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Effects of genetic merit for carcass weight, breed type and slaughter weight on performance and carcass traits of beef × dairy steers

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Crossbreeding of Holstein–Friesian dairy cows with both early maturing (e.g. Aberdeen Angus (AA)) and late maturing (e.g. Belgian Blue (BB)) beef breeds is commonly practised. In Ireland, genetic merit for growth rate of beef sires is expressed as expected progeny difference for carcass weight (EPD_{CWT}). The objective of this study was to compare the progeny of Holstein–Friesian cows, sired by AA and BB bulls of low (L) and high (H) EPD_{CWT} for performance and carcass traits. A total of 118 spring-born male progeny from 20 (9 AA and 11 BB) sires (8 L and 12 H) were managed together from shortly after birth to about 19 months of age. They were then assigned to one of two mean slaughter weights (560 kg (light) or 620 kg (heavy)). Following slaughter, carcasses were graded for conformation class and fat class, the 6th to 10th ribs joint was dissected as an indicator of carcass composition, and samples of subcutaneous fat and musculus longissimus *were subjected to Hunterlab colour measurements. A sample* of m. longissimus *was also chemically analysed. Slaughter and carcass weights per day of age for AAL, AAH, BBL and BBH were 747, 789, 790 and 805 (s.e. 10.5) g, and 385, 411, 427 and 443 (s.e. 4.4) g, respectively. Corresponding carcass weight, kill-out proportion, carcass conformation class (scale 1 to 5) and carcass fat class (scale 1 to 5) values were 289, 312, 320 and 333 (s.e. 4.0) kg, 516, 522, 542 and 553 (s.e. 3.5) g/kg, 2.5, 2.4, 3.0 and 3.1 (s.e. 0.10), and 3.4, 3.5, 2.9 and 2.8 (s.e. 0.11). There were few breed type × genetic merit interactions. Delaying slaughter date increased slaughter weight, carcass weight and all measures of fatness. It also reduced the proportion of carcass weight in the hind quarter and the proportions of bone and muscle in the ribs joint. None of these effects accompanied the increase in carcass weight due to higher EPD_{CWT}. It is concluded that BB have superior production traits to AA. Selection of sires for higher EPD_{CWT} increases growth rate, kill-out proportion and carcass weight of progeny with little effect on carcass or muscle traits. The extra carcass weight due to higher EPD_{CWT} is more valuable commercially than a comparable carcass weight increment from a delay in slaughter date because it comprises a higher proportion of muscle.*

Keywords: beef breeds, carcass, cattle, genetic merit, growth, muscle

Implications

Carcass weight is increased by the use of sires of higher genetic merit for growth or by delaying slaughter date. These approaches have different effects on feed intake and carcass traits. Increased genetic merit for growth has no effect on feed intake or efficiency, whereas delaying slaughter increases feed intake and reduces efficiency. Carcass and muscle composition are unaffected by genetic merit for growth, whereas delaying slaughter reduces muscle proportion and increases fat proportion in the carcass. Delaying slaughter also reduces moisture proportion and increases lipid proportion in the muscle. Thus, use of sires with higher genetic merit for growth facilitates an increase in carcass weight with no change in carcass or muscle composition.

Introduction

In Ireland, about 50% of all dairy cows are bred to beef bulls (AIM Bovine Statistics Report, 2008). As dairy cross calves do not meet the conformation standard for the high-value live export trade to the continental European Union they are reared to slaughter in Ireland and carcass weight is the main determinant of carcass value.

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To assist producers in the selection of sires that will increase the profitability of their enterprise, the Irish Cattle Breeding Federation (ICBF) undertakes and publishes genetic evaluations for a range of performance traits on all the main cattle breeds (including pure dairy breeds) used for beef production in Ireland. Genetic evaluations are carried out on an across-breed basis and production traits are individually weighted by their monetary value to produce a single aggregated economic value for beef genetic merit (Amer *et al.*, 2001). Carcass weights for all commercially slaughtered cattle (including culled cows) are captured in a central database and are used in the ICBF genetic evaluation programme as the measure of lifetime growth rate. Breeding value for carcass weight is derived using a multi-trait animal model and expressed as the expected progeny difference for carcass weight (EPD_{CWT}), estimated as a deviation from a common base carcass weight for Holstein–Friesian steers (Campion *et al.*, 2009a). Age at slaughter, among other factors, is adjusted for in the model as a fixed effect. All other EPDs are similarly expressed as deviations from a common base.

Generally, but not universally, the relationship between the EPD for a trait and measured performance for that trait is positive. Basarab *et al.* (1994) found that in straight-bred Herefords a 1 kg change in birth weight EPD corresponded to a 1.06 kg change in actual birth weight, while a 1 kg change in weaning or yearling weight EPD corresponded to 0.45 and 0.78 kg changes in 200-day and 365-day live weights, respectively. Similarly, Nunez-Dominguez *et al.* (1993) reported EPD regressions (kg/kg) on birth, weaning and yearling weights of 1.04, 0.88 and 1.40, respectively. In Ireland, Keane and Diskin (2007), using an earlier within-breed genetic evaluation system, found that a change in EPD for carcass weight matched the observed change in carcass weight. They also drew attention to the fact that while EPD_{CWT} is a constant, measured carcass weight differences are a function of overall growth rate and age at slaughter. To date, the ICBF beef genetic index and its components have not been widely evaluated. Clarke *et al.* (2009) compared progeny from beef cows of high and low Beef Carcass Index (BCI). This is an aggregate index comprising weaning weight, feed intake, carcass weight, carcass conformation class and carcass fat class. Dry matter (DM) intake or live weight (LW) gain during finishing did not differ significantly with BCI, but the high BCI calves were heavier at weaning and at slaughter. Regressions of measured traits on the corresponding EPD components of BCI showed that live weight, but not LW gain or carcass weight gain, was positively related to EPD for weaning weight and carcass weight. Feed intake was also related to EPD for intake, but carcass conformation class and carcass fat class were not related to the EPDs for these traits.

In a precursor to this study, Campion *et al.* (2009a and 2009b) compared progeny from Holstein–Friesian dairy cows and early Aberdeen Angus (AA) and late Belgian Blue (BB) maturing beef breed sires of high and low EPD_{CWT}. Pure-bred Friesians and Holsteins were also included. There was a beef sire breed × genetic merit interaction for carcass weight. Across the two beef sire breeds, the measured difference in carcass weight approximated to EPD_{CWT} but the effect was greater than predicted for AA and negligible for BB. It is important that these findings be either confirmed or amended on the basis of additional data.

The overall objective of this study was to further evaluate the ICBF beef genetic evaluation system. The specific objectives were (i) to compare growth, feed intake, slaughter traits and carcass traits of progeny of early and late maturing sire breeds, each of low and high EPD_{CWT}; (ii) to ascertain the effect of slaughter weight on these variables; and (iii) to examine possible interactions of breed type, genetic merit and slaughter weight.

