Irish Journal of Agricultural and Food Research **46:** 63–76, 2007

Performance and carcass traits of progeny of Limousin sires differing in genetic merit

M.G. Keane[1]† and M.G. Diskin[2]
[1]*Teagasc, Grange Research Centre, Dunsany, Co. Meath*
[2]*Teagasc, Athenry Research Centre, Athenry, Co. Galway*

Genetic indices for growth and carcass classification are published for beef sires used in Ireland for artificial insemination (AI). The objective of this study was to compare growth and carcass traits of progeny of Limousin sires of low and high genetic index for growth. A total of 70 progeny (42 males and 28 females) out of predominantly Holstein-Friesian cows by 7 AI Limousin sires were reared together to slaughter. The 7 sires were classified as low (n=3) or high (n=4) index based on their published genetic index for growth. The male progeny were reared entire and all animals were slaughtered at about 20 months of age. Carcasses were classified for conformation and fatness, and a rib joint (ribs 6 to 10) was separated into fat, muscle and bone. Growth rate did not differ significantly between the index groups but tended to be higher for the high index progeny. This higher growth rate, combined with a significantly higher kill out proportion, resulted in carcass weight and carcass weight per day of age being significantly higher for the high index progeny. Carcass conformation and fat class were not affected by genetic index, nor was the composition of the rib joint. Compared with males, females had a significantly lower growth rate and kill out proportion and, consequently, had a significantly lower carcass weight. The proportions of fat and bone in the rib joint were significantly higher, and the proportion of muscle was significantly lower for females than for males. It is concluded that carcass weight reflected sire group genetic index for growth but feed intake, carcass classification and rib joint composition were not affected.

Keywords: beef cattle; bulls; carcass traits; genetic index; heifers

†Corresponding author: gerry.keane@teagasc.ie

Introduction

A genetic improvement programme for Irish beef cattle is being implemented by the Irish Cattle Breeding Federation (ICBF), the objectives of which are to improve growth, carcass, calving and maternal traits (Amer *et al*., 2001). For sires, growth genetic index is defined in terms of carcass weight, carcass traits are defined as carcass conformation class and carcass fat class according to the EU Beef Carcass Classification Scheme (Commission of the European Communities, 1982), and calving traits are defined as calving difficulty, calf mortality and gestation length (ICBF, 2006).

Prior to the establishment of ICBF, the genetic merit of Irish beef sires was expressed in index form relative to the respective breed mean and the sire ranking was expressed relative to the base population (Grogan, 2000). Following the establishment of ICBF this changed, and the genetic indices of the sires then in use were converted to expected progeny differences (EPD) expressed in the units of measurement of the traits. Rather than report these units in absolute terms, which would not make comparisons of sires easy, they are reported relative to a common baseline of Holstein-Friesian sires, which had earlier been used as link sires in the beef progeny test programme. The conversion from the index form to the EPD units of trait form occurred during the course of the present study, so the sires used here were chosen on their index values.

Of the traits for which genetic values are published, growth (expressed as carcass weight) is the most important because live animals are traded, and carcasses are paid for predominantly on the basis of weight. Carcass grades are less important in Ireland than in other EU countries because the price differentials between the various categories are smaller (Drennan, 2002). While mindful of the importance of genetic merit for growth, it is also important to establish if there are associated effects on other traits, such as feed intake and carcass composition.

The objective of this study was to compare growth, feed intake, slaughter traits and carcass traits of progeny from Limousin sires originally of low or high genetic index for growth.

Materials and Methods

A total of 70 spring-born progeny (42 males and 28 females) out of Holstein-Friesian dairy cows (48) and Limousin × (Limousin × Hereford) beef heifers (22), by 7 Limousin artificial insemination (AI) bulls were reared together from a mean of 24 days after birth to slaughter. The 7 sires were classified on the basis of their original genetic index as Low (L; n=3) or High (H; n=4) for growth. There were 16 male and 14 female progeny of L sires (14, 12 and 4 per sire) and 26 male and 14 female progeny of H sires (16, 10, 7 and 7 per sire). All 7 sires had progeny from dairy cows (26 H and 22 L) and 5 (3 H and 2 L) of the sires had progeny from beef heifers (14 H and 8 L). The males were reared entire. In addition to their growth index, the sires also had genetic index values for carcass conformation class and carcass fat class. Twenty-four of the female and 28 of the male progeny were the result of planned matings in Teagasc research and college herds (these included the 22 calves from the beef heifers, which were born at Grange Research Centre). The remaining 4 females and 14 males were sourced from commercial dairy farms where the sires of interest had been used. All calves were tagged shortly after birth and those born outside Grange were transferred to Grange within 4 weeks of birth.

