

# Cattle stratified on genetic merit segregate on carcass characteristics, but there is scope for improvement<sup>1</sup>

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**ABSTRACT:** The study objective was to quantify the ability of genetic merit for a generated carcass index to differentiate animals on primal carcass cut weights using data from 1,446 herds on 9,414 heifers and 22,413 steers with weights for 14 different primal carcass cuts (plus 3 generated groups of cuts). The carcass genetic merit index was comprised of carcass weight (positive weight), conformation (positive weight), and fat score (negative weight), each equally weighted within the index. The association analyses were undertaken using linear mixed models; models were run with or without carcass weight as a covariate. In a further series of analyses, carcass weight and carcass fat score were both included as covariates in the models. Whether the association between primal cut yield and carcass weight differed by genetic merit stratum was also investigated. Genetic merit was associated ( $P < 0.001$ ) with the weight of all cuts evaluated even when adjusted to a common carcass weight ( $P < 0.01$ ); when simultaneously adjusted to a common carcass weight and fat score, genetic merit was not associated with the weight of the cuberoll or the group cuts termed minced-meat. The weight of the different primal cuts increased

almost linearly within increasing genetic merit, with the exception of the rump and bavette. The difference in mean primal cut weight between the very low and very high genetic merit strata, as a proportion of the overall mean weight of that cut in the entire data set, varied from 0.05 (bavette) to 0.28 (eye of round); the average was 0.17. Following adjustment for differences in carcass weight, there was no difference in cut weight between the very low and very high strata for the rump, chuck tender, and mince cut group; the remaining cuts were heavier in the higher index animals with the exception of the cuberoll and bavette, which were lighter in the very high index animals. The association between carcass weight and the weight of each of the evaluated primal cuts differed ( $P < 0.05$ ) by genetic merit stratum for all cuts evaluated with the exception of the rump, striploin, and brisket as well as the group cuts of frying and mincing. With the exception of these 5 primal (group) cuts, the regression coefficients of primal cut weight on carcass weight increased consistently for all traits with increasing genetic merit stratum, other than for the fillet, cuberoll, bavette, chuck and neck, and heel and shank.

**Key words:** conformation, heritability, primal cut

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## INTRODUCTION

The efficiency of processing operations can be improved with awareness of the type of raw material arriving onsite. For example, the processing characteristics of raw milk, which are known to vary by animal characteristics (Visentin et al., 2017a), including genetic merit (Visentin et al., 2017b), may affect how the raw milk is processed. The same could be true of meat processors having visibility of the expected carcass characteristics of animals in lairage, as a whole. Moreover, being able to identify, and subsequently purchase, cattle from farms that have a greater chance of meeting the immediate customer demand, could aid processing efficiency. Knowledge of the nongenetic factors associated with the macro-carcass characteristics of carcass weight, conformation score, and fat score in cattle has been documented elsewhere (Keane and Allen, 1998; Clarke et al., 2009a; Connolly et al., 2016).

Interanimal variability in carcass composition among cattle has been known to exist for many decades (Berg and Butterfield, 1966; Kempster and Jones, 1977). Primal yield cuts in cattle are known to be heritable (Pabiou et al., 2009, 2011). In fact, Pabiou et al. (2009) documented a heritability of between 0.03 and 0.91 for a series of 14 different primal carcass cuts (following adjustment to a common carcass weight) from a population of 1,048 Irish cattle. Heritability is a function of how closely the true genetic merit of an animal reflects its actual phenotypic value for that trait, once the impact of systematic environmental effects has been removed. Therefore, given the large reported heritability of carcass-related traits, (estimated) genetic merit for carcass traits should improve the precision of a statistical model within a decision support tool to differentiate carcasses on future phenotypic performance. Although the recording of the sire in cattle has historically been low in some populations, should genetic merit aid in predicting carcass merit, incentives could be provided for cattle with known sires purchased prior to the actual expression of the phenotype. Moreover, as the cost of procuring genomic information on individual animals reduce (Berry et al., 2016a), routine genotyping of all animals could become the norm, eliminating the necessity to record parentage but also providing even more precise phenotypic predictions via more accurate genetic evaluations. The upper threshold of the prediction

accuracy of the phenotype of an individual animal is, nonetheless, the square root of the heritability.

The objective, therefore, of the present study was to quantify the usefulness of estimated genetic merit of an animal for carcass traits as a tool not only to advance genetic gain in primal carcass cuts but also to be used by abattoirs to purchase animals suitable for specific customers. Of particular interest here was the carcass cut yields of animals stratified on parental average for an index composed of genetic merit for carcass weight, conformation score, and fat score. Such information also provides evidence of the phenotypic implications of cattle breeding programs that select for such traits.