Material and methods

Animal source

Male calves from Holstein–Friesian dams and 20 beef sires (9 AA and 11 BB), of either low (L, 8 sires) or high (H, 12 sires) EPD_{CWT}, were sourced from commercial dairy herds in spring 2007. All the calves were from sires that were available through artificial insemination and had high reliability for EPD_{CWT} based on the number of progeny with carcass records in the ICBF database. In total, 139 calves were sourced from 42 dairy herds and transferred to the Grange Beef Research Centre at 2 to 6 weeks of age. Following genotyping for sire verification (International Society of Animal Genetics, 2008), 14 animals with incorrectly identified sires were removed from this study. In addition, over the course of the study, a further seven animals were lost or removed due to mortality or accidents, leaving 118 animals comprising 29 AAL, 29 AAH, 30 BBL and 30 BBH for which complete data were available.

The mean sire EPDs for carcass weight, carcass conformation, carcass fatness, feed intake, suckler beef monetary value and carcass monetary value, together with the corresponding reliabilities, are shown in Table 1. Mean EPD_{CWT} values ranged from −12 kg for AAL to 30 kg for BBH. Within this range, individual bull values ranged from −15 to 52 kg. Mean carcass conformation class varied from 0.80 (AAL) to 2.76 (BBH), whereas mean carcass fat class varied from 0.98 (AAL) to −1.30 (BBH). Other than for feed intake where sire reliabilities were 80% to 85%, sire reliabilities exceeded 95%.

Management to start of finishing

After arrival, calves were penned individually and offered a total of 25 kg milk replacer per head over a 56-day period. Calf concentrates (750 g/kg coarsely rolled barley, 170 g/kg soyabean meal, 55 g/kg molasses, 25 g/kg mineral/vitamin pre-mix) were offered up to a maximum of 2 kg per head daily until turnout to pasture on 5 June, and at 1 kg per head daily for 4 weeks afterwards. Each calf received a total concentrate allowance of 100 kg. Hay was continuously available during the indoor rearing period. At pasture, calves preceded yearling steers in a leader/follower rotational grazing system and were treated with ivermectin (Qualimec, Janssen Animal Health, High Wycombe, Buckinghamshire, UK)

Table 1 *Mean sire estimated genetic merit, expressed as expected progeny difference for carcass weight (EPD_{CWT}), carcass conformation class (EPD_{CONF}), carcass fat class (EPD_{FAT}), daily dry matter intake (EPD_{DMI}), suckler beef value, carcass value, with corresponding reliabilities, weighted by number of progeny per sire for AA and BB bulls of L and H estimated genetic merit for carcass weight*

	AA		BB	
Trait	L	H	L	H
No. sires	4	5	4	7
No. progeny	29	29	30	30
EPD_{CWT} (kg)	−11.7	7.1	22.2	30.2
Reliability (%)	95	99	99	98
EPD_{CONF} (scale 1 to 15)	0.80	0.65	2.79	2.76
Reliability (%)	99	99	99	98
EPD_{FAT} (scale 1 to 15)	0.98	0.62	−1.09	−1.30
Reliability (%)	97	98	98	97
EPD_{DMI} (kg)	0.07	0.33	−0.56	−0.48
Reliability (%)	80	85	84	84
Suckler beef value (€)	−7	56	148	156
Reliability (%)	93	94	94	94
Carcass value (€)	−46	14	139	165
Reliability (%)	96	97	97	97

AA = Aberdeen Angus; BB = Belgian Blue; L = low; H = High.
Source: Irish Cattle Breeding Federation genetic evaluations (January, 2008).

at 3, 8 and 13 weeks after turnout for the control of gastrointestinal parasites. The calves were castrated on 10 October and were housed for the first winter on 15 November. The duration of the first grazing season was 163 days.

During the first winter, the animals were managed in three groups of 42, 42 and 34, each balanced for breed type, EPD_{CWT} and sire. All were offered grass silage (chemical composition: DM 231 g/kg, *in vitro* DM digestibility 729 g/kg, crude protein (CP) 149 g/kg, ash 84 g/kg, pH 4.0, *Unite Fourragere Viande* (UFV, Jarrige, 1989; O'Mara, 1996) 0.77) *ad libitum* and an average of 1.4 kg of cattle concentrates (875 g/kg rolled barley, 65 g/kg soyabean meal, 45 g/kg molasses, 15 g/kg mineral/vitamin pre-mix) per head daily for a 123-day winter period to 18 March when the concentrates were withdrawn. The animals were linear scored (ICBF, 2003) at about 10 months of age by a trained assessor. Skeletal scores (9-point scale) were recorded at three locations and muscular scores (15-point scale) were recorded at four locations. These scores were aggregated to give one overall skeletal and one overall muscular score per animal (Campion *et al*., 2009a). All animals were turned out to pasture together on 25 March for a second grazing season of 209 days. From early June onwards, they followed calves in a leader/follower rotational grazing system.

Management during finishing

At the end of the second grazing season (20 October), the animals were housed in slatted floor sheds and assigned to one of two slaughter weight groups (560 kg (light) and 620 kg (heavy)) balanced for breed type, genetic merit, previous winter management, LW and sire. Each of these slaughter weight groups were further sub-divided in a ratio of 2 : 1 into animals that were advanced or backwards relative to their target slaughter weight. Those in the advanced category were immediately placed on a finishing diet whereas those in the backwards category were placed on a growing diet until 2 February when they moved to the finishing diet. This was to allow the backward animals a further growing period before finishing. The growing diet consisted of grass silage *ad libitum* plus 2 kg cattle concentrates per head daily. The finishing diet consisted of a total mixed ration with a grass silage : cattle concentrate ratio of 33 : 67 on a DM basis. It was offered in a slatted floor shed fitted with Calan–Broadbent electronic doors for individual feed recording. The DM intake was recorded daily throughout finishing and feed refusals were discarded twice weekly. The same silage (chemical analysis: DM 204 g/kg, DMD 692 g/kg, CP 133 g/kg, ash 88 g/kg, pH 3.9, UFV 0.73) was used in the growing and finishing diets. The number of animals, mean start of finishing LW, mean slaughter weight and duration of the winter period were 39, 437 kg, 554 kg and 105 days (advanced light), 38, 440 kg, 629 kg and 183 days (advanced heavy), 20, 462 kg, 545 kg and 162 days (backwards light), and 21, 474 kg, 609 kg and 225 days (backwards heavy), respectively.

Slaughter and carcass assessment

Animals were weighed on the day before slaughter and on the morning of slaughter. These weights were averaged to give LW at slaughter (slaughter weight). The animals were transported approximately 130 km to a commercial beef processing plant and slaughtered within 1 h of arrival. Carcasses were dressed according to standard procedures and kill-out proportion was calculated as the proportion of cold carcass weight (hot weight × 0.98) in the slaughter weight. Carcass conformation and fat classes (Commission of the European Communities, 1982) were automatically recorded on a 5-point scale using a video imaging analysis carcass classification machine (VBS2000, E + V, Germany). Within the range ± one-third of a class, this machine had a correspondence with reference panel (three experienced classifiers) values of 100% for conformation class and 97% for fat class (Allen and Finnerty, 2000). Perirenal plus retroperitoneal fat weight, together with carcass measurements (DeBoer *et al*., 1974), were also recorded. Carcass measurements that were taken were carcass length, chest depth, leg length, leg width (maximum width of leg) and leg thickness (width of leg from the medial splitting surface of the symphysis pubis).

