Predicted carcass meat yield and primal cut yields in cattle divergent in genetic merit for a terminal index

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ABSTRACT: Several studies have clearly demonstrated the favorable impact of genetic selection on increasing beef cattle performance within the farm gate. Few studies, however, have attempted to quantify the value of genetic selection to downstream sectors of the beef industry, such as the meat processing sector. The objective of the current study was to characterize detailed carcass attributes of animals divergent in genetic merit for a terminal index as well as individual measures of genetic merit for carcass weight, conformation, and fat. The data used consisted of 53,674 young bulls and steers slaughtered between the years 2010 and 2013 in multiple Irish processing plants. All animals had a genetic evaluation as well as phenotypic measures of carcass characteristics. A terminal index, based on pedigree index for calving performance, feed intake, and carcass traits, calculated from the Irish national genetic evaluations, was obtained for each animal. Animals were categorized into four terminal index groups based on genetic merit estimates derived prior to the expression of the carcass phenotype by the animal. The association between genetic merit for terminal index with predicted phenotypic carcass red meat yield, carcass fat, carcass bone, and carcass composition, as well as between genetic merit for carcass weight, conformation, and fat with predicted phenotypic carcass red meat yield and composition were all quantified using linear mixed models. A greater terminal index value was associated with, on average, heavier phenotypic weights of each wholesale cut category. A greater terminal index value was also associated with a greater weight of meat and bone, but reduced carcass fat. Relative to animals in the lowest 25% genetic merit group, animals in the highest 25% genetic merit group had, on average, a greater predicted yield of very high value cuts (4.52 kg), high value cuts (13.13 kg), medium value cuts (6.06 kg), low value cuts (13.25 kg) as well as more total meat yield (37 kg). The results from the present study clearly signify a benefit to meat processors from breeding programs for terminal characteristics; coupled with the previously documented benefits to the producer, the benefits of breeding programs across the entire food production chain are obvious.

Key words: beef, carcass, carcass cuts, genetic merit

INTRODUCTION

The majority of published studies to date which have used large data sets to quantify the association

between animal genetic merit and phenotypic performance have been confined to comparison of parameters contributing to performance traits within the farm gate, such as live weight, average daily gain (ADG), weaning weight, age at slaughter, age at first calving, calving interval, and calving ease. Several studies, both at the (small) experimental level (Campion et al., 2009; Clarke et al., 2009a) and using larger (national) databases (McHugh et al., 2011; Connolly et al., 2016), have clearly demonstrated the favorable impact of genetic selection on increasing on-farm animal performance. Previously, for example, Connolly et al. (2016) reported that genetically superior animals (i.e., top 25% for a terminal index) produced, on average, a 38.7 kg heavier carcass, with 2.21 units greater carcass conformation, and 0.82 units less fat [based on the 1 to 15 linear scales, as outlined by Englishby et al. (2016)], compared to animals in the bottom 25% based on a terminal index. Genetically elite animals (i.e., top 25%) were, on average, slaughtered at a younger age, with superior carcass characteristics resulting in carcasses worth €187 more than the bottom 25% on genetic merit (Connolly et al., 2016). These monetary differences were, however, based on economic parameters realized within the farm gate (Connolly et al., 2016).

Few studies have attempted to quantify the value of genetic selection in cattle to downstream sectors of the beef industry, particularly the meat processing sector. One notable study in cattle by Moore et al. (2014) revealed that beef carcasses with the same weight, conformation, and fat score, based on the EUROP grading system, had a retail value differential of up to £100 (€114) between carcasses based on video image analysis (VIA) predicted retail yield for the meat processer, while incurring the same cost at purchase. Economic and production efficiency at the meat processor level is dictated by red meat yield, especially the proportion of higher value cuts, fat, and bone within the carcass (Drennan, 2006). Therefore, animals with a greater quantity of higher value cuts, with less fat and less bone, are favored by meat processors due to greater carcass value (Drennan et al., 2009). Sustainable beef production is a considerable challenge facing the beef industry (Kristensen et al., 2014); hence, producing carcasses with a higher proportion of red meat yield, with less fat and bone, would have a positive marketing impact on beef processing. However, measuring detailed carcass characteristics on a sufficiently large population of animals, from which to generate accurate genetic evaluations for these traits, is prohibitively expensive. Thus, carcass-related genetic evaluations in cattle are generally limited to traits which are routinely measured on all animals, such as carcass weight, carcass conformation, and fat-related characteristics (Englishby et al., 2016). It is important to highlight that VIA and other associated technologies are rapidly improving the ability to generate quality yield information on slaughtered animals and for use in genetic evaluations. The United Kingdom now has routine genetic evaluations based on predicted VIA yields measured in the abattoir. Given this, the tools are available to select animals based on the actual traits of interest to the abattoirs, which may aid accelerated genetic gain in more granular carcass metrics. Genetic analysis of a large database has clearly shown that greater carcass conformation, as measured within the European Union (EU), is positively correlated with a greater yield of higher value cuts when standardized to the same carcass weight (Pabiou et al., 2011). Furthermore, evidence exists, albeit based on a limited study population, which shows that cattle ranked higher for a terminal index composed of genetic merit for carcass weight, conformation, and fat score, yielded less fat and bone but more total meat compared to their lower genetic merit counterparts (Clarke et al., 2009b).

The objective of the current study was to characterize detailed carcass attributes of animals divergent in genetic merit for a terminal index as well as individual measures of genetic merit for carcass weight, conformation, and fat. The phenotypic carcass characteristics chosen were those of particular interest to the meat processing sector and included red meat yield (stratified into different primal cuts based on retail value), carcass fat, bone, and both the hind- and forequarter yield of each carcass; all measures were predicted from video image analyses. Results from this study should help instill confidence among processors that current breeding objectives are generating a more desirable animal for meat processors.