Calf rearing was as described by Fallon and Harte (1987). Calves were individu-

ally penned and offered 25 kg milk powder (205 g/kg fat) over a 42-day period. Hay was available *ad libitum* and calf concentrate (750 g/kg coarsely rolled barley, 50 g/kg molasses, 175 g/kg soya bean meal and 25 g/kg mineral vitamin premix) was offered *ad libitum* to a maximum of 2 kg per head daily. All calves were turned out to pasture on 31 May and rotationally grazed together until 4 October. Concentrate feeding (1 kg per head daily) continued for 4 weeks after turnout. At 3, 8 and 13 weeks after turnout animals were treated with ivermectin (Ivomec, MSD Agvet) for the control of gastrointestinal parasites. The male and female calves were separated on 4 October and from then until housing on 8 November they received 1 kg per head daily of cattle concentrate (875 g/kg rolled barley, 50 g/kg molasses, 60 g/kg soya bean meal and 15 g/kg mineral/ration mix). The duration of the first grazing season was 161 days.

During the first winter the animals were accommodated in a slatted shed and offered grass silage (dry matter (DM) 193 g/kg, crude protein (CP) 137 g/kg DM, *in vitro* DM digestibility (IVDMD) 689 g/kg, pH 3.9, estimated metabolisable energy (ME) concentration 10.1 MJ/kg DM) *ad libitum* plus 1.5 kg cattle concentrate per head daily. At 2 weeks after housing, animals were treated with oxfendazole (Synantic, Schering Plough) to control gastrointestinal parasites. Twice during the winter all animals were treated with deltamethrin (Spot-on, Hoechst Roussel Uclaf) to control skin lice. The duration of the winter feeding period was 140 days. The animals were then let to pasture (28 March) to prevent the possibility of lameness developing during the subsequent finishing period on a high concentrate diet in a slatted shed.

The animals were housed again on 16 May and offered the same grass silage as offered during the previous winter for 42 days until 27 June. Cattle concentrate was then introduced and gradually increased to *ad libitum* intake by 1 August. From then until slaughter on 20 November (females) or 27 November (males), concentrate was available *ad libitum*. To maintain normal rumen function the animals were also offered 1 kg silage DM per head daily. For the finishing period, the animals were moved to a separate shed and trained to use Calan-Broadbent doors for individual feed intake measurement over 42 days. One week before slaughter of the females, body measurements (height at withers, height at pelvis, back length, chest width and depth, pelvic width and circumference of round) were recorded. The mean interval from birth to slaughter was 607 days for females and 615 days for males. The corresponding intervals from arrival at Grange to slaughter were 584 and 590 days.

After slaughter at a commercial meat plant, cold carcass weight (0.98 of hot weight) and weight of perirenal plus retroperitoneal fat were recorded. Carcasses were classified for conformation and fatness according to the European Union Beef Carcass Classification Scheme (Commission of the European Communities, 1982). Carcass measurements (De Boer *et al.,* 1974) were also recorded for carcass and leg length, carcass and round width, and round thickness and circumference. After a 24 h chilling period (4 ^{o}C) the right side of each carcass was cut along the caudal edge of the 5th rib and through the spinal column. The abdominal muscles were separated from those of the pelvic limb and the side was cut along the edge of the *m. iliocostalis lumborum* through the ribs to the earlier cut at the 5th rib (Williams and Bergstrom, 1980). This divided the side into a pistola hind quarter (i.e., the hind quarter to the 5th rib without the area on the abdominal side of the *m. iliocostalis lumborum*) and a fore quarter

that included this area (Keane and Allen, 1998). The quarters were then weighed. A rib joint (ribs 6 to 10) was removed from the pistola (by cutting between the 10th and 11th ribs) and taken to the meat laboratory where it was placed in a chill (4 °C) for 24 h. Subcutaneous fat depth and *m. longissimus* area were measured at the 10th rib. The rib joint was weighed and separated into subcutaneous fat, intermuscular fat, *m. longissimus*, other muscle, bone and *ligamentum nuchae*. The latter was included with bone in the statistical analysis. A sample of *m. longissimus* at the 10th rib was chemically analysed for moisture, protein and lipid concentrations.

Statistical analysis

The data were statistically analysed as a 2 × 2 factorial using Proc MIXED of the Statistical Analysis Systems Institute (SAS, 2002–2003). Animal gender was included in the model as a fixed effect and genetic index of the sire was included as either a class variable or continuous variable. Sire and location of birth (Teagasc farm, commercial farm or Grange Research Centre) were included as random effects with a compound symmetry correlation structure assumed among records within sire and location of birth. Relevant growth and carcass variables were linearly regressed on the sire index values. Generally, the best fit model had a common slope and separate intercepts for each gender. The data are presented as main effects and where interactions occur the individual values are shown in footnotes.