After 48 h in the chill at 4°C, the right side of each carcass was quartered between the 5th and 6th ribs into a pistola hind quarter (without the flank) and a fore quarter that included the flank (Keane and Allen, 1998). Both quarters were weighed and the ribs joint (ribs 6 to 10 inclusive) was separated from the pistola by cutting between the 10th and 11th ribs. The *musculus longissimus* outline at the 10th rib

was traced on to translucent paper and the area was subsequently measured using a digital planimeter (Placom KP-90N, Sokkisha, Japan). The ribs joint was weighed and separated into fat, *m. longissimus*, other muscle, muscle trim and bone (including *ligamentum nuchae/supraspinale*). A sample of the subcutaneous fat over the 8th rib and a sample (2.5 cm thick) of *m. longissimus* from the 10th rib were taken for colour measurement. A second sample of *m. longissimus* was frozen for subsequent chemical analysis.

Colour measurements were carried out using a Hunterlab Ultrascan XE colorimeter (Hunter Associates Laboratory, Inc., Reston, VA, USA). Fat colour measurements were made the day after the samples were taken. The muscle samples were vacuum packaged and stored at 4°C for 12 days (14 days from slaughter). They were then removed from the package, over-wrapped with oxygen-permeable film and permitted to bloom at 4°C for 2 h. Colour measurements were then taken. For both the fat and muscle samples, L (lightness), a (redness) and b (yellowness) values were recorded using a D65 illuminant. Chroma and hue values were calculated and *m. longissimus* chemical composition was determined according to Dunne *et al*. (2004).

Statistical analysis

The data were statistically analysed according to the factorial design using mixed model methodology (PROC MIXED) of the Statistical Analysis Systems Institute (SAS, 2008). Up to the start of finishing the fixed effects included in the model were breed type (AA *v.* BB) and genetic merit (H *v.* L). For the finishing, slaughter and carcass data, slaughter weight (light *v.* heavy) was included as a factor, and the model also had a term for the finishing group (backwards or advanced). Management group in the first winter and birth year of dam were included in both models as fixed effects and sire was included as a random effect in both models.

The data are presented as the individual breed type × genetic merit means together with the main effect of slaughter weight as applicable. Where there were interactions with slaughter weight, the individual means are shown in table footnotes. Statistical significance is conventionally indicated (*$P<0.05$, **$P<0.01$, ***$P<0.001$) and where effects approached significance ($P>0.05$ but <0.10) the actual *P*-values are shown.

Results

Live weights and LW gains

There was no significant difference in birth date between the breed type and genetic merit groups, and neither was there a significant difference between the breed types in date of arrival at the Grange Beef Research Centre (Table 2). However, the low genetic merit animals arrived somewhat ($P=0.09$) later than their high merit counterparts (7 April *v.* 27 March). Arrival weight was not significantly affected by genetic merit, but BB were heavier ($P<0.05$) than AA. Thereafter, the BB animals tended to be heavier than AA throughout life but the differences at first housing (187 *v.* 167 kg) and at the second turnout (259 *v.* 236 kg) were not statistically significant. There was a LW difference at slaughter of 18 kg ($P=0.06$) in favour of BB. From the date of first housing to slaughter, the high-merit animals were significantly heavier than their low-merit comrades. The differences at the first turnout, first housing, second turnout, second housing and slaughter were 9, 21, 24, 30 and 29 kg, respectively. No breed type × genetic merit interaction was detected for any of the live weights. Days from birth to

Table 2 *Mean birth and arrival dates and mean live weights from arrival to slaughter for steer progeny of Holstein–Friesian dams and AA and BB sires of L and H estimated genetic merit for carcass weight*

	AA		BB		Slaughter weight			Significance/probability[2]			
Trait	L	H	L	H	Light	Heavy	s.e.[1]	B[3]	G[3]	S[3]	I[3]
Birth date	16 March	4 March	20 March	13 March	14March	12 March	4.65[4]	ns	ns	ns	ns
Arrival date	8 April	23 March	6 April	31 March	2 April	1 April	4.46[4]	ns	$P=0.09$	ns	G × S, $P=0.08$[5]
Live weights (kg) at:											
Arrival	50.9	51.3	56.8	58.1	–	–	1.95	*	ns	ns	ns
first turnout (5 June)	76.5	90.0	90.3	95.7	–	–	3.17	*	ns	ns	ns
first housing (15 November)	165	189	169	184	–	–	4.3	ns	**	ns	ns
second turnout (25 March)	232	257	239	261	–	–	5.4	ns	**	ns	ns
second housing (20 October)	393	432	415	436	416	422	5.3	*	***	ns	ns
Slaughter	562	604	593	609	556	628	7.0	$P=0.06$	**	***	ns
Birth to slaughter (days)	753	765	751	757	718	794	4.8	ns	ns	***	ns
Arrival to slaughter (days)	731	746	733	738	699	775	4.6	ns	ns	***	G × S, $P=0.07$[6]

AA = Aberdeen Angus; BB = Belgian Blue; L = low; H = high.
[1]Pooled standard error (s.e.) for main effect in this and subsequent tables.
[2]Where $P<0.1$ and >0.05, the *P*-value is shown, otherwise *$P<0.05$, **$P<0.01$, ***$P<0.001$, ns $P>0.1$ in this and subsequent tables.
[3]In this and subsequent tables B (Breed) = AA *v.* BB, G (Genetic merit) = L *v.* H, S (Slaughter weight) = Light *v.* Heavy, I = Interaction.
[4]Calculated on the number of days after 1 January.
[5]10 April, 4 April, 25 March and 29 March for L Light, L Heavy, H Light and H Heavy, respectively.
[6]Values of 691, 773, 707 and 777 for L Light, L Heavy, H Light and H Heavy, respectively.

slaughter and days from arrival to slaughter did not differ significantly for the breed types or genetic merits.

Daily LW gain from arrival to the first turnout was higher ($P < 0.05$) for BB than AA but the opposite was so ($P < 0.01$) from first turnout to first housing (Table 3). Thereafter to slaughter, there was no significant difference between the breed types in daily LW gain. However, slaughter weight per day of age was higher ($P < 0.05$) for BB. Daily LW gain was higher for the high-merit animals in the period from first turnout to first housing ($P < 0.01$) and from arrival to slaughter ($P < 0.05$). Slaughter weight per day of age was also higher ($P < 0.05$) for the high-merit animals. There was a breed type × genetic merit interaction ($P = 0.06$) for daily gain during the second grazing season because of a higher value for the high-merit AA but not for the high-merit BB. From the second housing to slaughter ($P < 0.05$) and during the finishing period ($P < 0.001$), daily LW gains were higher for the light than for the heavy slaughter weight group. However, daily gain from arrival to slaughter was higher ($P < 0.05$) for the heavy slaughter weight group.

Feed intake during finishing

Feed intake during finishing is shown in Table 4. Total DM intake did not differ between AA and BB, or between L and H, but was greater ($P < 0.001$) for the heavy than for the light slaughter weight group. UFV intake paralleled DM intake. As there were differences between the groups in mean LW during the finishing period there were differences in DM intake per kg mean LW with BB, H and the heavy slaughter weight categories having lower ($P < 0.001$) values than AA, L and the light slaughter weight categories, respectively. Efficiency of utilisation of UFV for LW gain (g LW gain per UFV) was not significantly affected by genetic merit but it tended ($P = 0.09$) to be better for BB than AA (119 *v.* 111 g/UFV) and was better ($P < 0.001$) for the light than for the heavy slaughter weight group.