MATERIALS AND METHODS

A detailed description of the data available, as well as the editing producers used, and their justification, is provided in Connolly et al. (2016) but is summarized below. The data used in the present study were obtained from a preexisting database managed by the Irish Cattle Breeding Federation (ICBF). Therefore, it was not necessary to obtain animal care and use committee approval in advance of conducting this study.

Phenotypic Data

Cold carcass weight, conformation, and fat information were available from the ICBF database

on 6,701,105 animals slaughtered between the years 2010 and 2013. Carcass fat and conformation are scored on a 15-point scale (Englishby et al., 2016) using VIA mechanical grading. Four groups of wholesale cut weights, henceforth referred to as wholesale cuts, were also generated from the VIA of each carcass, as described in detail by Pabiou et al. (2011); the individual cuts contributing to each wholesale cut group are based on retail value (Pabiou et al., 2009). The lower value cut (LVC) group includes fore- and hind-shins (shank), ribs 1 to 6, ribs 7 to 13, flank, brisket, neck, and lean trimmings. The medium value cut (MVC) group includes the weight of the shoulder [i.e., clod (beef chuck), blade steak, braising muscle, chuck tender, leg of mutton cut (LMC), and the chuck cuts]. The high value cut (HVC) group includes the sirloin (i.e., rump and tail of rump) and the round [i.e., silverside, topside, knuckle, salmon cut (part of the round in the United States)] cut weights. The very high value cut (VHVC) group comprises of the weights of the rib-roast [i.e., cap of ribs, cube roll (i.e., ribeye boneless)], striploin, and fillet (i.e., tenderloin). Total carcass meat weight, total carcass fat weight, and total bone weight are also routinely predicted from the VIA (Pabiou et al., 2011). Herein, the phenotypes of total meat, fat, and bone weight will be referred to as "overall weight." Carcass cut values were determined from a single point in time (March 2017), and were sourced from the Meat Trades Journal and from personal communications with meat industry experts.

Genetic Merit

Individual animal predicted transmitting ability (PTA) for the traits contributing to the Irish terminal index, as well as the terminal index values themselves, were available from the ICBF for the April 2010 Irish domestic genetic evaluations. Genetic evaluations in Ireland are multi-breed and are undertaken three times annually for each of the suites of traits: carcass, calving performance, live-animal linear scores, docility, milkability, and cow fertility. Most Irish beef cattle are crossbred and hence all evaluations adjust for the heterosis and recombination loss coefficient of the animal, as well as breed differences via the use of genetic groups in the genetic evaluation. Further details on the ICBF genetic evaluations are outlined in Connolly et al. (2016) and Evans et al. (2007, 2009).

Estimated breeding values (EBVs) for all traits in the present study were calculated for each animal as the sum of the sire PTA and dam PTA for the respective trait based on the April 2010 national genetic evaluation. A terminal index for each animal was calculated as (Connolly et al., 2016):

$$
\begin{aligned}
\text{Terminal index} = {} & -€5.27 * \text{calving difficulty EBV} \\
& -€1.72 * \text{gestation length EBV} \\
& -€5.34 * \text{mortality EBV} \\
& -€47.55 * \text{feed intake EBV} \\
& +€2.95 * \text{carcass weight EBV} \\
& +€14.77 * \text{carcass conformation EBV} \\
& -€7.86 * \text{carcass fat EBV.}
\end{aligned}
$$

Animals were categorized into four terminal index groups based on individual genetic merit (Connolly et al., 2016) as: 1) very high terminal index, 2) high terminal index, 3) low terminal index, and 4) very low terminal index groups. The thresholds imposed to distinguish between terminal index groups were chosen to achieve a relatively similar differential in mean terminal index between adjacent terminal index groups. This was undertaken within dairy-herd and beef-herd animals separately, and the categories subsequently combined resulting in four terminal index groups across all data, but with dairy-herd and beef-herd animals represented in each terminal index group (Connolly et al., 2016).

Data Edits

Only carcass data from young bulls and steers born between the years 2009 and 2010 were retained; predictions of whole sale cuts are currently not available for heifers. Only animals with a known sire and dam, each with a genetic evaluation for each trait were retained, due to the fact it would not be possible to accurately derive the genetic merit of an individual (without genomics) if the sire was not known. Following these edits, 239,821 records remained. Further data edits were introduced to remove animals with no VIA predicted cut yields or no VIA predicted overall weights. Bulls >24 mo of age at slaughter were not considered in the present study. Steers with a carcass price outside the range of €2.50/kg and €5.50/kg and young bulls with a carcass price outside the range of €2.80/kg and €5.50/kg were discarded. Only carcass weight records between 180 and 550 kg for steers and between 150 and 550 kg for young bulls were retained. Following these edits, 219,417 records remained.

Animals slaughtered younger than 1 yr of age were discarded. Animals from dams calving at <22 mo of age were also discarded, as were animals from dams calving >18 mo from the median age per parity. Only records from parity 1 to 10 cows were

retained and parity was categorized as 1, 2, 3, 4, and ≥5. Following edits, 156,433 records remained. Animals were categorized as born in a dairy herd or born in a beef herd and will henceforth be referred to as dairy-herd or beef-herd animals. The distinction was made by herd since dairy-herd calves are bucket reared, while beef-herd calves are allowed to suckle their dam for several months.

Contemporary group was defined as herd-year-season-sex of slaughter; in the present study, sex refers to either bull or steer. The definition of herd-year-season-sex was based on the algorithm described by Schmitz et al. (1991) and Crump et al. (1997) and used in previous Irish genetic studies (McHugh et al., 2011, 2014; Berry et al., 2013; Connolly et al., 2016). The algorithm is based on grouping the same-sex animals from the same herd slaughtered in close proximity. In the present study, all cattle of the same sex, within the same herd, slaughtered within 10 d of each other, were grouped together. Only contemporary groups with five or more records were retained. Following edits, observations from 53,674 carcasses were available for analysis.