Results

The sire codes and their breeding values in the original index form, in the converted EPD units of trait, and the current economically weighted beef production index are shown in Table 1. Weighted for

Table 1. Genetic index values for Limousin sires of High or Low genetic index for growth

Genetic index	Sire code	No. of progeny	Index[1]			Converted units of trait (EPD)[2]			BPSI[6] 2006 (€)
			Carcass	Conformation	Lean	Carcass[3]	Conformation[4]	Lean[5]	
Low	FL10	14	87	104	103	4.5	0.94	0.20	3
	CEE	12	107	111	96	17.0	1.00	0.07	46
	PAL	4	97	104	114	6.8	0.92	0.30	7
	Mean[7]		96	107	102	9.8	0.96	0.16	21
High	FL18	7	115	117	99	22.4	1.06	0.12	30
	DAD	7	123	119	108	27.7	1.06	0.24	73
	DWB	10	129	105	108	30.1	0.93	0.20	65
	PYR	16	128	126	83	32.3	1.15	−0.03	57
	Mean[7]		125	118	96	29.2	1.06	0.10	58

[1] Relative to breed mean = 100 and s.d. = 10, Department of Agriculture and Food (1998).
[2] Expected progeny difference (EPD) relative to 26-month old Friesian steers of 350 kg carcass weight, Irish Cattle Breeding Federation (2000), Genetic evaluation results of all beef sires tested to date, http://www.icbf.com/documents/all progeny-beef.htm.
[3] Expressed as carcass weight.
[4] Carcass conformation class.
[5] Equal to 200 – fatness index.
[6] Current beef production economic index.
[7] Weighted by number progeny per sire.

the number of progeny per sire, mean index of the H sires was 29 points higher for growth, 11 points higher for carcass conformation and 6 points lower for carcass leanness. The corresponding differences for EPD units of trait were 19.4 kg carcass, 0.1 units carcass conformation and –0.06 units carcass leanness. The economically weighted mean difference between the groups (2006 evaluation) was €37.

Live weight and gain

Live weight and feed intake of the progeny by genetic index group and gender are shown in Table 2. There was no genetic index × gender interaction for any of the live weight or feed intake measurements. At no time was the difference between the genetic index groups in live weight statistically significant, but the H progeny had numerically greater live weight at all times and the difference increased over time. At final weighing, the difference in favour of the H was 20 kg, which was close to statistical significance ($P < 0.08$). The males were significantly heavier than the females at all times throughout life except at turnout as calves.

Live-weight gains, together with slaughter and carcass weights per day of age, are shown in Table 3. There was no genetic index × gender interaction for any of the variables shown. The effect of genetic index on live-weight gain was not significant at any time, but live-weight gain was always numerically higher for the H progeny other than during calf rearing and the 7 week pasture period in the second grazing season. Carcass weight per day of age was significantly higher for the H progeny. Except for the periods from arrival to first turnout, and from second turnout to the start of *ad libitum* concentrate feeding, live-weight

Table 2. Live weight and feed intake for male and female progeny of Low and High genetic index Limousin sires

	Index (I)		Gender (G)		s.e.[1]	Significance[2]	
	Low	High	Male	Female		I	G
Live weight (kg) at:							
Start[3]	45.2	47.4	49.1	43.5	1.55		***
1st Turnout (31 May)	71.0	82.1	78.4	74.8	6.97		
1st Housing (8 November)	170	179	186	163	6.6		***
2nd Turnout (28 March)	252	266	274	243	8.0		***
2nd Housing (16 May)	275	288	299	264	8.3		***
Concentrates *ad libitum* (1 August)[4]	343	355	373	325	7.9		***
Last weigh day (31 October)[5]	486	506	540	452	8.8	$P < 0.08$	***
Slaughter[6]	507	528	567	468	10.3		***
Daily concentrate intake[7] (kg)	8.5	8.6	9.2	7.8	0.13		***

[1] For n = 30 (Low Index) in this and subsequent tables.
[2] There was no significant Index × Gender interaction for any trait.
[3] Including birth weight of those born at Grange.
[4] Start of *ad libitum* concentrate feeding.
[5] On which all animals were present.
[6] 20 November (females) and 27 November (males).
[7] During individual intake measurement.

Table 3. Live-weight and carcass gains of male and female progeny of Low and High genetic index Limousin sires

	Duration (days)	Index (I)		Gender (G)		s.e.	Significance[1]	
		Low	High	Male	Female		I	G
Live weight gain (g/day) from:								
Arrival to 1st turnout	46	667	565	621	611	57.2		
1st Turnout to 1st housing	161	615	619	674	560	33.3		**
1st Housing to 2nd turnout	140	584	615	632	567	21.6		*
2nd Turnout to 2nd housing	49	472	457	494	434	80.2		
2nd Housing to 1 August (concentrates *ad libitum*)	77	881	900	972	810	59.4		
1 August to slaughter	111 (118)[2]	1425	1497	1643	1279	41.4		***
Arrival to slaughter	587[3]	797	807	879	725	14.3		***
Slaughter weight for age (g/day)	611[4]	836	860	923	773	14.2		***
Carcass weight for age (g/day)	611[4]	456	478	513	421	7.8	*	***

[1] There was no significant Index × Gender interaction for any trait.
[2] Value for males.
[3] 584, 590, 590 and 584 days for Low, High, Male and Female, respectively.
[4] 610, 612, 615 and 607 for Low, High, Male and Female, respectively.

gain was significantly higher for males than females. Both slaughter weight and carcass weight per day of age were also significantly higher for the males.