Skeletal and muscular scores

All skeletal and muscular scores were significantly greater ($P = 0.06$ for height at withers) for BB than AA (Table 5). Other than length of back, which was not different, all skeletal scores were significantly greater for H than L. Muscular scores, other than hind quarter development, which was greater for H, were not significantly affected by genetic merit. There was a breed type × genetic merit interaction ($P = 0.08$) for average skeletal score due to a greater difference between L and H for AA than BB. There was also a genetic merit × slaughter weight interaction ($P = 0.08$) for average muscular score due to a greater difference between L and H at the light than at the heavy slaughter weight.

Table 3 *Lifetime live weight gains (g/day) for steer progeny of Holstein–Friesian dams and AA and BB sires of L and H estimated genetic merit for carcass weight*

	AA		BB		Slaughter weight			Significance/probability			
Trait	L	H	L	H	Light	Heavy	s.e.	B	G	S	I
Arrival to first turnout	433	503	530	555	487	523	26.6	*	ns	ns	ns
First turnout to first housing	547	608	477	542	544	543	16.5	**	**	ns	ns
First housing to second turnout	512	520	541	594	542	541	27.6	ns	ns	ns	ns
Second turnout to second housing	776	838	838	835	817	826	16.3	ns	$P = 0.09$	ns	B × G, $P = 0.06$
Second housing to slaughter	1005	1030	1067	1038	1073	997	30.3	ns	ns	*	ns
Finishing period[1]	1158	1160	1252	1181	1272	1004	41.9	ns	ns	***	ns
Daily gain from arrival (g)	700	740	731	746	719	739	10.1	ns	*	*	ns
Slaughter weight per day of age (g)	747	789	790	805	775	791	10.5	*	*	ns	ns

AA = Aberdeen Angus; BB = Belgian Blue; L = low; H = high.
[1]From start of finishing to slaughter.
See also Table 2 footnotes.

Table 4 *DMI, UFV intake and efficiency of UFV utilisation during finishing for steer progeny of Holstein–Friesian dams and AA and BB sires of L and H estimated genetic merit for carcass weight*

	AA		BB		Slaughter weight			Significance/probability			
Trait	L	H	L	H	Light	Heavy	s.e.	B	G	S	I
DMI (kg/day)	10.4	10.6	10.4	10.3	10.3	10.6	0.08	ns	ns	***	ns
DMI (g/kg LW)	21.1	19.8	19.8	19.1	20.4	19.4	0.17	***	***	***	ns
UFV intake/day	10.3	10.5	10.3	10.2	10.2	10.4	0.08	ns	ns	***	ns
LW/UFV (g)	112	110	122	116	125	106	3.8	$P = 0.09$	ns	***	ns

DMI = Dry matter intake; UFV = Unite Fourragere Viande (Jarrige, 1989), values of 1.12 and 0.73 UFV/kg DM for concentrates and silage, respectively; AA = Aberdeen Angus; BB = Belgian Blue; L = low; H = high; LW = Live weight.
See also Table 2 footnotes.

Table 5 *Mean skeletal and muscular scores at 10 months of age for steer progeny of Holstein–Friesian dams and AA and BB sires of L and H estimated genetic merit for carcass weight*

	AA		BB		Slaughter weight			Significance/probability			
Trait	L	H	L	H	Light	Heavy	s.e.	B	G	S	I
Skeletal scores[1]											
Height at withers	3.9	4.8	4.5	5.0	4.5	4.6	0.14	$P = 0.06$	**	ns	ns
Length of back	4.3	4.9	5.1	5.3	5.0	4.8	0.13	***	ns	ns	ns
Width at hips	3.6	4.3	4.3	4.7	4.2	4.3	0.13	***	***	ns	ns
Average skeletal score	3.9	4.7	4.6	5.0	4.5	4.6	0.10	***	***	ns	B × G, $P = 0.08$
Muscular scores[2]											
Width at withers	3.2	3.3	3.8	4.2	3.7	3.6	0.23	*	ns	ns	ns
Width behind withers	2.3	2.2	2.9	3.3	2.8	2.5	0.22	**	ns	$P = 0.06$	ns
Loin development	2.9	2.9	3.6	4.2	3.6	3.3	0.24	*	ns	$P = 0.07$	ns
Hind quarter development	3.2	3.5	4.2	4.8	3.9	3.9	0.19	***	*	ns	ns
Width of thigh	4.6	4.8	5.4	6.0	5.1	5.3	0.21	**	ns	ns	ns
Depth of thigh	3.7	4.0	4.1	4.5	4.3	3.9	0.18	*	$P = 0.06$	ns	ns
Average muscular score	3.2	3.4	4.0	4.5	3.9	3.8	0.17	**	ns	ns	G × S, $P = 0.08$[3]

AA = Aberdeen Angus; BB = Belgian Blue; L = low; H = high.
[1]Range 1 (short/narrow) to 9 (long/wide).
[2]Range 1 (hollow or poorly muscled) to 15 (bulging/thick muscled).
[3]Values of 3.6, 3.7, 4.1 and 3.8 for L Light, L Heavy, H Light and H Heavy, respectively.
See also Table 2 footnotes.

Table 6 *Slaughter traits and carcass measurements for steer progeny of Holstein–Friesian dams and AA and BB sires of L and H estimated genetic merit for carcass weight*

	AA		BB		Slaughter weight			Significance/probability			
Trait	L	H	L	H	Light	Heavy	s.e.	B	G	S	I
Carcass weight (kg)	289	312	320	333	294	333	4.0	***	***	***	ns
Carcass weight per day of age (g)	385	411	427	443	405	428	4.4	***	***	***	ns
Kill-out (g/kg)	516	522	542	553	522	545	3.5	***	*	***	B × S**[1]
Carcass conformation class[2]	2.5	2.4	3.0	3.1	2.7	2.8	0.10	***	ns	ns	ns
Carcass fat class[3]	3.4	3.5	2.9	2.8	2.9	3.4	0.11	***	ns	*	B × G × S*[4]
Perirenal + retroperitoneal fat (kg)	10.0	9.7	10.2	9.7	8.1	11.7	0.64	ns	ns	***	ns
Perirenal + retroperitoneal fat (g/kg)[5]	33.5	30.2	30.5	27.2	26.2	34.8	1.83	ns	ns	**	G × S, $P = 0.06$[6]
Carcass measurements (mm/kg)											
Carcass length	4.6	4.4	4.2	4.1	4.5	4.2	0.04	***	***	***	ns
Carcass width	1.7	1.6	1.5	1.5	1.6	1.5	0.02	***	*	***	B × S, $P = 0.06$[7]
Leg length	2.6	2.5	2.4	2.3	2.5	2.3	0.03	***	***	***	ns
Leg width	1.5	1.5	1.4	1.4	1.6	1.3	0.02	**	ns	***	B × S, $P = 0.08$[8]
Leg thickness	1.0	0.9	1.0	0.9	1.0	0.9	0.02	ns	ns	***	ns

AA = Aberdeen Angus; BB = Belgian Blue; L = low; H = high; EU = European Union.
[1]Values of 505, 534, 539 and 556 for AA light, AA heavy, BB light and BB heavy, respectively.
[2]EU beef carcass classification scheme: scale 1 (poorest) to 5 (best).
[3]EU beef carcass classification scheme: scale 1 (leanest) to 5 (fattest).
[4]Values of 3.2, 3.6, 3.2, 3.8, 2.5, 3.2, 2.7 and 2.9 for AAL light, AAL heavy, AAH light, AAH heavy, BBL light, BBL heavy, BBH light and BBH heavy, respectively.
[5]Of carcass.
[6]Values of 26.5, 37.4 25.8 and 32.2 for L light, L heavy, H light and H heavy, respectively.
[7]Values of 1.7, 1.5, 1.5 and 1.4 for AA light, AA heavy, BB light and BB heavy, respectively.
[8]Values of 1.6, 1.3, 1.5 and 1.3 for AA light, AA heavy, BB light and BB heavy, respectively.
See also Table 2 footnotes.