Statistical Analyses

The association between terminal index value with phenotypic carcass red meat yield and composition, as well as the association between carcass weight, carcass conformation, and carcass fat EBV with phenotypic carcass red meat yield and composition, were all quantified using mixed models in ASREML (Gilmour et al., 2009); contemporary group of herd-year-season-sex of slaughter was included in all models as a random effect. The dependent variable was either a wholesale cut yield (i.e., VHVC, HVC, MVC, LVC) or carcass composition yield (i.e., total meat yield, total bone yield, total fat yield, total forequarter or total hindquarter yield).

Fixed effects considered in all models were terminal index, dam parity (1, 2, 3, 4, 5+), whether the animal was a singleton or a twin, sex (i.e., bull, steer), age at slaughter in months, and whether or not the animal was from a dairy herd or a beef herd (i.e., dairy, beef). Terminal index was considered as either a continuous variable or as a class variable with four levels. In a separate series of analysis, phenotypic carcass weight was included as a covariate in the model to quantify the difference in the dependent variables between the genetic merit groups when standardized to a common carcass weight. When terminal index was included as a class effect with four levels, a covariate expressing the difference between the animal's terminal index value and terminal index center-point of the index group was also included in the model. In a separate analysis, predicted phenotypic wholesale cut yield (sum of VHVC, HVC, MVC, and LVC) was included as a covariate in the model to quantify the difference in the dependent variables (i.e., individual carcass wholesale cut yields and carcass composition) between the genetic merit groups when standardized to a common predicted total wholesale cut yield. Two-way interactions between sex (i.e., steer or young bull) and herd type (i.e., dairy or beef) with terminal index were also tested for significance in the mixed model.

RESULTS

Linear Regression Coefficients

A greater terminal index value was associated ($P < 0.01$) with, on average, heavier weights of each wholesale cut category (Table 1). Although the association differed ($P < 0.01$) by both herd type of origin and sex for HVC and by sex for VHVC ($P < 0.01$), the interaction was biologically of little consequence. A greater terminal index value was also associated ($P < 0.01$) with, on average, greater meat and bone yield, but reduced carcass fat yield, and although the association differed ($P < 0.01$) by both herd type of origin and sex, the interaction was biologically of little consequence (Table 2). A greater terminal index value was associated ($P < 0.01$) with, on average, more hindquarter yield and more forequarter yield, although the association differed ($P < 0.01$) by both herd type and sex for hindquarter yield and sex for forequarter yield (Table 3).

An increase in carcass weight EBV or carcass conformation EBV was associated ($P < 0.01$) with, on average, heavier weights of each wholesale cut category (Table 1). In contrast, an increase in carcass fat EBV was associated ($P < 0.01$) with a reduction in weight for each wholesale cut category (Table 1), which was relatively consistent between steers and young bulls. The associated reduction in wholesale cut yield for every unit increase in carcass fat EBV, with the exception of LVC cut yield, was greater in animals originating from beef herds (Table 1). An increase in carcass weight EBV or carcass conformation EBV was associated ($P < 0.01$) with an increase in meat yield, fat yield (Table 2), hindquarter yield, and forequarter yield (Table 3).

Table 1. The phenotypic change (SE in parenthesis)* in LVC, MVC, HVC, and VHVC per unit change in terminal index, carcass conformation estimated breeding value (EBV; Cconf EBV), carcass fat EBV (Cfat EBV), and carcass weight EBV (Carcwt EBV) for all animals, just dairy-herd animals, and just beef-herd animals as well as for young bulls (YB) and steers (S)

		LVC, kg	MVC, kg	HVC, kg	VHVC, kg
Terminal index	All	0.081 (0.001)	0.038 (0.006)	0.077 (0.001)	0.026 (0.0004)
	Dairy/Beef		0.073 (0.001) / 0.087 (0.001)	0.087 (0.002) / 0.071 (0.001)	0.029 (0.0006) / 0.024 (0.0005)
	YB/S				
Cconf EBV	All	3.62 (0.071)	1.71 (0.031)	3.64 (0.047)	1.46 (0.018)
	Dairy/Beef	3.40 (0.078) / 4.67 (0.16)	1.60 (0.035) / 2.23 (0.072)	3.26 (0.05) / 5.36 (0.11)	1.39 (0.02) / 1.80 (0.04)
	YB/S	4.64 (0.11) / 3.09 (0.08)	2.39 (0.048) / 1.36 (0.037)	4.54 (0.07) / 3.14 (0.05)	1.71 (0.026) / 1.33 (0.02)
Cfat EBV	All	−4.52 (0.21)	−2.13 (0.055)	−4.79 (0.08)	−1.27 (0.03)
	Dairy/Beef	−3.55 (0.15) / −1.46 (0.21)	−3.07 (0.092) / −1.98 (0.068)	−6.93 (0.14) / −4.54 (0.10)	−2.22 (0.06) / −1.12 (0.04)
	YB/S	−4.80 (0.21) / −4.38 (0.15)	−1.65 (0.067) / −2.92 (0.094)		
Carcwt EBV	All	0.30 (0.006)	0.14 (0.002)	0.26 (0.003)	0.09 (0.001)
	Dairy/Beef	0.28 (0.008) / 0.29 (0.006)	0.25 (0.004) / 0.26 (0.003)	0.28 (0.006) / −0.022 (0.002)	0.097 (0.002) / 0.10 (0.002)
	YB/S	0.31 (0.007) / 0.16 (0.003)	0.16 (0.003) / 0.013 (0.003)		

*Only the model solutions for Dairy/Beef and for YB/S are presented where the interaction existed (P < 0.05).

An increase in carcass fat EBV was associated with reduced meat and bone yield but increased fat yield (Table 2), while also associated with less hindquarter yield and forequarter yield (Table 3). The associated reduction in meat yield (Table 2), hindquarter yield, and forequarter yield (Table 3) for every unit increase in carcass fat EBV, was also greater in animals originating from the beef herd.

