Evaluation of beef genetic merit for growth rate in beef x dairy steers

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Abstract
The objective was to compare productivity and slaughter traits for progeny of Holstein-Friesian cows sired by bulls of Aberdeen Angus (AA) and Belgian Blue (BB) beef breeds selected for either low (L) or high (H) genetic merit for growth. Straight-bred Friesian (FR) and Holstein (HO) calves were also included. A total of 170 animals were used in the study and were slaughtered at either light (560 kg) or heavy (620 kg) weights. Slaughter and carcass weights per day of age for AAH, AAL, BBH, BBL, FR and HO were 782, 719, 795, 793, 804 and 783 (s.e. 12.9) g, and 415, 372, 438, 436, 413 and 401 (s.e. 5.8) g, respectively. There were significant interactions between genetic merit for growth and beef breed with the difference between L and H largely expressed for AA only. It is concluded that using beef sires of high genetic merit growth increases growth rate and carcass weight of the progeny but the effect may not be similar for all beef breeds.
Keywords: beef breeds, carcass, cattle, dairy breeds, genetic merit.

Introduction
In Ireland, beef genetic evaluations are carried out on an across-breed basis and traits are economically weighed to produce a total merit index. For dairy beef production, growth rate comprises ~70% of the monetary value of the total merit index. Breeding value for growth rate is expressed as expected progeny difference for carcass weight (EPD_{CWT}). The objective of this study was to evaluate EPD_{CWT} under standard production conditions.

Materials and Methods
Spring-born male progeny out of Holstein-Friesian cows and Aberdeen Angus (AA; 10 sires) and Belgian Blue (BB; 13 sires) sires of either high (H; 13 sires) or low (L; 10 sires) EPD_{CWT} were used. Pure-bred Friesians (FR; 7 sires) and Holsteins (HO; 12 sires) were also included. In total, 170 animals with sire verification, distributed across 6 genetic groups, namely AAH (n = 32), AAL (n = 24), BBH (n = 31), BBL (n = 27), FR (n = 28) and HO (n = 28) were reared to slaughter. At the start of the second (finishing) winter, the animals were assigned from within genetic group and sire to light and heavy slaughter weights of 560 kg and 620 kg, respectively. Dry matter intake (DMI) was recorded for all animals and ultrasonic measurements of *m. longissimus* and fat depth at the 3rd lumbar vertebra were recorded. Data were analysed using mixed model methodology with sire as a random effect and week of age and parity of dam as factors. When the dependent variables were slaughter group related, genetic group, slaughter group, and age nested within slaughter group, were included as fixed effects. In all analyses, the individual animal was considered the experimental unit. Contrast statements were used to partition the variation into orthogonal components namely H v L, AA v BB, interaction between genetic merit and beef breed, FR v HO, beef breeds v. dairy strains, slaughter group, and relevant interactions.

Results and Discussion
Mean sire EPD_{CWT} values, weighted by number of progeny per sire, for AAH, AAL, BBH, BBL, FR and HO were 3.4, -13.4, 26.7, 13.0, -8.1 and 0.9 kg, respectively. Slaughter weight, slaughter weight per day of age, carcass weight and carcass weight per day of age were significantly greater for H than L (Table 1). However, because of significant genetic merit x beef breed interactions, all these effects were evident for AA only. Slaughter weight, *m. longissimus* depth, kill-out proportion, carcass weight, together with slaughter and carcass weights per day of age, were all significantly higher for BB than AA, while DMI and fat depth were lower. Compared to HO, *m. longissimus* depth, fat depth, and kill-out proportion were significantly higher for FR. Compared with the beef breeds, the dairy strains were significantly heavier and had a significantly greater slaughter weight per day of age. However, these differences were mainly between the dairy strains and AA, with BB generally similar to the dairy strains. The beef breeds had greater *m. longissimus* depth and superior feed efficiency to the dairy strains. Despite a significantly higher kill-out proportion for the beef breeds, there was no significant difference in carcass weight per day of age. *M. longissimus* and fat depths, together with kill-out proportion and carcass weight, increased significantly with increasing slaughter weight, while relative feed intake and feed efficiency declined.

Conclusions
With increasing genetic merit for growth, live weights and carcass weight increased for AA but not for BB. DMI and feed efficiency were not affected by genetic merit and the extra weight due to H was not accompanied by any increase in fatness. BB were superior to AA for all important production traits other than feed efficiency which was not different. FR had greater *m. longissimus* and fat depths, and a higher kill-out proportion than HO, but slaughter weight and carcass weight were not significantly different. Kill-out proportion, fat depth and carcass weight increased with increasing slaughter weight while relative feed intake and feed efficiency decreased.

Table 1. Effects of genetic merit, beef breed and dairy strain on live weight and slaughter traits.

	AA		BB		Dairy		S (kg)[1]				Significance of contrasts[1]				
	H	L	H	L	FR	HO	560	620	s.e[2]	G[1]	B	G x B	D	A	S
Slaughter weight (kg)	596	547	605	605	612	597	565	623	10.0	**	***	*	NS	*	***
DMI (g/kg LW)	20.6	21.3	20.1	20.2	20.5	21.1	21.5	19.8	0.25	NS	**	NS	NS	NS	***
Efficiency[3]	93	92	93	98	78	87	95	85	4.9	NS	NS	NS	NS	**	***
M. longissimus (mm)	65.7	62.4	70.0	70.9	65.2	60.0	63.5	67.9	0.96	NS	***	*	***	***	***
Fat depth (mm)	4.7	4.6	2.0	2.2	3.9	2.9	2.9	3.8	0.25	NS	***	NS	**	NS	***
Slaughter LW (g/day)[4]	782	719	795	793	804	783	779	779	12.8	**	**	*	NS	*	NS
Carcass (kg)	314	283	334	333	317	305	294	335	4.7	***	***	**	NS	NS	***
Kill-out (g/kg)	527	518	553	553	519	511	523	537	3.3	NS	***	NS	*	***	***
Carcass (g/day)[4]	415	372	438	436	413	401	406	419	5.8	***	***	***	NS	NS	*

[1]G = H v L; B = AA v BB; D = FR v HO; A = Beef v Dairy; S = Slaughter group; [2]Pooled standard error for genetic group; [3]LW gain/Unite Fourragere Viande;
[4]Of age; DMI = dry matter intake; LW = live weight.