i> DMD (g/kg)	Net energy ² (UFV(I)/ kg DM)
<i>Grass silage</i>								
1	Bulls	197	3.7	–	144	83	774	0.84
1	Heifers	163	3.8	–	155	92	713	0.76
2	Bulls	169	4.0	630	143	87	680	0.71
2	Heifers	159	3.8	–	142	82	743	0.80
3	Bulls	194	3.8	610	135	92	667	0.70
3	Heifers	158	3.9	–	–	89	697	0.74
<i>Mixed diet</i>								
3	Bulls	371	–	–	132	86	703	0.74
<i>Concentrates</i>								
1	Bulls & heifers	842	–	–	127	38	879	1.13
2	Bulls & heifers	855	–	–	128	39	882	1.13
3	Bulls & heifers	861	–	–	121	39	863	1.13

¹Weaning heifers were offered the same silage as bulls each year.

²UFV(I) (Unité Fourragère Viande – Feed Unit for meat calculated by reference to O'Mara (1996)).

The live weight used to express intake relative to live weight was the mean of weights recorded at the start and end of the recording period. Net energy intake, expressed in Unité Fourragère Viande (UFV(I); Feed Unit for meat), was calculated by reference to O'Mara (1996).

Live weight, ultrasound and skeletal measurements, and visual muscularity scores

Live weight was recorded at birth, turnout to pasture, weaning, pre-slaughter and intermittently throughout the study. *In vivo* measurements of *m. longissimus dorsi* muscle depth, and area and fat depth were determined prior to slaughter in Years 2 and 3 using ultrasound scanning equipment (Aloka 500 v ultrasound unit (Animal Ultrasound Services Inc., Ithaca, New York, USA) or Dynamic Imaging Concept MLV unit (Dynamic Imaging Ltd., Livingston, Scotland)) equipped with a 12.5 cm long 3.5 MHz linear assay transducer probe. Muscle area was measured on stored images using the Auskey

software package (Animal Ultrasound Services, Inc., Ithaca, New York, USA). Fat depth, and muscle depth and area were determined at both the 13th rib and at the 3rd lumbar vertebrae. The mean of measured fat depths at points that were approximately 0.2, 0.4, 0.6 and 0.8 (proportionately) across the width of the muscle at the 13th rib and at points that were 0.25, 0.50 and 0.75 (proportionately) across the width of the muscle at the 3rd lumbar vertebrae were used to give a fat depth for each location, whereas muscle depth consisted of one reading at the deepest point of the muscle. Skeletal measurements were obtained pre-slaughter in Years 1 and 2. Animals were measured at 11 positions, namely, height at withers, height at pelvis, chest circumference, chest depth, chest width, pelvic length, pelvic width, hip width, hind-quarter length and back length (× 2) as described by Doorley (2001).

A visual muscular score (mean of the roundness of the hind-quarter, width of hind-quarter and width/depth of loin on

a scale of 1 to 15) using the Signet system (Collins, personal communication) was assigned to all animals pre-slaughter in Years 1, 2 and 3 by two trained operators on each occasion. Additionally, animals were scored for muscularity on a 1 to 15 point scale pre-slaughter, using the Irish Cattle Breeding Federation (ICBF) scoring system (ICBF, 2002), by a trained operator.

Carcass classification score, measurements and dissection

Following slaughter at a commercial abattoir, perinephric plus retroperitoneal fat was weighed. Hot carcass weight was recorded from which cold carcass weight was calculated (hot carcass weight \times 0.98). The carcasses were scored using the EU carcass classification system (Commission of the European Communities, 1982) for conformation (E, U, R, O, P (worst)) and fat (1 to 5 (fattest)). The five scores for both conformation and fat were subdivided into 3 categories, giving a 15 point scale for each. Carcass measurements were carried out as per de Boer *et al.* (1974) in years 1 and 3. These included carcass length, carcass depth, leg length, round width, round circumference and leg width.