When carcass weight was included as a covariate in the statistical model, a greater terminal index value remained associated ($P < 0.01$) with heavier weights for each wholesale cut category (Table 4), as well as more meat yield (Table 5) and hindquarter yield (Table 6), although the size of the association reduced; the terminal index remained associated with reduced fat yield (Table 5). In contrast, when carcass weight was included as a covariate in the statistical model, both bone yield (Table 5) and forequarter yield (Table 6) reduced for every unit increase in the terminal index.

Wholesale Cut Yield

Phenotypic VHVC, HVC, MVC, and LVC weight increased ($P < 0.01$) with increasing terminal index group (Table 7). When the sum of all predicted wholesale cut yields was included as a covariate in the statistical model, the difference between extreme terminal index groups reduced further for both the VHVC and HVC cuts (Table 7). The association between terminal index group and VHVC, HVC, MVC, and LVC cut weight differed ($P < 0.001$) by both herd type and sex. The difference in VHVC and HVC weight between extreme terminal index animals was greatest in young bulls (4.78 kg for VHVC; 13.47 kg for HVC) compared to steers (4.27 kg for VHVC; 12.79 kg for HVC).

Carcass Meat, Bone, and Fat Yield

Carcass meat and bone yield increased ($P < 0.01$) with increasing terminal index group, but the differential in bone yield was not consistent between the some adjacent terminal index groups (Table 8). Carcasses from the very high genetic merit group had the least fat yield, while the low genetic merit group had the greatest fat yield, when adjusted to a fixed carcass weight (Table 8). Once adjusted to a common carcass weight, the difference in total meat yield between extreme terminal index groups reduced from 37.13 kg (SE = 1.09 kg) to 10.07 kg (SE = 0.42 kg) (Table 8). Moreover, when carcass weight was included as a covariate in the statistical model, mean bone and fat yield

Table 2. The phenotypic change (SE in parenthesis)* in total fat, total bone, and total meat per unit change in terminal index, carcass conformation estimated breeding value (EBV; Cconf EBV), carcass fat EBV (Cfat EBV), and carcass weight EBV (Carcwt EBV) for all animals, just dairy-herd animals, and just beef-herd animals as well as for young bulls (YB) and steers (S)

		Total fat, kg		Total bone, kg		Total meat, kg	
Terminal index	All	−0.004 (0.0016)		0.017 (0.007)		0.23 (0.003)	
	Dairy/Beef	0.0014 (0.002)	0.016 (0.003)	0.018 (0.0009)	0.013 (0.001)	0.22 (0.004)	0.24 (0.006)
	YB/S	0.005 (0.002)	−0.010 (0.002)	0.025 (0.001)	0.012 (0.0009)	0.27(0.005)	0.21 (0.004)
Cconf EBV	All	0.23 (0.078)		−0.74 (0.04)		10.14 (0.16)	
	Dairy/Beef	0.54 (0.086)	−1.15 (0.18)	−0.96 (0.039)	0.22 (0.082)	9.19 (0.17)	14.50 (0.36)
	YB/S	0.60 (0.11)	0.016 (0.09)	0.24 (0.05)	−1.28 (0.04)	14.13 (0.23)	8.01 (0.18)
Cfat EBV	All	2.83 (0.14)		−2.34 (0.062)		−13.57 (0.28)	
	Dairy/Beef	3.47 (0.17)	1.65 (0.23)	−2.55 (0.075)	−1.65 (0.10)	−10.60 (0.33)	−19.40 (0.46)
	YB/S	1.49 (0.23)	3.51 (0.17)			−15.13 (0.47)	−12.79 (0.34)
Carcwt EBV	All	0.034 (0.006)		0.086 (0.002)		0.80 (0.01)	
	Dairy/Beef	0.051 (0.007)	−0.0005 (0.009)	0.09 (0.003)	0.08 (0.004)		
	YB/S	0.056 (0.0008)	0.020 (0.007)	0.12 (0.004)	0.07 (0.003)	0.92 (0.016)	0.73 (0.013)

*Only the model solutions for Dairy/Beef and for YB/S are presented where the interaction existed ($P < 0.05$).

Table 3. The phenotypic change (SE in parenthesis)* in total hindquarter weight, total forequarter weight, and total fat weight (kg) per unit change in terminal index, carcass conformation estimated breeding value (EBV; Cconf EBV), carcass fat EBV (Cfat EBV), and carcass weight EBV (Carcwt EBV) values for all animals, just dairy-herd animals or just beef-herd animals as well as for young bulls (YB) and steers (S)

		Total hindquarter, kg		Total forequarter, kg	
Terminal index	All	0.13 (0.002)		0.12 (0.003)	
	Dairy/Beef	0.13 (0.002)	0.14 (0.004)		
	YB/S	0.15 (0.003)	0.12 (0.002)	0.17 (0.004)	0.01 (0.003)
Cconf EBV	All	5.76 (0.10)		5.021 (0.19)	
	Dairy/Beef	5.23 (0.11)	8.22 (0.23)	4.67 (0.15)	6.67 (0.30)
	YB/S	7.75 (0.15)	4.69 (0.12)	8.49 (0.19)	3.15 (0.15)
Cfat EBV	All	−7.50 (0.18)		−5.95 (0.23)	
	Dairy/Beef	−5.65 (0.22)	−11.11 (0.30)	−3.99 (0.28)	−9.76 (0.38)
	YB/S	−8.62 (0.30)	−6.94 (0.22)	−8.15 (0.39)	−4.85 (0.28)
Carcwt EBV	All	0.49 (0.007)		0.49 (0.009)	
	Dairy/Beef			0.50 (0.011)	0.46 (0.015)
	YB/S	0.56 (0.01)	0.46 (0.008)	0.62 (0.013)	0.41 0.010)

*Only the model solutions for Dairy/Beef and for YB/S are presented where the interaction existed ($P < 0.05$).

decreased ($P < 0.01$) with increasing terminal index group (Table 8). The association between terminal index group and meat yield differed ($P < 0.001$) by herd type (Table 8). Although the difference in meat yield between the extreme terminal index groups originating from the dairy herd or from the beef herd was similar (Table 8), the difference in meat yield between adjacent genetic merit groups was not consistent among animals originating from the dairy herd and the beef herd (Table 8).