Carcass traits

There was no genetic index × gender interaction for any slaughter traits except carcass fat class, which was higher for L than H males but higher for H than L females (Table 4). Both kill out proportion and carcass weight were significantly higher for the H progeny. There was no difference in carcass classification score or in perirenal plus retroperitoneal fat weight or proportion due to genetic index group. All carcass traits, except carcass conformation ($P < 0.08$), were

Table 4. Slaughter traits of male and female progeny of Low and High genetic index Limousin sires

Variable	Index (I)		Gender (G)		s.e.	Significance	
	Low	High	Male	Female		I	G
Kill out proportion (g/kg)	545	558	557	545	4.7	*	**
Carcass weight (kg)	276.5	296.1	316.5	256.1	7.69	*	***
Carcass conformation class[1]	3.00	3.09	3.20	2.89	0.188		*
Carcass fat class[2,3]	4.00	4.06	3.93	4.13	0.078		*
Perirenal + retroperitoneal fat weight (kg)	7.8	7.8	6.4	9.2	0.35		***
Perirenal + retroperitoneal fat[4] (g/kg)	28.5	26.9	19.7	35.8	1.56		***

[1] EU Beef Carcass Classification Scheme: scale 1 (poorest) to 5 (best).
[2] EU Beef Carcass Classification Scheme: scale 1 (leanest) to 5 (fattest).
[3] I × G interaction ($P < 0.05$); values for Male Low, Male High, Female Low and Female High were 4.01, 3.86, 3.99 and 4.26, respectively.
[4] As proportion of carcass weight.

significantly affected by gender. Males had a significantly greater carcass weight and kill out proportion, and tended ($P < 0.08$) to have better carcass conformation. Females had a significantly higher carcass fat class and a significantly greater weight and proportion of perirenal plus retroperitoneal fat.

There was no genetic index × gender interaction for any of the scaled live animal or carcass measurements (Table 5). Body measurements scaled for live weight did not differ significantly between the sire index groups, but for all measurements except chest width and pelvic width, the L progeny had numerically higher values. All carcass measurements scaled for carcass weight were significantly ($P < 0.07$ for leg thickness) greater for the L progeny. Taken together, the live animal and carcass measurements indicate that the L carcasses were less compact (longer per unit weight) but this was not reflected in carcass conformation although it was slightly poorer for the L progeny. All live animal and carcass measurements scaled for carcass weight were significantly lower for males than females indicating more compact carcasses for the males.

Other than subcutaneous fat proportion which was higher for L males but lower for L females, there was no genetic index × gender interaction for any of the carcass or rib joint composition measurements (Table 6). Pistola weight as a proportion of the side weight was greater ($P < 0.01$) for the L than for the H progeny. Fat depth and *m. longissimus* area, both absolutely and scaled for carcass weight, were not affected by genetic index. Females had a higher ($P < 0.01$) proportion of their side weight in the pistola than males, while *m. longissimus* area was greater ($P < 0.001$) for males. When *m. longissimus* area was scaled for carcass weight however, there was no significant effect of gender.

With the exception of other muscle, which was greater for the high index progeny,

Table 5. Live animal and carcass measurements for male and female progeny of Low and High genetic index Limousin sires

Variable	Index (I)		Gender (G)		s.e.	Significance[1]	
	Low	High	Male	Female		I	G
Body measurements (cm/kg live weight)							
Height at withers	0.249	0.244	0.228	0.263	0.0035		***
Height at pelvis	0.263	0.258	0.242	0.280	0.0036		***
Back length	0.244	0.237	0.229	0.252	0.0035		***
Chest width	0.094	0.095	0.086	0.102	0.0016		***
Chest depth	0.131	0.127	0.121	0.137	0.0012		***
Pelvic width	0.099	0.099	0.093	0.105	0.0020		***
Round circumference	0.383	0.375	0.352	0.406	0.0045		***
Carcass measurements (cm/kg carcass)							
Carcass length	0.460	0.435	0.411	0.484	0.0118	*	***
Carcass width	0.175	0.163	0.154	0.183	0.0037	*	***
Leg length	0.253	0.238	0.226	0.266	0.0062	*	***
Leg width	0.145	0.139	0.135	0.149	0.0023	*	***
Leg thickness	0.093	0.090	0.084	0.099	0.0013	$P < 0.07$	***
Round circumference	0.420	0.402	0.377	0.445	0.0056	*	***

[1] There were no significant Index × Gender interactions.