In Year 1 the entire carcass was dissected into meat, fat and bone using commercial procedures. The two sides of each carcass were quartered into the hind- and fore-quarters between the 12th and 13th rib, and 10th and 11th rib for the bull and heifer progeny, respectively. There were seven retail cuts in the hind-quarter (silverside, topside, striploin, rump, knuckle, fillet and flank steak) and six in the forequarter (chuck, cube roll, brisket, clod, shoulder blade and flat rib). The weight of each meat cut (from which bone and dissectible fat had been removed, except for the cube roll where bone remained, and the cube roll and striploin where a standard level

of fat cover remained) was recorded individually. The weight of fat and bone from each meat cut was combined for the hind-quarter and the fore-quarter separately. The total weight of meat was equal to the sum of meat cuts and lean trim weight.

To obtain subcutaneous fat depth and *m. longissimus* area the carcass was cut between the 12th and 13th rib for all progeny in Year 2 and for the bull progeny in Year 3, and between the 10th and 11th rib for the heifer progeny in Year 3. In Years 2 and 3, an eight rib Italian pistola (no flank) from the right side of each carcass was dissected. The pistola was dissected into eleven meat-only retail cuts (topside, silverside, knuckle, rump, cube roll, striploin, fillet, heel, shin, cap of rib and tail of rump) and the procedure adopted was as outlined for year 1.

Statistical analysis

Preliminary analyses showed that there was no significant effect of grassland production system (Semi-intensive and Extensive) for the traits examined and so this factor was omitted from subsequent analysis. For male and female data combined over years, analysis of variance was carried out using the MIXED procedure of SAS (SAS, 2001) with repeated measures. The fixed effects in the model, were cow genotype, parity, year, sire within parity and gender. The interaction terms included were cow genotype \times parity and gender \times year. Individual animal within genotype was included as a random variable. Data for year 1 only were subjected to analysis of variance using the GLM procedure of the SAS (SAS Institute, Inc., 2001). The fixed effects in the model were cow genotype and gender. The cow genotype \times gender interaction term was not significant for any variable and so was not included in the final model. Data

pertaining to intake for the bull progeny were analysed for each year separately, using Proc MIXED with fixed effects in the model for cow genotype and week and the interaction term of cow genotype \times week. Individual animal was included as a random variable in Year 2 and pen as a random variable in Year 3. Birth day was included as a covariate in all models. The Tukey-Kramer multiple range test within SAS was used to compare least squares means.

Results

Feed intake and feed efficiency

In year 2 net energy intake was higher ($P < 0.01$) for the progeny of SLF and LLF cows than L cows, with C and LF being intermediate (Table 2). In year 3, there were no significant effects of genotype on net energy intake. Net energy intake expressed relative to live weight, and feed

conversion ratio did not differ between the genotypes in either year.

Growth, slaughter traits and carcass classification scores

There was no effect ($P > 0.05$) of genotype on daily gain from weaning to slaughter (Table 3). Daily gain from birth to slaughter was higher ($P < 0.001$) for progeny of LF and SLF cows than for L and LLF, whereas the progeny of C cows had intermediate gains for this period and differed only from LF progeny. Live weight at slaughter ($P < 0.001$), cold carcass weight ($P < 0.01$) and carcass gain per day of age ($P < 0.01$) were greater for progeny of LF and SLF cows than for L and LLF cows, with C being intermediate. Kill-out proportion was greater ($P < 0.001$) for the progeny of L cows than all other genotypes except LLF, which was intermediate. Carcass

Table 2. Least squares means for net energy (NE) intake, NE intake relative to live weight and energy conversion ratio for the bull progeny of five beef cow genotypes for years 2 and 3

	Year ¹	Cow genotype ²					s.e. ³	Significance
		LF	LLF	L	C	SLF		
Number of animals	2	8	7	8	5	17	–	
	3	6	6	6	–	12	–	
Net energy intake								
	UFV(I) ⁴ /day	2	8.34 ^{ab}	8.41 ^b	8.11 ^a	8.29 ^{ab}	8.38 ^b	0.107
	3	10.72	10.39	10.85	–	10.67	0.393	
UFV(I)/100 kg live weight ⁵	2	1.72	1.68	1.77	1.72	1.73	0.046	
	3	1.75	1.87	1.97	–	1.83	0.070	
Feed conversion ratio ⁶	2	7.13	7.58	7.64	7.16	7.60	0.600	
	3	6.18	6.20	6.22	–	6.54	0.720	

^{ab} Within rows, means without a common superscript differ ($P < 0.05$).