Carcass Hindquarter and Forequarter Yield

Carcass hindquarter yield and forequarter yield increased ($P < 0.01$) with increasing terminal index group, but the differential in hindquarter and forequarter yield between adjacent terminal index groups was not always consistent (Table 9). When carcass weight was included as a covariate in the statistical model, the differential in hindquarter yield between extreme terminal index groups reduced, relative to the model that did not adjust for carcass weight as a covariate in the model (Table 9). When carcass weight was included as a covariate in the model, mean forequarter yield decreased ($P < 0.01$) with increasing terminal index group. Although this association differed ($P < 0.01$) by herd type of origin and animal sex, the interaction was biologically of little consequence.

Table 4. The phenotypic change (SE in parenthesis)* in low value cut weights (LVC), medium value cut weights (MVC), high value cut weights (HVC), and very high value cut weights (VHVC) per unit change in terminal index, carcass conformation estimated breeding value (EBV; Cconf EBV), carcass fat EBV (Cfat EBV), and carcass weight EBV (Carcwt EBV) for all animals, just dairy-herd animals, and just beef-herd animals as well as for young bulls (YB) and steers (S) when carcass weight was included as covariate in the statistical model

		LVC, kg	MVC, kg	HVC, kg	VHVC, kg
Terminal index	All	0.012 (0.0005)	0.008 (0.0003)	0.034 (0.0006)	0.009 (0.0002)
	Dairy/Beef	0.081 (0.0008)	0.030 (0.0007)	0.426 (0.001)	0.008 (0.0003) 0.011 (0.0004)
	YB/S	0.015 (0.0006)	0.034 (0.0009)	0.342 (0.0007)	0.007 (0.0004) 0.010 (0.0003)
Cconf EBV	All	0.71 (0.024)	0.458 (0.014)	1.76 (0.030)	0.725 (0.011)
	Dairy/Beef	0.66 (0.03)	0.424 (0.015)	1.52 (0.032)	0.787 (0.026)
	YB/S	0.47 (0.04)	0.611 (0.031)	2.82 (0.007)	0.784 (0.013)
Cfat EBV	All	−0.82 (0.041)	−0.591 (0.024)	−2.46 (0.052)	−0.316 (0.020)
	Dairy/Beef	−0.76 (0.05)	0.529 (0.029)	−2.02 (0.063)	
	YB/S	−0.70 (0.05)	−0.718 (0.040)	−3.33 (0.085)	−0.764 (0.034)
Carcwt EBV	All	0.03 (0.002)	0.023 (0.001)	0.092 (0.003)	0.024 (0.0008)
	Dairy/Beef	0.014 (0.003)	0.025 (0.001)	0.081 (0.003)	0.031 (0.001)
	YB/S	0.040 (0.002)	0.019 (0.002)	0.114 (0.004)	0.027 (0.001)

*Only the model solutions for Dairy/Beef and for YB/S are presented where the interaction existed ($P < 0.05$).

DISCUSSION

The current EUROP carcass grading system adopted in EU countries attempts to characterize each carcass based on expected red meat yield and quality (Allen and Finnerty, 2000). Using data from 662 cattle, however, Conroy et al. (2009) documented a correlation of only 0.73 between EUROP carcass conformation score and meat yield. While measuring the actual meat yield on every carcass is currently prohibitively expensive, attempts have been made to predict meat yield and high value primal cuts using VIA of carcasses (Pabiou et al., 2011). Indeed, Pabiou et al. (2010) documented an accuracy of 0.91 when using VIA to predict total meat yield in a population of 627 Irish steers.

Because payment to producers within the EU is based on the relatively crude EUROP carcass conformation score, genetic evaluations, and hence breeding objectives, generally only focus on evaluations of the EUROP classification. Previously, using data from 156,864 animals from 7,301 herds, Connolly et al. (2016) reported that genetically elite animals performed better on-farm, potentially realizing a difference of up to €213.86 in carcass value between animals in the top 10% for the terminal index, relative to the average. However, this analysis was restricted to animals divergent for a terminal index (predominantly focused on returning profit to producers), and focused on the benefits that are likely to accrue within the farm gate from embarking on such a breeding strategy to improve the terminal index value of a herd. Indeed, the benefits of genetic selection on a whole gamut of performance traits in many domesticated species such as beef cattle (McHugh et al., 2014), dairy cattle (Berry and Evans, 2014), and sheep (Dawson and Carson, 2002) have been previously reported, but all confined their analyses to economic (and societal) benefits within the farm gate. In the present study, the impact of genetic selection on downstream industries, namely the meat processing sector, was evaluated. A major focus of processors is to maximize the percentage of (high value) red meat yield while reducing the quantity of carcass bone, but still maintaining the required external fat cover to ensure a pleasant eating experience, irrespective of markets and customers.