Slaughter traits

Carcass weight and carcass weight per day of age were significantly affected by breed type, genetic merit and slaughter weight but no interactions were detected (Table 6). Carcass weight of BB was 26 kg heavier ($P < 0.001$) than for AA, whereas carcass weight of the H animals was 18 kg heavier ($P < 0.001$) than for the L animals. There were corresponding breed type and genetic merit differences in carcass weight per day of age. The carcass weight difference between the light and heavy slaughter weight groups was

39 kg ($P < 0.001$). Kill-out proportion was higher for BB than AA ($P < 0.001$), for H than L genetic merit ($P < 0.05$), and for the heavy than for the light slaughter weight group ($P < 0.001$). There was a breed type × slaughter weight interaction ($P < 0.01$) for kill-out proportion due to a greater difference between the slaughter weight groups for AA than BB. Carcass conformation class was better ($P < 0.001$) for BB than AA but was unaffected by either genetic merit for carcass weight or slaughter weight. Carcass fat class was lower ($P < 0.001$) for BB than AA, was unaffected by genetic merit for carcass weight, and was higher ($P < 0.05$) for the heavy than for the light slaughter weight group. There was a breed type × genetic merit × slaughter weight interaction ($P < 0.05$) for carcass fat class because of a smaller difference between the light and heavy slaughter weight groups for BBH than for the other groups. Both perirenal plus retroperitoneal fat weight, and its proportion of carcass weight, were unaffected by breed type and genetic merit, but both were significantly greater for the heavy than for the light slaughter weight. There was a genetic merit × slaughter weight interaction ($P = 0.06$) for perirenal plus retroperitoneal fat proportion because of a greater difference between L and H for the light than for the heavy slaughter weight group.

Scaled for carcass weight, all carcass measurements except leg thickness were significantly lower for BB than AA. Similarly, all carcass measurements, except leg width and leg thickness, which were similar, were significantly lower for H than L. All carcass measurements scaled for carcass weight were lower ($P < 0.001$) for the heavy than for the light slaughter weight group. There were breed type × slaughter weight interactions for both carcass width ($P = 0.06$) and leg width ($P = 0.08$) scaled for carcass weight due to a greater decrease from the light to the heavy slaughter weight for AA than BB.

Carcass traits

The effects of breed, genetic merit and slaughter weight on hind quarter proportion, *m. longissimus* area and ribs joint composition are shown in Table 7. Hind quarter proportion was higher ($P < 0.001$) for BB than AA and for the light than for the heavy slaughter weight group, but there was no effect of genetic merit on hind quarter proportion. The *m. longissimus* area was greater ($P < 0.001$) for BB than AA and for the heavy than for the light slaughter weight group but again there was no effect of genetic merit. When *m. longissimus* area was scaled for carcass weight, breed effect persisted but slaughter weight effect disappeared. There were significant breed × slaughter weight interactions for both *m. longissimus* area ($P < 0.001$) and *m. longissimus* area scaled for carcass weight ($P < 0.01$) due to a greater increase from the light to the heavy slaughter weight for BB than AA.

Ribs joint bone proportion was not significantly affected by breed type but *m. longissimus*, other muscle and total muscle proportions were higher ($P < 0.001$), and fat proportion was lower ($P < 0.001$) for BB than AA. Ribs joint composition was not affected by genetic merit but bone ($P < 0.001$), muscle trim ($P < 0.01$) and total muscle ($P < 0.05$) proportions were lower, and fat proportion was higher ($P < 0.001$), for the heavy than for the light slaughter weight group. There were breed type × slaughter weight interactions for proportions of other muscle, muscle trim, total muscle and fat. The muscle proportion interactions ($P < 0.05$) were due to greater decreases with increasing slaughter weight for AA than BB, whereas the fat proportion interaction ($P = 0.07$) was due to a greater increase with increasing slaughter weight for AA than BB.

Table 7 *Carcass traits and ribs joint composition for steer progeny of Holstein–Friesian dams and AA and BB sires of L and H estimated genetic merit for carcass weight*

	AA		BB		Slaughter weight			Significance/probability			
Trait	L	H	L	H	Light	Heavy	s.e.	B	G	S	I
Pistola proportion (g/kg side)	455	459	471	469	470	457	2.21	***	ns	***	ns
Musculus longissimus (cm^2)	64.9	71.1	86.3	85.3	70.9	83.0	2.50	***	ns	***	B × S***[1]
M. longissimus (cm^2/kg carcass)	0.23	0.23	0.27	0.25	0.24	0.24	0.008	**	ns	ns	B × S**[2]
Ribs joint composition (g/kg)											
Bone	202	210	208	208	221	193	4.1	ns	ns	***	ns
M. longissimus	179	183	211	213	198	194	4.0	***	ns	ns	ns
Other muscle	230	245	277	292	253	269	7.1	***	ns	*	B × S*[3]
Muscle trim	194	178	170	162	188	164	7.8	$P = 0.08$	ns	**	B × S*[4]
Total muscle	603	602	657	666	638	626	7.3	***	ns	*	B × S*[5]
Fat	195	188	135	126	140	182	8.4	***	ns	***	B × S, $P = 0.07$[6]

AA = Aberdeen Angus; BB = Belgian Blue; L = low; H = high.
[1]Values of 65.1, 70.9, 76.6 and 95.0 for AA light, AA heavy, BB light and BB heavy, respectively.
[2]Values of 0.24, 0.22, 0.25 and 0.27 for AA Light, AA Heavy, BB Light and BB Heavy, respectively.
[3]Values of 223, 251, 283 and 287 for AA Light, AA Heavy, BB Light and BB Heavy, respectively.
[4]Values of 206, 165, 170 and 162 for AA Light, AA Heavy, BB Light and BB Heavy, respectively.
[5]Values of 614, 591, 662 and 661 for AA Light, AA Heavy, BB Light and BB Heavy, respectively.
[6]Values of 166, 218, 115 and 146 for AA Light, AA Heavy, BB Light and BB Heavy, respectively.
See Table 2 footnotes.