¹ Silage and concentrates (4.55 kg/day per head) were offered separately in year 2 but as total mixed ration (silage:concentrates = 2:1) in year 3.

² LF = Limousin \times Holstein-Friesian; LLF = Limousin \times (Limousin \times Holstein-Friesian); L = Limousin; C = Charolais; SLF = Simmental \times (Limousin \times Holstein-Friesian).

³ Maximum s.e.

⁴ UFV(I) (Unité Fourragère Viande) calculated by reference to O'Mara (1996).

⁵ Calculated using mean of start and end live weights during the recording period.

⁶ UFV(I) per kilogram of daily gain.

Table 3. Mean values for slaughter weight, carcass weight, kill-out proportion, growth and carcass traits for the progeny of five beef cow genotypes for years 1, 2 and 3

Variable	Cow genotype ¹					s.e. ²	Significance	
	LF	LLF	L	C	SLF		Genotype	Genotype × parity
Number of animals	53	51	47	39	55			
Slaughter weight (kg)	573 ^b	536 ^a	532 ^a	553 ^{ab}	568 ^b	7.8	***	* ⁵
Cold carcass (kg)	318 ^b	302 ^a	304 ^a	310 ^{ab}	317 ^b	4.8	**	* ⁶
Kill-out proportion (g/kg)	554 ^a	562 ^{ab}	571 ^b	559 ^a	558 ^a	3.3	***	* ⁷
Carcass conformation score ³	3.23 ^a	3.23 ^a	3.55 ^b	3.54 ^b	3.36 ^{ab}	0.093	**	
Carcass fat score ⁴	2.88 ^c	2.81 ^{bc}	2.52 ^{ab}	2.46 ^a	2.83 ^c	0.100	***	
Perinephric & retroperitoneal fat (kg)	7.5 ^b	6.4 ^{ab}	5.3 ^a	5.4 ^a	7.0 ^b	0.37	***	
Daily live-weight gain (g)								
Weaning to slaughter	960	953	961	985	982	21.2		
Birth to slaughter	1014 ^c	950 ^a	931 ^a	969 ^{ab}	1004 ^{bc}	14.9	***	* ⁸
Carcass weight per day of age (g)	614 ^b	583 ^a	585 ^a	596 ^{ab}	613 ^b	9.5	**	

^{abc} See footnotes Table 2.

^{1,2} See footnotes Table 2.

³ Scale 1 to 5 (best).

⁴ Scale 1 to 5 (fattest).

⁵ Subclass means, by parity, for LF, LLF, L, C and SLF were: **Parity 1:** 515^b, 491^{ab}, 475^a, 520^b, 518^b; **Parity 2:** 599^b, 562^a, 564^a, 552^a, 575^{ab}; **Parity 3:** 606, 555, 557, 587, 610.

⁶ Subclass means, by parity, for LF, LLF, L, C and SLF were: **Parity 1:** 291, 280, 282, 297, 295; **Parity 2:** 326, 311, 317, 303, 317; **Parity 3:** 337, 314, 312, 329, 340.

⁷ Subclass means by parity, for LF, LLF, L, C and SLF were: **Parity 1:** 563^a, 570^a, 593^b, 572^a, 570^a; **Parity 2:** 544^a, 552^a, 561^a, 548^a, 549^a; **Parity 3:** 555^a, 564^a, 558^a, 558^a, 556^a.