## MATERIALS AND METHODS

Primal cut yields were available on 127,635 steers and 64,606 heifers slaughtered in a single abattoir between the years 2013 and 2017, inclusive. Greater details of the data set are presented by Judge et al. (2019). For inclusion in the present study, animals could not have resided in >3 herds during their lifetime and had to be resident for at least 70 d in the herd from which they were slaughtered. The sire and dam had to be known for all animals and a carcass genetic evaluation (described later) also had to be available on both parents. Following these edits, data from 66,215 steers and 34,643 heifers remained. All animals were categorized as born in either a dairy herd or a beef herd and will hereon in be referred to as dairy-herd or beef-herd animals. The distinction was based on the breed composition of the dams (Ring et al., 2018) and was undertaken in the present study for subsequent use in the statistical model because dairy herds bucket rear calves while calves are allowed to suckle for several months in beef herds. For consideration in the present study, all animals had to be slaughtered between 16 and 36 mo of age. Only carcass weight records between 200 and 550 kg were retained for steers with the carcass weight limits for heifers being between 180 and 550 kg. A total of 64,490 steers and 34,198 heifer records remained.

Although the weights of all primal cuts were available for each side of each carcass, the actual cuts, and the specifications of those cuts, differed temporally within and among retailers. For the

present study, only primal cuts with the same cut specification from a large number of carcasses in the data set were considered. Fourteen primal cuts remained where a weight was available for both sides of the carcass for the cut in question, and the intra-animal coefficient of variation of both weights was <10%. Primal cuts weight > 4 SD from the mean cut weight of the respective animal gender (i.e., steer or heifer) were discarded. The 8 primal cuts with available weights in the hind quarter were the topside, silverside flat, eye of round, knuckle, rump, striploin, fillet, and cuberoll. The 5 cuts with available weights in the forequarter were the bavette, brisket, chuck tender, leg of mutton and miscellaneous forequarter cuts, and chuck and neck. The weight of the heel and shank combined was also available. The weight of the striploin, fillet, and rump were summed in the present study to generate a group of “frying cuts,” which was only generated if weight records existed for each of the 3 contributing primal cuts in the edited data set; the cuberoll was not included because fewer number of records existed for this cut. Similarly, where weight information on all relevant primal cuts were available, the topside, knuckle, silverside flat, and eye of round were summed to generate a group of cuts, here termed “roasting cuts” for use in the subsequent analyses. Finally, a group of cuts termed “mince cuts” was generated as the sum of the bavette, chuck and neck, heel and shank, chuck tender, and leg of mutton and forequarter miscellaneous. Only animals with a weight observation, after all edits, for at least 5 of the 14 primal cuts were retained.

The parity number of each dam was recoded to 1, 2, 3, 4, 5+. A general heterosis coefficient for each animal was categorized into 0%, >0 and ≤10%, >10% and ≤20%, ... >90% and <100%, and 100%. The general recombination loss coefficient for each animal was categorized as 0%, >0 and ≤10%, >10% and ≤20%, >20% and ≤30%, >30% and ≤40%, >40% and ≤50%, and >50%. Contemporary groups of herd-year-season-gender of slaughter were generated using an algorithm used in Irish national genetic evaluations (McHugh et al., 2011; Berry and Evans, 2014; Berry et al., 2017b). Within a herd, the algorithm clusters together animals of the same gender that are slaughtered in close proximity (≤10 d) of each other; where <10 animals are initially clustered together, the group is amalgamated with an adjacent contemporary group to form a single larger group. This process is repeated until the contemporary group contains ≥10 animals, provided the number of days between the initial and final slaughter date does not exceed 30. Only animals within contemporary groups of at least 4 animals were retained. The final data set consisted of 31,827 animals (9,414 heifers and 22,413 steers) from 3,566 contemporary groups originating from 1,446 herds. The number of records per primal cut is summarized in Table 1. Of the edited data set, the overwhelming majority of the animals were crossbred with the major breed component of almost two thirds of the animals being either Limousin (27% of the entire population), Charolais (17% of the entire population), or Hereford (15% of the entire population). A total of

**Table 1.** Number of records in the analyses for each primal cut (group) by genetic merit stratum

Cut	Genetic merit stratum				Total
	Very low	Low	High	Very high	
Topside	1,871	14,293	11,224	2,434	29,822
Silverside flat	1,510	11,256	8,606	1,909	23,281
Eye of round	1,450	10,748	8,112	1,797	22,107
Knuckle	1,754	13,039	9,730	2,109	26,632
Rump	1,786	13,758	10,718	2,340	28,602
Striploin	492	6,925	6,650	1,550	15,617
Fillet	1,299	9,621	7,417	1,606	19,943
Cuberoll	392	4,865	4,600	1,098	10,955
Bavette	946	7,625	6,247	1,374	16,192
Brisket	1,289	9,544	7,959	1,729	20,521
Chuck tender	1,125	8,541	6,639	1,446	17,751
Leg of mutton and forequarter miscellaneous	1,717	13,374	10,433	2,276	27,800
Chuck and neck	1,797	13,933	11,029	2,413	29,172
Heel and shank	1,801	13,699	10,590	2,289	28,379
Frying	367	5,083	4,801	1,099	11,350
Roasting	1,235	9,067	6,771	1,487	18,560
Mincing	456	3,579	2,701	597	7,333

42% of the animals in the final data set were born in dairy herds.