Table 8 *Subcutaneous fat colour and* m. longissimus *colour and chemical composition for steer progeny of Holstein–Friesian dams and AA and BB sires of L and H estimated genetic merit for carcass weight*

	AA		BB		Slaughter weight			Significance/probability			
Trait	L	H	L	H	Light	Heavy	s.e.	B	G	S	I
Fat colour[1]											
L (lightness)	67.0	67.1	65.8	65.2	65.8	66.8	0.42	**	ns	*	ns
a (redness)	11.3	11.5	10.8	10.9	11.4	10.9	0.33	ns	ns	ns	ns
b (yellowness)	22.8	23.1	22.3	23.0	21.9	23.6	0.50	ns	ns	***	ns
Hue	63.6	63.6	64.2	64.7	62.8	65.2	0.59	ns	ns	***	ns
Chroma	25.5	25.8	24.8	25.6	24.8	26.1	0.52	ns	ns	**	ns
m. longissimus colour[1]											
L (lightness)	38.8	38.8	40.6	39.9	38.5	40.5	0.37	*	ns	***	ns
a (redness)	13.1	13.3	12.1	12.6	13.1	12.5	0.36	$P = 0.08$	ns	ns	ns
b (yellowness)	8.7	8.7	8.9	9.0	8.6	9.1	0.16	ns	ns	*	ns
Hue	33.8	33.5	36.7	35.6	33.4	36.4	0.53	**	ns	***	ns
Chroma	15.7	15.9	15.1	15.5	15.7	15.4	0.38	ns	ns	ns	ns
m. longissimus composition (g/kg)											
Protein	221	223	227	226	225	223	1.32	**	ns	ns	ns
Moisture	716	726	741	740	735	726	2.29	***	ns	***	B × G, $P = 0.06$
Lipid	55	43	23	23	30	42	3.00	***	ns	***	ns

AA = Aberdeen Angus; BB = Belgian Blue; L = low; H = high.
[1]Hunterlab values; L (lightness) scale 0 (black) to 100 (white), a (redness) scale + (red) to − (green), b (yellowness) scale + (yellow) to − (blue), Hue = $[\tan^{-1}({}^{b}/_{a})] \times [180/\pi]$, Chroma (saturation/colour intensity) = $\sqrt{(a^2 + b^2)}$.
See also Table 2 footnotes.

Muscle traits

Subcutaneous fat and *m. longissimus* colour data, together with *m. longissimus* chemical composition, are shown in Table 8. Other than L (lightness) value, which was lower ($P < 0.01$) for BB, there was no effect of breed type or genetic merit on subcutaneous fat colour values. However, slaughter weight did affect subcutaneous fat colour values with significantly higher L (lightness), b (yellowness), chroma and hue values for the heavy than for the light slaughter weight group. *M. longissimus* had higher L (lightness; $P < 0.05$) and hue ($P < 0.01$) values for BB than AA and tended ($P = 0.08$) to have a lower a (redness) value. L (lightness; $P < 0.001$), b (yellowness; $P < 0.05$) and hue ($P < 0.001$) values for *m. longissimus* were also higher for the heavy than for the light slaughter weight group but were unaffected by genetic merit. There were no statistically significant interactions between the main effects for any colour traits measured.

M. longissimus chemical composition was significantly affected by both breed type and slaughter weight but not by genetic merit. BB had higher protein ($P < 0.01$) and moisture ($P < 0.001$) concentrations, and a lower ($P < 0.001$) lipid concentration, than AA, whereas the heavy slaughter weight animals had a lower ($P < 0.001$) moisture concentration and a higher ($P < 0.001$) lipid concentration than the light slaughter weight animals. There was a breed type × genetic merit interaction ($P = 0.06$) for moisture concentration, which was higher for AAH than AAL but not for BBH compared with BBL.

Discussion

Context of study

This study was comparable with those of Campion *et al.* (2009a and 2009b) insofar as it evaluated the effects of sire estimated genetic merit for carcass weight on a range of production and carcass traits. However, it differs from those of Campion *et al.* (2009a and 2009b) in that it did not include dairy strains, carcasses were not completely dissected and *m. longissimus* chemical composition was measured. Twelve of the 20 sires used in this study were common to the studies of Campion *et al.* (2009aand 2009b).

The AA and BB sire breeds were specifically chosen for the study because they represent extremes in fatness (at a fixed age/weight), carcass conformation and muscling (Kempster *et al.*, 1982; Keane, 2002). These traits may be differentially affected by changes in EPD_{CWT}. Progeny of these sire breeds are readily available from Irish dairy farms as AA is the beef breed of choice for crossing on dairy cows, whereas BB is the second most common late maturing beef breed used in dairy herds (AIM Bovine Statistics Report, 2008). Within both sire breeds, available EPD values for traits other than carcass weight were similar so the measured effects can reasonably be attributed to the difference in EPD_{CWT}.

Live weights and LW gains

As there were no significant differences between the breed types or genetic merit groups in birth or arrival dates these can be eliminated as affecting subsequent production traits.

BB were heavier than AA at arrival even though they were on average 4 days younger suggesting heavier birth weights. A similar conclusion can be inferred from the literature. Mee and Dings (1989) reported that BB sired calves had heavier birth weights than Friesian sired calves, while both Carter (1975) and Everitt *et al*. (1978) showed that Friesian calves were heavier than AA cross calves. The absence of differences between the genetic merit groups in arrival weight suggests no effect of EPD_{CWT} on birth weight. The differences between the breed types in live weights and slaughter weight were similar to these observed by Keane and Drennan (2008) and Keane and Moloney (2009). From arrival, when the mean LW difference was just 1 kg, live weights of the two genetic merit groups diverged consistently up to 30 kg at the time of the second housing. There was no further divergence during the second winter. This pattern of LW change over time is almost identical to that observed by Campion *et al*. (2009a) and similar to that reported by Clarke *et al*. (2009), who studied progeny from Irish beef cows. Unlike previously (Campion *et al*., 2009a), where breed type by genetic merit interactions for live weights were detected no such interactions were detected in this study, indicating that EPD_{CWT} effects were consistent across the two breed types. The 72 kg greater slaughter weight for the heavy compared with the light slaughter weight group was commensurate with their 76 days greater age.

The absence of significant LW gain differences between AA and BB but the generally higher numerical values for BB, supports previous findings (Keane and Drennan, 2008; Keane and Moloney, 2009; Campion *et al*., 2009a) as does the higher value for slaughter weight per day of age for BB (Keane and Moloney 2009; Campion *et al*., 2009a). Although from the end of the first grazing season LW was significantly greater for H than L, significant LW gain differences were not detectable in this period. However, slaughter weight per day of age was significantly greater for H. Campion *et al*. (2009a) also found that slaughter weight per day of age was greater for high EPD_{CWT} animals even though the only significant difference in LW gain was during the first grazing season. Thus, the results of all three studies (Clarke *et al*., 2009; Campion *et al*., 2009a and this study) that have evaluated the Irish beef genetic evaluation system agree that genetic merit for growth, as measured by $EPD_{CWT,}$ is more strongly expressed early in life than during finishing.

The lower LW gain during finishing for the heavy than for the light slaughter weight group reflects the decline in LW gain that occurs with increasing length of finishing period (Keane *et al*., 2006). Campion *et al*. (2009a) also reported a lower finishing LW gain for animals taken to a heavier slaughter weight. The higher daily gain from arrival to slaughter for the heavy slaughter weight group may appear at variance with their lower LW gain during finishing compared with the light slaughter weight group. This is explained by the fact that LW gain during finishing was higher than observed in earlier production phases. Thus, the longer finishing period of higher LW gain for the heavy slaughter weight group, when averaged over the entire period from arrival to slaughter, more than offset the higher LW gain over the shorter finishing period for the light slaughter weight group.