Table 6. Carcass traits, rib joint composition and *m. longissimus* chemical composition of male and female progeny of Low and High genetic index Limousin sires

Variable	Index (I)		Gender (G)		s.e.	Significance	
	Low	High	Male	Female		I	G
Pistola weight (g/kg side weight)	475	467	467	475	2.93	*	**
Fat depth (mm)	11.4	12.3	12.0	11.7	0.52		
M. longissimus area (cm^2)	96.2	100.4	107.1	89.5	2.81		***
M. longissimus area (cm^2/kg carcass weight)	0.348	0.343	0.339	0.352	0.0071		
Rib joint composition (g/kg)							
Subcutaneous fat[1]	75	78	72	80	2.4		*
Intermuscular fat	165	156	146	175	5.3		***
M. longissimus et thoracis	223	216	222	217	4.5		
Other muscle	371	388	401	358	6.9	*	***
Total fat	240	235	219	256	7.5		***
Total muscle	594	604	623	575	6.7		***
Total bone	166	160	158	168	4.5		**
M. longissimus compositon (g/kg)							
Moisture	738	739	738	739	2.4		
Protein[2]	222	223	227	218	1.2		***
Lipid	34	31	28	37	1.5		***

[1] I × G interaction ($P < 0.05$), values for Male Low, Male High, Female Low and Female High of 74, 71, 75 and 86, respectively.
[2] I × G interaction ($P < 0.05$), values for Male Low, Male High, Female Low and Female High of 216, 220, 228 and 225, respectively.

rib joint composition was not significantly affected by genetic index, but the proportions of all rib joint tissues were significantly affected by gender. Females had more subcutaneous, intermuscular and total fat, more bone, and less other muscle and total muscle than males. There was no effect of genetic index on the *m. longissimus* chemical composition, but males had higher ($P < 0.001$) protein and lower ($P < 0.001$) lipid concentrations than females.

Regression on genetic values

The regressions of growth and carcass traits on the original sire genetic index values are shown in Table 7. The regressions of slaughter weight per day of age and carcass weight per day of age on sire index for growth were not statistically significant, although in both instances the coefficients were positive, indicating a trend towards greater slaughter and carcass weights per day of age, with increasing genetic index for growth. Slaughter and carcass weights per day of age were not significantly related to conformation index, but the coefficients were positive, indicating a tendency towards higher growth in progeny of higher conformation index sires. There was no relationship between carcass conformation class and sire conformation index. Kill out proportion was not significantly related to sire conformation index either, but again, the coefficient was positive. Rib joint muscle proportion increased significantly with increasing sire conformation index. The relationship between bone proportion and conformation index was not significant but the coefficient was negative, indicating a trend towards a decrease in

Table 7. Regressions of growth and carcass traits on the original genetic index values of Limousin sires

Original index	Intercept		s.e.[1]	Slope	s.e.	R^2	Significance	
	Male	Female					Model	Slope
Growth index								
Slaughter weight per day[2]	854	698	68.0	0.64	0.588	0.50	***	
Carcass weight per day[2]	451	356	41.1	0.57	0.356	0.51	***	
Conformation index								
Slaughter weight per day[2]	861	703	139.0	0.58	1.210	0.49	***	
Carcass weight per day[2]	471	370	88.3	0.57	0.767	0.49	***	
Carcass conformation class	2.80	2.58	0.940	0.003	0.0082	0.02		
Kill out proportion	505	494	26.8	0.45	0.233	0.14	***	
Pistola proportion[3]	251	256	13.2	–0.15	0.114	0.11	***	
Rib joint muscle proportion	479	431	47.1	1.26	0.409	0.49	***	**
Rib joint bone proportion	171	181	25.9	–0.10	0.225	0.08	**	
M. longissimus area[4]	0.354	0.367	0.069	–0.0001	0.0006	0.001		
Lean index								
Carcass fat class	4.65	4.88	0.524	-0.008	0.0053	0.08	*	
Perirenal + retroperitoneal fat proportion[5]	14.4	30.2	6.42	0.059	0.0648	0.72	***	
Rib joint fat proportion	157	196	39.7	0.61	0.401	0.30	***	

[1] For male.
[2] From birth.
[3] Of carcass weight.
[4] Per kg carcass weight.
[5] Per kg carcass weight.

bone proportion with increasing sire conformation index. There was no evidence of a relationship between *m. longissimus* area scaled for carcass weight and conformation index. Carcass fat class was not significantly related to sire index for leanness, but the coefficient was negative indicating a trend in the expected direction.

Discussion

Sire selection

At the commencement of this study the genetic values for Irish beef sires were expressed in index form using best linear unbiased predication (BLUP) methodology (Department of Agriculture and Food, 1998). BLUP derived deviations were scaled to a standard deviation of 10 and expressed relative to a breed mean of 100. Later, these indices were converted to EPDs expressed in units of the original measurement and are reported on an across-breed basis. Heretofore, Holstein-Friesian sires were used as link sires in the beef progeny test programme so their breeding values now serve as the base against which the beef sire EPDs are calculated (Grogan, 2000). Thus, the EPD value of a beef sire for growth is the extra carcass weight, over the base (350 kg), of his steer progeny out of Holstein-Friesian cows slaughtered at 26 months of age. The Beef Carcass Classification (Commission of the European Communities, 1982) conformation and fat classes are expressed

as EPDs on the EUROP grid scale. The alphabetic conformation scores are converted to a numeric scale by replacing EUROP with 5, 4, 3, 2, 1, respectively. The beef sire values are expressed relative to the Holstein-Friesian steer progeny test base of 2.02 for conformation class and 3.39 for fat class.