Meeting the Processors Desired Carcass Characteristics

In support of previous findings demonstrating superior carcass characteristics at the macro

Table 5. The phenotypic change (SE in parenthesis)* in total fat weight, total bone weight, and total meat weight per unit change in terminal index, carcass conformation estimated breeding value (EBV; Cconf EBV), carcass fat EBV (Cfat EBV), and carcass weight EBV (Carcwt EBV) for all animals, just dairy-herd animals, and just beef-herd animals as well as for young bulls (YB) and steers (S) when carcass weight was included as a covariate in the statistical model

		Total fat, kg		Total bone, kg		Total meat, kg	
Terminal index	All	−0.057 (0.0015)		−0.001 (0.0005)		0.060 (0.0012)	
	Dairy/Beef	−0.050 (0.002)	−0.072 (0.002)	−0.012 (0.0006)	−0.017 (0.001)	0.056 (0.001)	0.071 (0.002)
	YB/S	−0.063 (0.002)	−0.054 (0.002)				
Cconf EBV	All	−1.87 (0.070)		−2.09 (0.024)		2.89 (0.061)	
	Dairy/Beef	−1.347 (0.076)	−4.340 (0.159)	−2.20 (0.026)	−1.59 (0.053)	2.49 (0.061)	4.72 (0.137)
	YB/S	−2.543 (0.095)	−1.506 (0.078)	−1.75 (0.035)	−2.27 (0.027)	3.41 (0.089)	2.61 (0.007)
Cfat EBV	All	5.48 (0.120)		−0.698 (0.044)		−4.70 (0.105)	
	Dairy/Beef	5.17 (0.145)	6.07 (0.197)	−1.43 (0.052)	0.749 (0.072)	−4.23 (0.126)	−5.60 (0.173)
	YB/S	5.12 (0.020)	5.65 (0.143)	−0.253 (0.0739)	−0.921 (0.05)	−4.27 (0.177)	−4.91 (0.127)
Carcwt EBV	All	−0.163 (0.005)		−0.029 (0.002)		0.151 (0.004)	
	Dairy/Beef	−0.143 (0.006)	−0.203 (0.008)	−0.026 (0.002)	−0.035 (0.003)		
	YB/S	−0.190 (0.007)	−0.148 (0.006)	−0.021 (0.003)	−0.034 (0.002)		

*Only the model solutions Dairy/Beef and YB/S are presented where a interaction existed ($P < 0.05$).

Table 6. The phenotypic change (SE in parenthesis) in total hindquarter weight, total forequarter weight, and total fat weight (kg) per unit change in terminal index, carcass conformation estimated breeding value (EBV; Cconf EBV), carcass fat EBV (Cfat EBV), and carcass weight EBV (Carcwt EBV) for all animals, just dairy-herd animals or just beef-herd animals as well as for young bulls (YB) and steers (S) when carcass weight was included as a covariate in the statistical model

		Total hindquarter, kg		Total forequarter, kg	
Terminal index	All	0.023 (0.0008)		−0.024 (0.0011)	
	Dairy/Beef	0.021 (0.0009)	0.028 (0.0013)	−0.022 (0.001)	−0.028 (0.002)
	YB/S	0.017 (0.0011)	0.027 (0.0009)	−0.013 (0.001)	−0.031 (0.001)
Cconf EBV	All	1.05 (0.037)		−1.21 (0.049)	
	Dairy/Beef	0.874 (0.040)	1.890 (0.084)	−1.07 (0.053)	−1.89 (0.113)
	YB/S	0.805 (0.051)	1.189 (0.042)	−0.643 (0.065)	−1.53 (0.054)
Cfat EBV	All	−1.75 (0.064)		1.61 (0.006)	
	Dairy/Beef	−1.52 (0.078)	−2.17 (0.116)	1.30 (0.105)	2.21 (0.143)
	YB/S	−1.43 (0.108)	−1.90 (0.077)		
Carcwt EBV	All	0.075 (0.003)		−0.075 (0.004)	
	Dairy/Beef	0.069 (0.003)	0.088 (0.004)	−0.067 (0.004)	−0.091 (0.006)
	YB/S	0.058 (0.004)	0.085 (0.003)	−0.041 (0.005)	−0.095 (0.004)

*Only the model solutions Dairy/Beef and YB/S are presented where a interaction existed ($P < 0.05$).

level (i.e., EUROP conformation grade) in animals genetically elite for a terminal index (Clarke et al., 2009b), results from the present study also observed that such animals produced more red meat yield (Table 8) and heavier higher value primal cuts (Table 7), even when adjusted to a common carcass weight (Table 8). The heavier higher value cut is despite these traits not directly being included in the terminal index. Given that Pabiou et al. (2011) previously reported genetic correlations of 0.55 to 0.84 between EUROP carcass conformation score and both red meat yield and higher value primal cuts, indirect improvement in primal cut weights as a consequent of genetic selection for EUROP is not surprising. While producers directly benefit from the improved carcass conformation (through payment schemes), the superior concentration (and weight) of higher value primal yields also benefits the meat processor. For example, 1 kg of fillet (tenderloin) steak is worth €40.08, while 1 kg of beef braising steak (e.g., brisket) is worth only €10.61 (Meat Trades Journal, 2017). High value cuts, namely the "steak" cuts, defined as the fillet (tenderloin), striploin, cube roll (ribeye boneless), and sirloin, typically account for only 13% of the carcass weight, but contribute to, on average, 37% of the carcass value (Meat Industry Ireland, 2017). Based on the results from the present study, it is

Table 7. Least squares phenotypic mean and pooled SE for very high value cuts (VHVC), high value cuts (HVC), medium value cuts (MVC), low value cuts (LVC) and when adjusted to a fixed wholesale cut yield (Yield$_{FIX}$) for very high, high, low, or very low terminal index animals categorized by herd type: all animals (All), animals just from dairy herds (Dairy), or animals just from beef herds (Beef)