⁸ Subclass means by parity, for LF, LLF, L, C and SLF were: **Parity 1:** 905^b, 871^{ab}, 822^a, 909^b, 914^b; **Parity 2:** 1054^b, 1000^a, 986^a, 966^a, 1015^{ab}; **Parity 3:** 1083, 980, 986, 1032, 1084.

conformation score was higher ($P < 0.01$) for the progeny of L and C cows than for LF and LLF, with SLF being intermediate. Carcass fat score was lower ($P < 0.001$) for the progeny of C and L cows than LF and SLF. The progeny of LLF cows had similar fat scores to all genotypes except C. Perinephric and retroperitoneal fat weight was higher ($P < 0.001$) for progeny of LF and SLF cows than for progeny of L and C, with LLF being intermediate. The genotype × parity interaction was significant for daily gain from birth to slaughter ($P < 0.05$), slaughter weight ($P < 0.05$), kill-out proportion

($P < 0.05$) and cold carcass weight ($P < 0.05$).

Ultrasound and skeletal measurements, and visual muscularity scores

Muscle depth and area and fat depth did not differ ($P > 0.05$) between the progeny of the cow genotypes when measured pre-slaughter (Table 4). However, muscle depth expressed relative to live weight at slaughter was greater for progeny of L cows than LF and SLF cows with C and LLF being intermediate.

Chest depth was significantly greater for the progeny of LF and SLF cows than

Table 4. Mean pre-slaughter values for ultrasonic muscle and fat measurements (years 2 and 3), skeletal measurements (years 1 and 2) and muscularity scores (years 1, 2 and 3) for the progeny of five beef cow genotypes

Variable	Cow genotype ¹					s.e. ²	Significance
	LF	LLF	L	C	SLF		
Number of animals	36	35	27	26	38		
Ultrasound muscle							
Area (cm ²) at 13 th rib	98.3	97.6	100.9	98.7	97.1	3.39	
Depth (cm) at 13 th rib	8.7	8.7	8.9	8.9	8.5	0.23	
Area (cm ²) at 3 rd lumbar	70.9	69.6	69.6	72.9	70.2	2.92	
Depth (cm) at 3 rd lumbar	7.3	7.4	7.4	7.5	7.2	0.22	
Ultrasound fat							
Depth (mm) at 13 th rib	3.7	3.6	2.8	2.7	3.9	0.52	
Depth (mm) at 3 rd lumbar	3.1	2.7	2.2	2.2	2.9	0.39	
Ultrasound muscle per 100 kg live weight							
Area (cm ²) at 13 th rib	17.4 ^a	18.4 ^{ab}	19.5 ^b	17.7 ^a	17.3 ^a	0.63	***
Depth (cm) at 13 th rib	1.55 ^a	1.65 ^{ab}	1.75 ^b	1.59 ^{ab}	1.52 ^a	0.056	***
Area (cm ²) at 3 rd lumbar	12.5	13.1	13.4	13.0	12.4	0.51	
Depth (cm) at 3 rd lumbar	1.30 ^a	1.39 ^{ab}	1.43 ^b	1.34 ^{ab}	1.29 ^a	0.045	***
Skeletal measurements							
Number of animals	37	36	33	25	36		
Height at withers	133.9	132.0	132.5	131.6	132.9	1.17	
Height at pelvis	143.9	141.4	141.8	141.6	141.7	1.29	
Chest circumference	190.3	186.1	186.5	186.2	189.2	1.89	
Chest depth	73.8 ^b	72.7 ^{ab}	70.5 ^a	72.7 ^{ab}	74.1 ^b	1.06	**
Chest width ³	47.2	46.5	46.5	44.3	46.8	1.59	
Pelvic length	48.0	47.2	47.0	47.4	47.3	0.98	
Hip width	47.3	45.6	46.3	46.1	45.6	1.01	
Hind-quarter length	64.1	63.6	62.8	61.3	63.4	1.20	
Back length 1	137.0	136.5	136.8	138.4	139.5	2.22	
Back length 2	87.6	87.6	88.2	89.6	90.7	2.03	
Ratios							
Weight/height at withers	4.13 ^b	3.96 ^a	3.93 ^a	4.08 ^{ab}	4.09 ^{ab}	0.084	*
Weight/height at pelvis	3.84 ^b	3.70 ^a	3.67 ^a	3.79 ^{ab}	3.84 ^b	0.076	*
Muscularity score (scale 1–15)							
Number of animals	53	51	47	39	55		
Signet	7.4 ^a	7.5 ^a	8.5 ^b	8.3 ^b	7.7 ^{ab}	0.37	**
ICBF	9.1 ^a	9.1 ^a	9.7 ^{ab}	9.9 ^b	9.5 ^{ab}	0.29	**

^{ab} See footnotes Table 2.^{1,2} See footnotes Table 2.³ Year 2 only.