Feed intake

The absence of any difference between AA and BB in daily DM intake, together with the lower DM intake per kg LW for BB, agrees with the findings of Campion *et al*. (2009a). However, while the latter observed no significant effect of genetic merit on DM intake, in this study, H had a lower DM intake per kg LW than L. The decrease in DM intake per kg LW with increasing slaughter weight has been reported previously (Keane *et al*., 2006; Campion *et al*., 2009a) as has the decrease in efficiency of net energy utilisation for LW gain (Andersen, 1975; Bailey *et al*., 1985). Measured mean daily DM intake did not closely reflect the mean EPD_{DMI} value for the breed effect but did for the genetic merit effect. The measured mean breed effect was 0.17 kg DM/day compared with a mean EPD_{DMI} value of 0.72 kg/day, and the measured mean genetic merit effect was 0.06 kg/day compared with a mean EPD_{DMI} value of 0.17 kg/day. Similar findings were reported by Campion *et al*. (2009a). As feed intake is a function of LW it would seem that EPD_{DMI} value should either be scaled for LW or specified to a LW range.

Skeletal and muscular scores

The greater skeletal and muscular linear scores of BB compared with AA would be expected given the well-documented greater muscularity of the BB breed (Cuvelier *et al*., 2006) and they were also heavier. Campion *et al*. (2009a) evaluated various body measurements together with linear scores. Both skeletal and muscular scores were generally greater for BB than AA, whereas body measurements per kilogram LW were greater for AA. The differences between the genetic merit groups in skeletal scores paralleled the breed differences, in that the high genetic merit animals were heavier and had higher scores. Campion *et al*. (2009a) also found a genetic merit effect for average skeletal score but not for muscular score. The absence of differences between the genetic merit groups in muscular scores (other than hind quarter development) contrasts with the clearly evident breed differences.

Slaughter traits

The 26 kg extra carcass weight for BB over AA is mid-way between the values of 30 kg (Keane and Drennan, 2008) and 22 kg (Keane and Moloney, 2009) reported previously for the same breed types. Campion *et al*. (2009a) reported differences between AA and BB of 20 and 50 kg for high and low EPD_{CWT} animals, respectively. The 29 g/kg difference between AA and BB in kill-out proportion is identical to that observed by Campion *et al*. (2009a) and similar to the values of 24 g/kg (Keane and Drennan, 2008), 19 g/kg (Keane and Moloney, 2009) and 24 g/kg (Keane and Drennan, 2009) reported previously. The differences between AA and BB in carcass conformation and fat classes are also similar to values reported previously (Keane and Drennan, 2008 and 2009;

Keane and Moloney, 2009). The lower values for all carcass measurements except leg thickness for BB compared with AA, indicate greater carcass compactness for BB and support earlier findings (Keane and Drennan, 2008 and 2009; Keane and Moloney, 2009; Campion *et al*., 2009a).

The carcass weight superiority for H over L of 23 kg for AA and 13 kg for BB compare with corresponding EPD_{CWT} values of 19 and 8 kg, respectively. When carcass weight is the measure of life-time growth rate (as in the ICBF beef genetic index), it is theoretically possible that all of the difference in carcass weight arising from a difference in $EPD_{CWT,}$ could be due to a difference in kill-out proportion. Keane and Diskin (2007) estimated that about one-third of the extra carcass weight from higher sire EPD_{CWT} was due to a higher kill-out proportion and Campion *et al*. (2009a) reported a superior ($P = 0.06$) kill-out proportion for higher EPD_{CWT} animals. These findings suggest that animals of higher genetic merit for carcass weight may have a higher kill-out proportion, and that the entire EPD_{CWT} effect may not be reflected in live weight. The proportions of the carcass weight differences between L and H due to differences in kill-out proportion in this study were about 15% for AA and 55% for BB.

The absence of differences between H and L in carcass conformation and fat classes suggests that EPD_{CWT} has no effect on carcass classification grades. Although this would be expected at constant carcass weight, it is of interest to compare the effects of an increase in carcass weight attributable to higher EPD_{CWT} with that due to later slaughter. Within breed type, carcass conformation class normally increases with increasing carcass weight (Steen and Kilpatrick, 1995; Keane *et al*., 2006). Although in this study the increase (0.16 class) in carcass conformation class from the light to the heavy slaughter weight was not statistically significant, the numerical increase for a fixed increment of carcass weight was greater for the slaughter weight effect than for the genetic merit effect (0.041 *v.* 0.028 class per 10 kg carcass weight).

In contrast to carcass conformation class, carcass fat class did differ significantly for the light and heavy slaughter weight groups. Across the two breed types, the carcass fat class increase per 10 kg increase in carcass weight was 0.118 due to heavier slaughter weight compared with 0.022 due to higher $EPD_{CWT.}$ This suggests that the onset and/or rate of fattening were retarded (relative to carcass weight) in the higher genetic merit animals, and that both genetic groups were of similar fatness at similar ages rather than at similar slaughter weights. For both AA and BB, perirenal plus retroperitoneal fat weight was marginally lower for the H animals even though carcass weight was 18 kg higher. This also suggests delayed fat deposition relative to carcass weight.

Carcass traits

The 13 g/kg greater hind quarter proportion for BB over AA compares with previous values of 18 g/kg (Keane and Drennan, 2008), 17 g/kg (Keane and Drennan, 2009), 20 g/kg (Keane and Moloney, 2009) and 17 g/kg (Campion *et al*., 2009b). The absence of a difference between the breeds in ribs joint bone proportion also agrees with previous findings (Keane and Drennan, 2008; Keane and Moloney, 2009), whereas the higher *m. longissimus*, other muscle and total muscle proportions, together with the lower fat proportion of BB compared with AA, have been documented previously (Keane and Drennan, 2008; Keane and Moloney, 2009; Campion *et al*., 2009b). It is noteworthy that even though all other muscle proportions were higher for BB, muscle trim proportion tended ($P = 0.08$) to be higher for AA. This may reflect the greater fragmentation of the AA muscle associated with the removal of the higher proportion of fat, resulting in muscle portions categorised as other muscle for BB being included as trim for AA. The absence of significant effects of genetic merit on pistola proportion, *m. longissimus* area, ribs joint composition or *m. longissimus* chemical composition supports the findings of Keane and Diskin (2007) and Campion *et al*. (2009b).

There are inconsistencies in the literature on whether genetic differences in growth rate should be accompanied by differences in carcass or muscle composition. As the rate of protein accretion is a function of the relative rates of protein synthesis and degradation, more rapidly growing animals should have a higher ratio of synthesis to degradation than slower growing animals (Castro Bulle *et al*., 2007). However, this would not necessarily result in a higher muscle protein concentration or muscle proportion in the carcass if the higher protein synthesis was matched by higher rates of lipid and mineral deposition in faster growing animals. Castro Bulle *et al*. (2007) confirmed a higher rate of protein gain in animals selected for higher growth rate but as fat gain was even higher, the high growth rate animals were actually fatter as indicated by carcass back fat thickness. In contrast, Oddy *et al*. (1998) observed that cattle selected for high growth rate had lower rates of both protein synthesis and degradation than those selected for low growth rate. However, both the high and low growth rate lines had similar subcutaneous fatness levels.