The present study had fewer progeny per sire and fewer sires than originally intended. Initially it was planned to select 5 sires each with a growth index of 100 or less and 5 with a growth index of 120 or more but at the time there were not 5 Limousin AI sires in each of these categories in commercial use. Consequently, one sire (CEE) with an index of 107 was selected in the L category and one sire (FL18) with an index of 115 was selected in the H category. (In the most recently published sire evaluations, these two sires have exchanged ranking and CEE has now a somewhat higher beef production index value than FL18). In addition to being unable to obtain progeny from 5 sires in each category, over 30 calves from one high index sire and two low index sires were lost from the study because of tuberculosis outbreaks on their farms of birth.

The mean difference between the L and H sires was 29 units (96 v. 125) of growth index or an EPD of 19.4 kg carcass (9.8 kg v. 29.2 kg). No account was taken of carcass conformation or fat scores when selecting the sires but the H sires had 11 units index (EPD 0.1 of a class) better conformation, and 6 units index (EPD 0.06 of a class) lower leanness than the L sires. Genotyping of calves to confirm sire parentage was not considered necessary as 52 of the animals came from Teagasc herds with accurate records and the remainder came from commercial farms that had used only the one AI beef sire of interest.

Live animal and carcass weights and gains

The differences in growth and live weight between males and females were in the expected range. Yearling weight was about 30 kg greater for males, which is similar to the value reported by Drennan, Davis and O'Neill (2000). There are few comparisons of bulls and heifers reared together to slaughter at the same age. Keane and Drennan (1987) reared heifers and anabolic implanted steers together to slaughter. The implanted steers, which can be considered similar to bulls in growth rate (Keane, 1988), were 113 kg heavier than the non-implanted heifers at slaughter. This is in good agreement with the 101 kg difference between the males and females in the present study at a lower slaughter age. The growth difference between males and females provides a perspective for the magnitude of differences between the genetic index groups. Although these differences were not significant for any period, lifetime live-weight gains were consistently higher for the high merit progeny and amounted to 24 g slaughter weight per day of age. When combined with the 13 g/kg greater kill out proportion, the outcome was a significantly greater 22 g carcass weight per day of age for the high merit animals.

As the current growth genetic index of sires is expressed as carcass weight rather than live weight, there is no indication if the differences in carcass weight are due to differences in live weight, or differences in kill out proportion, or both. Strict interpretation of the present results, where live-weight gain did not differ significantly but kill out proportion did, would imply that the difference between the genetic index groups in carcass weight per day of age were due entirely to a difference in kill out proportion. A more pragmatic interpretation, however, is that both live-weight gain and kill out proportion contributed. The

22 g/day difference between the genetic index groups in carcass weight per day of age comprised about 13 g/day slaughter weight per day of age (the difference in slaughter weight per day of age multiplied by the mean kill out proportion) and 9 g/day kill out proportion.

Slaughter and carcass weights per day were 150 and 92 g, respectively greater for males than females. Keane and Drennan (1987) reported corresponding values of 154 and 99 g/day for the differences between heifers and anabolic implanted steers. Despite a difference between the genders of over 60 kg in carcass weight, the difference in carcass conformation was small and not significant. Similarly, the difference in carcass fat class, although significant, was small despite the quite large differences in perirenal plus retroperitoneal fat weight and proportion, and rib joint fat proportion.

Carcass measurements and classification scores

The absence of significant differences between the genetic index groups in live animal measurements was surprising considering that most carcass measurement differences were significant. Because complete restraint is impractical, live animal measurements, especially on bulls, are likely to be more variable than carcass measurements. The differences between the genetic index groups for carcass measurements were relatively large compared with the small differences in carcass conformation, indicating that carcass conformation is a poor indicator of carcass compactness (carcass length measurements per unit weight). The significantly greater values for females than for males of all live animal and carcass measurements (scaled for carcass weight), is in line with general experience. Keane and Allen (1998) showed that bulls have lower carcass measurements than steers, and steers in turn have lower body measurements (scaled for weight) than heifers (Keane and Drennan, 1990). Despite the large differences between the genders in carcass measurements, and by extension compactness, the difference in carcass conformation class was numerically small and not significant.

Better carcass conformation and compactness is popularly associated with a higher proportion of side weight in the hind quarter. However, in the present study, it was the L animals, with their poorer carcass conformation and compactness, that had a significantly higher proportion of their side weight in the pistola. Clearly, better carcass conformation and compactness do not necessarily indicate a greater proportion of hind quarter.