L cows, with LLF and C being intermediate. The progeny of LF cows had a greater ($P < 0.05$) ratio of weight to height at withers than those of LLF and L cows,

with C and SLF being intermediate. The ratio of weight to height at pelvis was greater for LF and SLF progeny than LLF and L progeny, with C being intermediate.

Other skeletal measurements did not differ significantly between the genotypes.

Muscular score at slaughter using the Signet system was greater ($P < 0.01$) for the progeny of L and C cows than for LF and LLF, with progeny from SLF being intermediate. Using the ICBF scoring system, the progeny of C cows had greater ($P < 0.01$) muscle scores than progeny of LF and LLF cows, with L and SLF being intermediate.

Carcass dimensions and muscle and fat measurements

Carcass dimensions and carcass muscle and fat measurements for the progeny are presented in Table 5. The progeny of LF

cows had a greater carcass ($P < 0.001$) and leg ($P < 0.05$) lengths than LLF and L cows, with C and SLF being intermediate. Carcass depth was greater ($P < 0.001$) for the progeny of LF cows than all except L, there being no difference between the other genotypes. Leg width was greater ($P < 0.01$) for the progeny of L cows than the other genotypes, which were similar ($P > 0.05$). There was no effect of genotype on carcass muscle area or depth. Carcass fat depth was greater ($P < 0.05$) for the progeny of LF cows than L cows, with LLF, C and SLF being intermediate.

The genotype \times parity interaction was significant for carcass depth ($P < 0.001$), leg width ($P < 0.01$) and fat depth ($P < 0.05$).

Table 5. Least squares means values for carcass measurements for progeny of five beef cow genotypes

Variable	Cow genotype ¹					s.e. ²	Significance	
	LF	LLF	L	C	SLF		Genotype	Genotype \times parity
Carcass dimensions³								
No. of animals	31	29	33	26	34			
Carcass length (cm)	132.9 ^b	127.5 ^a	126.5 ^a	129.7 ^{ab}	129.9 ^{ab}	1.43	***	
Carcass depth (cm)	48.0 ^b	44.2 ^a	45.0 ^{ab}	44.6 ^a	43.7 ^a	0.94	***	*** ⁵
Round width (cm)	42.6	42.5	40.6	43.9	42.7	1.39		
Round circumference (cm)	120.4	118.8	117.1	120.5	121.1	1.61		
Leg length (cm)	72.2 ^b	69.9 ^a	69.9 ^a	70.9 ^{ab}	70.2 ^{ab}	0.89	*	
Leg width (cm)	28.3 ^a	27.7 ^a	31.6 ^b	28.4 ^a	28.5 ^a	0.79	**	** ⁶
Muscle and fat measurements⁴								
No. of progeny	36	35	27	26	38			
Muscle area (cm ²)	111	107	118	110	109	4.2		
Muscle depth (cm)	8.5	8.4	8.5	8.6	8.5	0.53		
Fat depth (mm)	5.2 ^b	4.5 ^{ab}	3.4 ^a	4.1 ^{ab}	4.8 ^{ab}	0.67	*	* ⁷

^{abc} See footnotes Table 2.

^{1,2} See footnotes Table 2.

³ Years 1 and 3 combined.

⁴ Years 2 and 3 combined.

⁵ Subclass means, by parity, for LF, LLF, L, C and SLF were: **Parity 1:** 43.5, 44.3, 43.3, 44.6, 44.0; **Parity 2:** 55.1^b, 43.6^a, 46.8^{ab}, 44.8^a, 43.2^a; **Parity 3:** 45.2, 44.8, 45.0, 44.3, 43.9.