Genetic merit group	Herd type	VHVC Yield, kg	VHVC Yield$_{FIX}$, kg	HVC Yield, kg	HVC Yield$_{FIX}$, kg	MVC Yield, kg	MVC Yield$_{FIX}$, kg	LVC Yield, kg	LVC Yield$_{FIX}$, kg
Very high	All	31.21[a]	26.71[a]	75.96[a]	63.73[a]	60.56[a]	52.97[a]	105.33[a]	87.23[a]
High	All	29.24[b]	26.27[bc]	70.70[b]	62.63[b]	58.41[b]	53.27[bc]	100.47[b]	88.32[b]
Low	All	28.32[c]	26.23[b]	67.70[c]	62.03[c]	57.00[c]	53.33[c]	97.54[c]	82.82[c]
Very low	All	26.69[d]	26.23[bd]	62.83[d]	61.50[d]	54.50[d]	53.34[dbc]	92.08[d]	89.30[d]
SE		0.13	0.05	0.33	0.15	0.21	0.08	0.48	0.14
Very high	Dairy	30.08[a]	26.46[a]	73.07[a]	63.26[a]	59.46[a]	53.16[a]	102.61[a]	87.60a
High	Dairy	26.73[b]	25.80[bc]	64.37[b]	61.83[b]	55.66[b]	53.62[b]	93.80[b]	89.08[b]
Low	Dairy	26.09[c]	25.90[cd]	62.17[c]	61.64[b]	54.26[c]	53.52[b]	91.02[c]	89.22[b]
Very low	Dairy	25.44[d]	26.00[d]	60.12[d]	61.55[b]	52.98[d]	53.44[b]	88.32[d]	89.38[b]
SE		0.07	0.03	0.18	0.08	0.13	0.07	0.29	0.11
Very high	Beef	32.35[a]	26.95[a]	78.84[a]	64.19[a]	61.66[a]	52.77[a]	108.05[a]	86.87[a]
High	Beef	31.75[b]	26.74[a]	77.03[b]	63.44[b]	61.16[a]	52.92[ab]	107.13[a]	87.57[b]
Low	Beef	30.55[c]	26.57[b]	73.22[c]	62.42[c]	59.73[b]	53.14[bc]	104.06[b]	88.42[c]
Very low	Beef	27.95[d]	26.46[cb]	65.54[d]	61.44[d]	56.02[c]	53.24[c]	95.85[c]	89.21[d]
SE		0.11	0.06	0.27	0.12	0.19	0.09	0.42	0.14

[a–d]Superscripts indicate the significance level between terminal index groups.

Table 8. Least squares phenotypic mean and pooled SE for meat yield (Total meat), bone yield (Total bone), fat yield (Total fat) and when adjusted to a fixed carcass weight (Yield$_{FIX}$) for very high, high, low, or very low terminal index animals categorized by herd type: all animals (All), animals just from dairy herds (Dairy), or animals just from beef herds (Beef)

Genetic merit group	Herd type	Total meat Yield, kg	Total meat Yield$_{FIX}$, kg	Total bone Yield, kg	Total bone Yield$_{FIX}$, kg	Total fat Yield, kg	Total fat Yield$_{FIX}$, kg
Very high	All	280.36[a]	250.41[a]	75.37[ab]	69.99[a]	39.67[a]	30.79[a]
High	All	266.65[b]	245.52[b]	75.76[a]	71.95[b]	41.47[bc]	35.30[b]
Low	All	257.91[c]	242.78[c]	75.14[b]	72.42[c]	42.11[b]	37.82[c]
Very low	All	243.23[d]	240.34[d]	73.45[c]	72.94[d]	40.45[ac]	40.09[d]
SE		1.09	0.42	0.25	0.17	0.58	0.51
Very high	Dairy	272.80[a]	249.28[a]	75.60[a]	71.36[a]	38.89[a]	32.06[a]
High	Dairy	248.54[b]	242.09[b]	75.90[a]	74.69[b]	39.57[a]	38.04[b]
Low	Dairy	240.86[c]	240.54[c]	74.67[b]	74.58[b]	39.09[a]	39.43[bc]
Very low	Dairy	234.44[d]	240.11[dc]	73.27[c]	74.31[b]	37.07[b]	39.17[b]
SE		0.60	0.23	0.14	0.10	0.30	0.25
Very high	Beef	287.92[a]	251.53[a]	75.14[a]	68.63[a]	40.45[a]	29.52[a]
High	Beef	284.76[a]	248.94[b]	75.62[ab]	69.21[b]	43.38[b]	32.57[b]
Low	Beef	274.96[b]	245.02[c]	75.62[ab]	70.25[c]	45.13[c]	36.21[c]
Very low	Beef	252.03[c]	240.57[d]	73.62[c]	71.57[d]	43.83[bc]	41.00[d]
SE		0.90	0.35	0.21	0.14	0.45	0.40

[a–d]Superscripts indicate the significance level between terminal index groups.

clear that every unit increase in the terminal index is associated with heavier high value cut weight (Table 1) and red meat yield (Table 2), as well as the morphology and shape of the carcass changing with proportionally more high value cuts (i.e., when adjusted to a common carcass weight).

Using estimated industry average monetary values of €17.00, €7.50, €5.00, and €3.13 for VHVC,

Table 9. Least squares phenotypic mean and pooled SE for hindquarter meat yield (Total hindquarter), forequarter meat yield (Total forequarter) and when adjusted to a fixed carcass weight (Yield$_{FIX}$) for very high, high, low, or very low terminal index animals categorized by herd type: all animals (All), animals just from dairy herds (Dairy), or animals just from beef herds (Beef)

Genetic merit group	Herd type	Total hindquarter		Total forequarter	
		Yield, kg	Yield$_{FIX}$, kg	Yield, kg	Yield$_{FIX}$, kg
Very high	All	188.59[a]	169.10[a]	204.26[a]	178.82[a]
High	All	180.41[b]	166.73[b]	199.63[b]	181.58[b]
Low	All	175.59[c]	165.74[c]	195.24[c]	182.44[c]
Very low	All	166.44[d]	164.64[d]	185.98[d]	183.71[d]
SE		0.70	0.27	0.93	0.37
Very high	Dairy	183.26[a]	167.98[a]	199.84[a]	179.77[a]
High	Dairy	169.17[b]	164.99[b]	188.77[b]	183.53[b]
Low	Dairy	164.74[c]	164.50[bc]	183.81[c]	183.82[b]
Very low	Dairy	160.38[d]	164.21[c]	179.11[d]	184.09[b]
SE		0.53	0.19	0.69	0.27
Very high	Beef	193.92[a]	170.21[a]	208.69[bc]	177.88[a]
High	Beef	191.66[a]	168.46[b]	210.49[b]	179.64[b]
Low	Beef	186.44[b]	166.98[c]	206.68[c]	181.06[c]
Very low	Beef	172.49[c]	165.08[d]	192.05[a]	183.33[d]
SE		0.73	0.27	0.97	0.37

[a-d]Superscripts indicate the significance level between terminal index groups.