Compared with the males, the females, which tended to have poorer carcass conformation and were significantly less compact, had a higher proportion of their side weight in the hind quarter. The differences between genders in this respect are well documented. Keane and Allen (1998) showed that steers have a higher proportion of pistola than bulls, and Keane and Drennan (1990) showed that heifers have a higher proportion of high-priced meat cuts than steers. The similarity in *m. longissimus* area scaled for carcass weight for males and females agrees with earlier findings (Keane and Drennan, 1990; Keane and Allen, 1998). Fat depth was not a good indicator of true fatness as indicated either by perirenal plus retroperitoneal fat weight and proportion or rib joint fat proportion.

Carcass composition

While there was no significant effect of genetic index on rib joint composition, the H carcasses were heavier, and so would be expected to have higher fat, lower bone

and lower muscle proportions (Keane *et al.,* 1990). They did have a slightly lower bone proportion, but they also had somewhat lower fat and higher muscle proportions. Using the equations of Moloney and Keane (2001), the composition of the "extra" carcass weight of the H animals was estimated as 140 g/kg bone, 745 g/kg muscle and 115 g/kg fat. This indicates that the 19.6 kg extra carcass weight of the H animals yielded 14.6 kg extra muscle. The higher fat and lower muscle proportions of females compared to males is in agreement with previous findings (Keane and Drennan, 1987).

There are few published reports with which the present data can be directly compared. Most publications in this area relate to animals that have been differentially selected over a number of generations for various traits rather than for animals that are the progeny of sires differing in genetic index for growth. In a comparison of Angus cattle previously selected for high and low growth rate, the low growth rate line had a slower rate of protein accretion than the high growth rate line (Dobos and Oddy, 1997), which appeared to be due to a higher rate of protein degradation in the low growth rate line (Oddy *et al.,* 1998). Despite the differences in rate of protein accretion there was no difference between the growth lines in subcutaneous fatness implying that fat accretion was proportional to protein accretion thus keeping body composition similar for the two lines.

Regressions on genetic values

Generally, the regression equations show that relationships between the measured traits and genetic indices were poor. There is a widespread perception in the cattle industry that live animal (and carcass) conformation is positively associated with growth rate, kill out proportion, hind quarter proportion, carcass muscle proportion and muscle size. Although the proportion of carcass conformation variance explained by conformation genetic index was small, the higher index group did have somewhat better carcass conformation and significantly better compactness as indicated by carcass measurements. In addition, they also had a higher growth rate, a higher kill out proportion and a higher proportion of muscle in the rib joint (only the kill out difference was statistically significant). However, they did not have a greater *m. longissimus* area and they actually had a lower pistola proportion.

As for carcass conformation, carcass fat class genetic index accounted for little of the variation in carcass fat but it was closely related to perirenal plus retroperitoneal fat proportion and moderately related to rib joint fat proportion. It is probable that these measured continuous variables are better indicators of carcass fatness than a class variable such as fat class. In the present study, the vast majority of carcasses within a gender would have fallen into one of two fat classes.

Feed efficiency

Cattle selected for high and low growth rate do not necessarily respond in the same way to changes in nutrition. As level of feeding is increased, cattle selected for high growth increase protein gain through reductions in both synthesis and degradation, whereas cattle selected for low growth rate increase protein gain by increasing both synthesis and degradation (Oddy *et al.,* 1998). This suggests that low growth rate animals have inherently higher rates of muscle protein turnover than high growth rate animals. In the present study, there was no evidence of a differential response to feeding level between the two genetic groups. The animals were on a low to moderate plane of nutrition

up to the start of finishing and were then on a high plane of nutrition during finishing. There was no difference in relative growth rate during finishing compared to earlier for the two genetic groups. High growth rate cattle are considered to be more efficient in converting feed to live-weight gain, which is more likely due to reduced maintenance requirements than to increased efficiency of gain, as composition of the gain is not altered (Herd, Speck and Wynn, 1991). In line with the present results, Parnell *et al.* (1994) reported that, at the same age, animals selected for high growth rate had heavier carcasses but there was no difference in carcass composition. At the same carcass weight however, which was reached earlier, the high growth rate selected animals tended to be leaner.

It has been shown that steers selected for high growth rate consumed less feed per unit live weight to reach any particular live weight target, and so had higher feed efficiency (Herd, Speck and Wynn, 1991; Parnell *et al*., 1994). This greater efficiency was largely due to the need to maintain their body weight for a shorter time as a consequence of their higher growth rate, rather than to increased efficiency of feed use for live-weight gain. Thus, if taken to the same slaughter age (as in the present study) the higher maintenance requirement of the greater body weight of the high merit animals would likely offset any advantage in live-weight gain efficiency thus leaving gross feed efficiency unaltered.

Conclusions

It is concluded that the progeny of sires of high genetic index for growth produced heavier carcasses than progeny of low growth genetic index sires. About two-thirds of the extra carcass weight was due to higher live-weight gain and one third was due to a higher kill out proportion. There was no difference between the progeny groups in feed intake. While there was little difference in carcass conformation, the high index progeny had more compact carcasses, as indicated by carcass measurements scaled for carcass weight. High index progeny had a lower proportion of pistola in the side weight, but there was no difference in rib joint composition between the two genetic index groups. Males grew faster, had a higher kill out proportion, better carcass conformation and a lower carcass fat class than females. They also had more compact carcasses with less fat and bone and more muscle. There were no biologically important interactions between genetic index and gender.