⁶ Subclass means, by parity, for LF, LLF, L, C and SLF were: **Parity 1:** 28.0, 27.0, 27.3, 27.9, 27.2; **Parity 2:** 28.7^a, 28.0^a, 38.8^b, 29.0^a, 28.5^a; **Parity 3:** 28.3, 28.1, 28.7, 28.3, 29.8.

⁷ Subclass means, by parity, for LF, LLF, L, C and SLF were: **Parity 1:** 3.6, 2.7, 1.6, 3.6, 3.7; **Parity 2:** 6.1, 5.4, 4.3, 3.9, 4.0; **Parity 3:** 5.9, 5.4, 4.5, 5.0, 6.7.

Proportions of meat, fat and bone and high-value cuts in the carcass and hind-quarter

In year 1, there was no difference between the progeny of the cow genotypes in the proportion of hind-quarter in the carcass (Table 6). The proportion of meat in the carcass was higher ($P < 0.001$) and bone lower ($P < 0.001$), and meat-to-bone ratio higher ($P < 0.001$) for the progeny of L cows than all other genotypes, between which there were no differences. Carcass fat proportion was similar for progeny of L and C cows and lower ($P < 0.001$) than LLF and SLF, with LF being intermediate. The combined meat

in the striploin, cube roll and fillet (high value cuts – HVC) expressed relative to cold carcass weight was greater for the progeny of L cows than LLF and SLF cows, with LF and C being intermediate, whereas HVC expressed relative to carcass meat did not differ ($P > 0.05$) between the genotypes.

In years 2 and 3, the proportion of hind-quarter in the carcass was higher ($P < 0.001$) for progeny of L and C cows than LF and SLF, with LLF being intermediate (Table 6). There was no effect ($P > 0.05$) of genotype on meat or fat proportion in the hind-quarter, whereas bone proportion was higher ($P < 0.01$)

Table 6. Mean values for carcass (year 1) and hind-quarter (years 2, 3) composition for progeny of five beef cow genotypes

Variable	Cow genotype ¹					s.e. ²	Significance	
	LF	LLF	L	C	SLF		Genotype	Genotype × parity
Carcass composition (Year 1)								
No. of animals	15	14	20	13	15			
Hind-quarter (g/kg)	493	496	498	494	488	2.8		
Carcass meat (g/kg)	725 ^a	711 ^a	760 ^b	726 ^a	714 ^a	6.6	***	
Carcass fat (g/kg)	90 ^{ab}	102 ^b	69 ^a	88 ^a	106 ^b	6.1	***	
Carcass bone (g/kg)	185 ^b	188 ^b	170 ^a	186 ^b	180 ^b	2.7	***	
HVC ³ in the carcass (g/kg)	85 ^{ab}	82 ^a	87 ^b	85 ^{ab}	84 ^a	1.1	**	
HVC in the meat (g/kg)	117	115	114	118	118	1.2		
Meat-to-bone ratio	3.9 ^a	3.8 ^a	4.5 ^b	3.9 ^a	4.0 ^a	0.08	***	
Hind-quarter composition (Years 2 and 3)								
No. of animals	38	37	27	26	40			
Hind-quarter (g/kg)	488 ^a	497 ^{ab}	500 ^b	505 ^b	488 ^a	4.9	***	* ⁴
Meat (g/kg)	752	761	768	756	756	7.3		
Fat (g/kg)	63	61	54	51	61	5.8		
Bone (g/kg)	185 ^{ab}	178 ^a	177 ^a	193 ^b	183 ^a	4.5	**	
HVC ¹ in the carcass (g/kg)	76	77	79	77	76	1.6		
HVC ¹ in the hind-quarter (g/kg)	207	203	204	201	205	3.7		
Meat to bone ratio	4.07 ^{ab}	4.28 ^{ab}	4.34 ^a	3.95 ^b	4.17 ^{ab}	0.135	*	

^{abc} See footnotes Table 2.

^{1,2} See footnotes Table 2.