As the H animals in this study had heavier carcasses, a difference in carcass composition would be expected due to its association with carcass weight (Keane *et al*., 2006). Compared with L, the H carcasses were 18 kg heavier, and compared with the light slaughter weight, the heavy slaughter weight carcasses were 39 kg heavier. Thus, if the association of carcass weight and compositional traits was independent of the reason for the carcass weight difference, then the genetic merit effects on carcass composition would be proportional to the slaughter weight effects. This was not so; the effects of an increase in slaughter weight due to later slaughter were much greater than those due to higher EPD_{CWT}. From the light to the heavy slaughter weight, pistola proportion decreased by 13 g/kg. On this basis, a 6 g/kg decrease would be expected due to the higher EPD_{CWT} but there was actually an increase of 1 g/kg. Similarly, ribs joint bone proportion decreased by 28 g/kg from the light to the heavy slaughter weight but increased by 4 g/kg from the L to H genetic merit. Total muscle proportion decreased by 12 g/kg from the light to the heavy slaughter weight but

increased by 4 g/kg from the L to H genetic merit, and fat proportion increased by 42 g/kg from the light to the heavy slaughter weight but decreased by 8 g/kg from the L to the H genetic merit. Taken together these data indicate that an increment of carcass weight due to higher EPD_{CWT} had less effect on carcass composition than a comparable increment due to delayed slaughter. Thus, animals of higher EPD_{CWT} can be taken to the carcass weight commensurate with their growth genetic potential without affecting carcass composition.

Fat and muscle colour and muscle composition

There are few published reports on fat colour with which the present data can be directly compared. Dunne *et al*. (2004) measured the fat colour of BB (but not AA) and two strains of Holstein–Friesians and found little difference in L (lightness) value. The increases in fat yellowness, hue and chroma values with increasing slaughter weight reflect either the longer finishing period or the greater age of the animals at slaughter (Dunne *et al*., 2009). As the finishing diet contained grass silage the heavy slaughter weight animals received carotenoids for a longer period. Assuming only a small or negligible turnover of these carotenoids, once deposited in the fat, their extended accumulation in the heavy slaughter weight group would have accounted for the increased yellowness. That the heavy slaughter weight animals were fatter than their light slaughter weight counterparts indicates ongoing triacylglycerol accumulation in their adipose tissue, and β-carotene, which is responsible for much of the variation in yellowness of bovine fat (Dunne *et al*., 2006), can be simultaneously incorporated into the adipose tissue with triacylglycerols (Arias *et al*., 2009). The greater yellowness, hue and chroma values for the heavy slaughter weight group suggest that carotenoid accumulation matched that of triacylglycerols.

The higher *m. longissimus* L (lightness) value for BB compared with AA agrees with the findings of Campion *et al*. (2009b). Although the BB animals did not exhibit muscular hypertrophy phenotypically, their higher L (lightness) value may have been associated with this condition as such animals have lower myoglobin content (Fiems *et al*., 1995) and a higher muscle L (lightness) value (Van Eenaeme *et al*., 1997). Dunne *et al*. (2004) also observed that the progeny of BB bulls had a higher muscle L (lightness) value than progeny of Holstein–Friesian bulls whereas Cuvelier *et al*. (2006) reported a significantly higher L (lightness) value for BB than for AA bulls. The lower a (redness) value for BB compared with AA agrees with the findings of Cuvelier *et al*. (2006) but is at variance with the findings of both Dunne *et al*. (2004) and Campion *et al*. (2009b). The difference in hue value reflects the differences in the a (redness) and b (yellowness) values from which it was calculated.

That there were no genetic merit effects on *m. longissimus* colour traits is consistent with there being no compositional effects, but it is at variance with the findings of Campion *et al*. (2009b) who did observe a lower L (lightness) value for higher EPD_{CWT} animals. The available data on the effects of slaughter weight on muscle colour traits are inconsistent. Campion *et al*. (2009b) found that both L (lightness) and hue values decreased with increasing slaughter weight, whereas Dunne *et al*. (2004) found no consistent effect of slaughter weight. Differences between experiments in growth to any particular slaughter weight mean that animals reach similar slaughter weights at different ages (Shorthose and Harris, 1991). Thus, anomalies or inconsistencies in colour values are not surprising as muscle surface colour may reflect intramuscular lipid (Muir *et al*., 1998) and pigment (Boccard *et al*., 1979) contents as well as the type and distribution of muscle fibres (Lefaucheur 2010), all of which change with age and growth rate.

M. longissimus chemical compositional differences are consistent with the physical composition of the ribs joint. The higher protein and moisture, and lower lipid concentrations of BB compared with AA reflect the higher muscle and lower fat proportions in the ribs joint of BB. Similarly, the absence of any significant effect of genetic merit on chemical composition is consistent with the absence of a genetic merit effect on ribs joint composition. The lower moisture and higher lipid concentration of *m. longissimus* from the heavy slaughter weight animals would be expected from their lower ribs joint muscle and higher ribs joint fat proportions. A close relationship between muscle chemical composition and carcass physical composition has been widely documented (Berg and Butterfield, 1976; Keane *et al*., 1990 and 1991; Robelin and Tulloh, 1992).

Conclusions

It is concluded that differences in growth rate of AA and BB were small, particularly in animals of high genetic merit for carcass weight. However, because of a higher kill-out proportion, BB had heavier carcasses, which were of better conformation and lower fatness. All skeletal and muscular scores were superior for BB, and carcass measurements scaled for carcass weight were lower, indicating greater carcass compactness. Animals of higher genetic merit generally had higher LW gains resulting in a higher slaughter weight per day of age. They also had a higher kill-out proportion but there was no difference in carcass conformation or carcass fatness. The EPD_{CWT} difference between the L and H genetic groups was 19 kg for AA and 8 kg for BB. The measured carcass weight differences were 23 kg for AA and 13 kg for BB. A greater proportion of the extra carcass weight attributable to higher EPD_{CWT} was due to a higher kill-out proportion for BB than AA. Although breed × genetic merit interactions were not significant, the differences between the breeds in growth rate and slaughter weight tended to be greater for L than for H. For example, the differences between AA and BB for L were 43 g slaughter weight per day of age and 31 kg slaughter weight. The corresponding differences for H were 16 g slaughter weight per day of age and 5 kg slaughter weight.

Daily feed DM intake was not affected by breed type or genetic merit but DM intake per kg LW was lower for BB and H than for AA and L, respectively. While DM intake increased

with increasing slaughter weight, it did so more slowly and as a result DM intake per kg LW decreased. Efficiency of net energy utilisation for LW gain was 18% poorer for the heavy than for the light slaughter weight group.

Delaying slaughter date increased slaughter weight, carcass weight and carcass fatness. It also reduced the proportion of pistola in the carcass, the proportions of bone and muscle in the ribs joint and the proportions of moisture and protein in *m. longissimus*. It increased the proportion of fat in the ribs joint and the proportion of lipid in *m. longissimus*. None of these effects were associated with the increase in carcass weight attributable to higher EPD_{CWT}. Thus, an increment of carcass weight due to higher EPD_{CWT} is more valuable than a similar increment due to a delay in slaughter because it comprises higher proportions of pistola and muscle and a lower proportion of fat. As carcass conformation improves with increasing carcass weight due to delayed slaughter but not due to higher $EPD_{CWT,}$ it follows that where carcass payment is based on conformation, the better-conformed carcasses from delayed slaughter receive a premium even though they have lower proportions of pistola and muscle. In contrast, the higher pistola and muscle proportions of higher EPD_{CWT} carcasses go unrewarded because conformation is not correspondingly improved.

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