Acknowledgements

The authors thank Mr. T. Darby, Mr. J. Farrell and Mr. E. Vesey for skilled technical assistance, Mr. B. Duffy for expert care and management of the animals, the staff of Grange Laboratories for feed analysis and Dr. D. Berry for statistical analysis and helpful comments on the manuscript.

References

Amer, P.R., Simm, G., Keane, M.G., Diskin, M.G. and Wickham, B.W. 2001. Breeding objectives for beef cattle in Ireland. *Livestock Production Science* **67**: 223–239.

Commission of the European Communities. 1982. Commission of the European Communities (Beef Carcass Classification) Regulations. Council Regulations 1358/80, 1208/82. Commission Regulations 2930/81, 563/82, 1557/82. Commission of the European Communities, Brussels.

De Boer, H., Dumont, B.L., Pomeroy, R.W. and Weniger, J.H. 1974. Manual on EAAP reference methods for the assessment of carcass characteristics in cattle. *Livestock Production Science* **1**: 151–164.

Department of Agriculture and Food. 1998. Genetic values for growth, carcass and calving ease traits for beef AI bulls. Department of Agriculture and Food, Dublin, 11 pages.

Dobos, R.C. and Oddy, V.H. 1997. Protein accretion and compensatory growth. In: "Proceedings

Growth and Development Workshop, Co-operative Research Centre for the Cattle and Beef Industry" (Ed. D.W. Hennessy, S.R. McLennan and V.H. Oddy), University of New South Wales, Armidale, Australia.

Drennan, M. 2002. Important factors in suckler beef production and influence of calving season on income. *Irish Grassland and Animal Production Association Journal* **36**: 129–136.

Drennan, M.J., Davis, W. and O'Neill, B.J. 2000. Suckler beef systems. In: "Profitable Production of Quality Beef" (Ed. M.G. Keane), Teagasc, pages 18–22.

Fallon, R.J. and Harte, F.J. 1987. Calf feeding and management. Beef Series No. 1, An Foras Talúntais, Dublin, 26 pages.

Grogan, A.J. 2000. Beef genetic evaluations for 2000 and future developments. Irish Cattle Breeding Federation, 6 pages.

ICBF (Irish Cattle Breeding Federation). 2006. Economic indexes for selection of beef cattle in Ireland – current status. ICBF publication, 27 pages.

Herd, R.M., Speck, P.A. and Wynn, P.C. 1991. Feed requirements for maintenance and growth of 1-year old Angus steers selected for either fast or slow yearling growth rate. *Australian Journal of Experimental Agriculture* **31**: 591–595.

Keane, M.G. 1988. Beef production in the absence of anabolic agents. *Irish Grassland and Animal Production Association Journal* **22**: 79–92.

Keane, M.G. and Allen, P. 1998. Effects of production system intensity on performance, carcass composition and meat quality of beef cattle. *Livestock Production Science* **56**: 203–214.

Keane, M.G. and Drennan, M.J. 1987. Lifetime growth and carcass composition of heifers and steers non-implanted or sequentially implanted with anabolic agents. *Animal Production* **45**: 359–369.

Keane, M.G. and Drennan, M.J. 1990. Comparison of growth and carcass composition of heifers in three production systems and steers, and effects of implantation with anabolic agents. *Irish Journal of Agricultural and Food Research* **29**: 1–13.

Keane, M.G., More O'Ferrall, G.J., Connolly, J. and Allen, P. 1990. Carcass composition of serially slaughtered Friesian, Hereford × Friesian and Charolais × Friesian steers finished on two dietary energy levels. *Animal Production* **50**: 231–243.

Moloney, A.P. and Keane, M.G. 2001. The relationship between plasma creatinine concentration or 6–10th rib joint composition and skeletal muscle weight in cattle. Proceedings of the Agricultural Research Forum, 2001, Ireland, page 69.

Oddy, V.H., Herd, R.M., McDonagh, M.B., Woodgate, R., Quinn, C.A. and Zirkler, K. 1998. Effect of divergent selection for yearling growth rate on protein metabolism in hind-limb muscle and whole body of Angus cattle. *Livestock Production Science* **56**: 225–231.

Parnell, P.F., Herd, R.M., Perry, D. and Bootle, B. 1994. The Trangie Experiment – responses in growth rate, size, maternal ability, reproductive performance, carcass composition, feed requirements and herd profitability. *Proceedings of the Australian Society of Animal Production* **20**: 17–20.

SAS 2002–2003. Version 9.1. SAS Institute Inc., Cary, NC, USA.

Williams, D.R. and Bergstrom, P.L. 1980. Anatomical jointing, tissue separation and weight recording proposed as the EEC standard method for beef. Commission of the European Communities, Brussels, EUR 6878EN, 27 pages.

Received 25 April 2005