³ High-value cuts = cube roll, striploin and fillet.

⁴ Subclass means, by parity, for LF, LLF, L, C and SLF were: **Parity 1:** 507^a, 514^a, 531^b, 528^{ab}, 500^a; **Parity 2:** 484 494 483 498 488; **Parity 3:** 474 483 487 490 477.

for progeny of C cows than LLF, L and SLF, with LF being intermediate. The meat-to-bone ratio was higher ($P < 0.05$) for progeny of L cows than C, with the other three genotypes being intermediate. The proportion of HVC in the carcass and in the hind-quarter did not differ ($P > 0.05$) between the genotypes. The genotype \times parity interaction was significant ($P < 0.05$) for the proportion of hind-quarter in the carcass.

Discussion

Significant cow breed \times parity interactions

The cow genotype \times parity interactions involving the C and L breeds may be due to positive individual heterotic effects. In parity one, the C progeny produced were crossbred (Limousin \times Charolais), whereas in later parities they were purebred (Charolais \times Charolais). Conversely, the progeny of L cows were purebred (Limousin \times Limousin) in parity one and crossbred (Charolais \times Limousin) in subsequent parities.

Growth and slaughter traits

The similar daily live-weight gain from weaning to slaughter among the genotypes is consistent with other studies comparing the progeny of Hereford \times Friesian with Limousin \times Friesian (Drennan and McGee, 2004) or Charolais (>0.875 ancestry) (Drennan, McGee and Keane, 2005) cows. Likewise, Young *et al.* (1978) found that steers from Charolais, Simmental and Limousin crossbred cows had similar post-weaning growth rates. Rahnefeld *et al.* (1988) reported that the progeny from Charolais-sired dams had 5% and 2.5% greater post-weaning gain than progeny from Limousin- and Simmental-sired dams, respectively. Effectively, this means that the difference between the genotypes

in live weight at slaughter predominantly reflected the differences in pre-weaning growth (Murphy *et al.*, 2008) largely due to the diversity in milk yield of the dam genotypes (McGee *et al.*, 2005b; Murphy *et al.*, 2008). In accord with the findings of Drennan and McGee (2004) and Drennan *et al.* (2005) this limited capacity of the suckler calf to compensate post-weaning for growth retardation experienced pre-weaning means that in spring-calving, pasture-based systems in temperate regions, live weight differences at weaning are largely retained until slaughter.

The higher kill-out proportion of the L progeny concurs with Rahnefeld *et al.* (1984) who found that the progeny of Limousin crossbred cows had a higher dressing percentage than progeny of Simmental crossbreds, with progeny of Charolais crossbreds being intermediate. Rahnefeld *et al.* (1983) reported that progeny from Limousin and Charolais crossbred cows had a higher dressing percentage than those of Simmental crossbred cows. The decline in kill-out proportion as the percentage of dairy breeding increased in the Limousin is consistent with studies showing a higher kill-out proportion in late-maturing beef breed crosses than in Holstein or Friesian (e.g. McGee *et al.*, 2005c).

Despite the differences in kill-out proportion, the differentiation between the genotypes in carcass weight still mirrored those in live weight at slaughter. In accord with the present results, Rahnefeld *et al.* (1984) found that progeny of Simmental crossbred cows had significantly higher and numerically higher carcass weight than progeny of Limousin or Charolais crossbred cows, respectively. Similarly, Morris *et al.* (1987) reported that progeny of Limousin crossbred cows had a lower carcass weight than Charolais and Simmental crossbred cows, which were

similar. In an on-farm study, Kirkland *et al.* (2004) reported that carcass weight did not differ between the progeny of Continental \times Friesian and continental ($\geq 75\%$ ancestry) breed dams, whereas more specifically, from the same study, Keady *et al.* (2004) found that carcass weight was similar for the progeny of Limousin \times Friesian, Limousin and Charolais cows. These findings agree with the carcass weight results obtained for LF compared to SLF but not for LF compared to LLF, L or C.