HVC, MVC, and LVC groups, respectively, carcasses of animals in the very high genetic merit terminal index group would generate, on average, €252 more through greater red meat yield and extra value cuts, compared to the very low genetic merit terminal index group. Even when adjusted to a common carcass weight, carcasses of animals in the very high genetic merit terminal group were expected to generate, on average, €90 more revenue for processors through greater red meat yield and extra value cuts, compared to the very low genetic merit group. The monetary impact of the results from the present study are similar to previous studies and signify considerable differences in carcass retail value between beef carcasses. Moore et al. (2014) investigated the relationship between VIA predicted retail yield in different beef carcasses, revealing a £300 (€341) variation in retail value between carcasses of the same weight, while carcasses within the same weight, conformation, and fat score (based on the EUROP grading) had a retail value differential of up to £100 (€114). Previously, Connolly et al. (2016) reported that animals of higher genetic merit based on the terminal index yielded €168 more revenue for the primary producer through a combination of heavier carcass weight, superior carcass quality, fewer days on farm, and less feed intake. Therefore, not only does improvement in genetic merit benefit the producer, it also benefits the processor through

higher red meat yield and a greater proportion of higher value cuts, even at a common carcass weight. Furthermore, the expected fewer days on farm and lesser feed intake per day (Connolly et al., 2016) should also result in a lower environmental footprint of the entire sector.

The benefits of genetic selection can be extrapolated to a national level. For example, the slaughtering of one million very high genetic merit animals relative to the very low genetic merit animals would equate to an extra 37 million tons of red meat (i.e., 37 kg extra red meat per carcass × 1 million carcasses), 4.8 million tons of extra very high value cuts, 13.1 million tons of high value cuts, 6.1 million tons of low value cuts, and 13.3 million tons of very low value cuts being produced. Using the meat costs outlined previously, this would be worth €252 million to the beef processing industry per million animals harvested.

Use of Genetic Indexes in Cattle Procurement

Beef animals in most countries are purchased by either a processor procurement team or local cattle buyer. In Australia, the strategic sourcing of cattle that are likely to meet market specification is a critical challenge for purchasers of animals (Slack-Smith et al., 2009). When beef animals fail to reach target specifications, carcass value is

compromised, and this negatively impacts the supplier's ability to meet customer requirements as well as the processors' cost of production (Slack-Smith et al., 2009). At present, animals are purchased on visual appearance and there is considerable expense associated with sourcing animals for processing. Exploiting available information on the genetic merit of the animal could aid in optimizing the selection of animals for purchasing and may even alleviate the necessity to visually appraise the animal (Berry et al., 2017), thus considerably reducing the costs of procurement. Expansion of the suite of animal-level traits genetically evaluated, such as meat sensory characteristics, could further improve our ability to differentiate live animals, even over and above that achieved through visual appraisal. This is similar to the Australian meat grading system (meat standards of Australia) and the American grading system (USDA system) which facilitates animal grading based on yield and meat quality (Polkinghorne and Thompson, 2010).

Implications for Dairy Beef Production

Beef cow numbers are predicted to reduce in Europe by 10% by 2030, while dairy cow numbers are expanding in some European countries such as Ireland and Austria following the abolition of milk quotas (EU Agricultural Outlook report, 2017). The number of dairy cows in Ireland, for example, increased from 1.3 million in 2015 to 1.4 million in 2017 (CSO, 2017), and is expected to reach 1.6 million by 2025 (Kelly, 2017). Furthermore, with improvements in key technologies, such as sexed semen, more beef-cross dairy animals will be produced from the dairy herd (Cerchiaro et al., 2007). The anticipated deterioration in carcass conformation and red meat yield of animals from dairy herds (Clarke et al., 2009b) is a cause for concern for many beef processors. Previous studies have shown a 1-unit increase in carcass conformation score, on a 15-point scale, was associated with an increase in carcass meat proportion of 11.8 g/kg of carcass weight, whereas a 1-unit increase in carcass fat score, on a 15-point scale, was associated with a decrease in carcass meat proportion of 9.6 g/kg of carcass weight (Conroy et al., 2009). However, based on previous research, the correlations between dairy milk traits and carcass attributes suggest favorable associations (Milk Development Council report, 2008); indicating that improving the carcass merit of dairy animals can be undertaken without repercussions for dairy traits, and thus it is possible to make genetic gain for carcass

traits on the dairy population. Results from the present study clearly show that the terminal index worked equally well in animals born in beef herds as it does in animals born in dairy herds. Therefore, resources need to be deployed for the development of terminal indexes for beef animals tailored to the demands of the dairy farmer (i.e., short gestation and easy calving). Such an approach might well mitigate any anticipated deterioration in carcass quality in slaughtered animals born to dairy cows.

CONCLUSION

The main objective of the current study was to characterize detailed carcass attributes, such as red meat yield and cut weights, from animals divergent in genetic merit for a terminal index. Based on the results from the present study, animals of higher genetic merit on a terminal index produced more red meat, combined with a greater relative proportion of high value cuts in the carcass. The results clearly indicate a benefit to the processer of breeding programs for terminal characteristics; coupled with the previously documented benefits to the producer (Connolly et al., 2016), the benefits of breeding programs across the entire food production chain are obvious. The results also raise the question of the payment for beef cattle based on meat yield, which would send a strong market signal to the primary producers, encouraging accelerated genetic improvement for meat yield. It is also important to highlight that the gains achieved through breeding are cumulative and permanent and, with future improvement in VIA (and other) technology, increased genetic gain could be made to further increase carcass meat yield and carcass composition for the beef industry.

Conflict of interest statement: None declared.

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