Carcass classification scores and fat and muscle measurements

The higher carcass conformation score of the progeny from L and C cows than LF cows concurs with the findings of Kirkland *et al.* (2004) who compared the progeny of Continental \times Friesian and continental ($\geq 75\%$ ancestry) breed dams, whereas Keady *et al.* (2004) found that carcass conformation score did not differ between the progeny of Limousin \times Friesian, Limousin or Charolais cows. The discrepancies in the latter case probably reflect limitations associated with on-farm studies.

The absence of a difference between genotypes in absolute ultrasound measures of muscle depth and area on the live animal were in agreement with subsequent carcass muscle area and depth measurements. However, in the present study, when expressed relative to live weight, ultrasound muscle measurements were generally highest for the L genotype. Similarly, Rahnefeld *et al.* (1983) found that the progeny of Limousin crossbred cows had a greater muscle area relative to carcass weight than progeny of Charolais crossbreds, who in turn were greater than the progeny of Simmental crossbred cows.

The Signet muscular scores of progeny at slaughter followed an identical pattern

to subsequent carcass conformation scores of the genotypes. This would be expected as previous studies have shown good correlations between live animal muscular score and carcass conformation score (Drennan, Keane and McGee, 2007).

The lower fat score of the progeny of L and C cows compared with progeny of LF is in agreement with the findings of Kirkland *et al.* (2004) who compared the progeny of Continental \times Friesian and continental ($\geq 75\%$ ancestry) breed dams, whereas Keady *et al.* (2004) found that carcass fat class was lower for Limousin than Limousin \times Friesian with Charolais being intermediate. The increasing weight of perinephric and retroperitoneal fat with increasing proportion of dairy breeding in the L crossbreds, is consistent with results showing that dairy breeds deposit more of their fat in the abdominal cavity than do beef breeds (Truscott, Wood and Macfie, 1983).

Although ultrasound measures of fat depth did not differ between the genotypes and carcass fat measurements differed significantly, in general, all measures of fatness on the live animal and carcass followed the same trend, whereby they were lower for the C and L than LF and SLF, with LLF being intermediate.

Carcass composition

The higher proportion of the carcass as pistola or hind-quarter in the progeny of C and L cows than LF cows is consistent with the results of Drennan *et al.* (2005) comparing the progeny of Charolais ($\geq 87.5\%$ ancestry) and Hereford \times Friesian dams. As the pistola is up to three times more valuable than the fore-quarter this is of major commercial importance. The greater meat-to-bone ratio in the carcass of the L progeny agrees with the findings of Rahnefeld *et al.* (1983) who reported that progeny of Limousin cross-

bred cows had a greater lean-to-bone ratio than progeny of Charolais crossbreds, who in turn were greater than Simmental cow progeny. Morris *et al.* (1987) also found that progeny of Limousin crossbred cows had numerically greater carcass meat proportion than progeny of Charolais and Simmental dams, which were similar and that Limousin crossbred cow progeny tended to have a lower carcass bone proportion than Simmental progeny with Charolais being intermediate.

Differences in the proportion HVC relative to weight of meat in the carcass and hind-quarter were relatively small. Newman *et al.* (1994) found that progeny of Charolais crossbred cows has less dissectible fat and more lean in the preferred cuts than the progeny of Simmental crossbred cows. Robelin and Tulloh (1992) pointed out that, commercially, the most important differences between breeds is in the total amount of muscle, as differentiation in the muscle distribution are comparatively unimportant.

Sire breed studies comparing growth and carcass traits have shown that there are relatively large differences between dairy breeds, or early-maturing beef breeds, and late-maturing beef breeds, whereas difference between breeds within each category are generally smaller (Keane, 1993b). The fact that all the progeny compared in the current study had at least 75% late-maturing beef breed ancestry, the magnitude of the cow genotype differences post-weaning would be reduced.

In conclusion, there was no effect of cow genotype on the performance of their progeny from weaning to slaughter. However, crossbred cows with good maternal (milk) traits produced progeny with a higher carcass weight per day of age, whereas the purebred continental cows produced progeny with superior carcass classification. Genotype

effects were relatively small for carcass composition.

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