### Genetic Merit

Genetic evaluations for carcass traits in Ireland are undertaken using a multibreed multitrait model that includes carcass weight, carcass conformation, carcass fat score, live-weight measures at different ages, feed intake, and skeletal measures (Evans et al., 2007, 2008). The pedigree index value for carcass weight, carcass conformation, and carcass fat score for all animals was calculated from their parents based on the December 2017 national genetic evaluation. The pedigree of all animals was available from the Irish Cattle Breeding Federation database. A carcass genetic index was subsequently created for each animal in the present study as follows:

$$Index = \widetilde{CWT} + \widetilde{CONF} - \widetilde{FAT}$$

where  $\widetilde{CWT}$  was the pedigree index of the animal for carcass weight standardized within the edited data set to have a variance of 1,  $\widetilde{CONF}$  was the pedigree index of the animal for carcass conformation standardized within the edited data set to have a variance of 1, and  $\widetilde{FAT}$  was the pedigree index of the animal for carcass fat standardized within the edited data set to have a variance of 1.

The edited data set was subsequently stratified into 4 groups differing in the calculated carcass genetic index. This was done separately for dairy-herd animals and beef-herd animals to avoid any confounding in the subsequent analyses. Furthermore, the thresholds imposed to differentiate between the different genetic index strata was such to try and ensure the difference in mean index value of each stratum was relatively consistent between adjacent strata. A new variable was created per animal, which was the deviation of that animal's calculated genetic index value from the mean of the stratum the animal resided in; this was to be used as a covariate in the statistical model.

### Analyses

The association between genetic merit stratum and each primal cut (group) weight was quantified using linear mixed models in SAS 9.4 software (SAS Institute Inc., Cary, NC); contemporary group was included as a random effect in all models. Fixed effects included in all models, along with genetic merit stratum, were dam parity number, whether the animal was born into a dairy or a beef herd,

heterosis coefficient, recombination coefficient, the difference in genetic index value of the animal relative to the mean of the respective genetic merit stratum (covariate), and a 2-way interaction between animal gender and month of age at slaughter. In a separate series of analyses, carcass weight was included as a covariate in the model, whereas in an additional series of analyses, both carcass weight and carcass fat score were also included as covariates in the models. Furthermore, as well as evaluating the association between stratum based on genetic merit for the index, the associations with strata based on just genetic merit for either carcass weight, conformation, or fat score were also quantified. The referent animal for the derivation of least squares means was a 27-mo-old steer (i.e., average in the data set) from a third-parity dam born into a beef herd with no heterosis or recombination; when carcass weight was included in the model as a covariate, the least squares means were for a 360-kg carcass weight, which was the average in the data set of steers. An additional series of analyses using the aforementioned models was used to quantify whether the association between each primal cut weight and carcass weight differed by genetic merit stratum; this was investigated by including a 2-way interaction term between carcass weight and genetic merit strata as an independent variable in the mixed model.

## RESULTS

The number of records per genetic index stratum for each of the primal carcass cuts and cut groups is in Table 1. Because genetic index per animal was normally distributed, and the thresholds imposed to differentiate strata were such to retain, within primal cut, a relatively equidistance in genetic index value between the consecutive index strata, the number of weight records in the very high and very low strata were fewer. The least squares means for the different primal cuts and groups of cuts by stratum of genetic merit are in Table 2, with or without adjustment to a common carcass weight. Genetic merit was associated ( $P < 0.001$ ) with the weight of all cuts evaluated even when adjusted to a common carcass weight ( $P < 0.01$ ). The least squares means for the different primal cuts and groups of cuts by stratum of genetic merit for carcass weight, conformation, or fat score are in Supplementary Tables 1, 2, and 3, respectively; however, only the associations pertaining to the overall index are discussed hereafter.

Because of the stratification approach employed in the present study, the hypothesis was that the differential, within primal cut, in (unadjusted) weight

**Table 2.** Least squares means (kg) and weighted pooled SE for the yields of different carcass primal cuts (with or without adjustment to common carcass weight) in animals stratified as very low, low, high, and very high on genetic merit index

Cut	No adjustment for carcass weight						With adjustment for carcass weight					
	Very low	Low	High	Very high	SE	<i>P</i> -value	Very low	Low	High	Very high	SE	<i>P</i> -value
Topside	22.13 <sup>a</sup>	24.16 <sup>b</sup>	26.00 <sup>c</sup>	27.91 <sup>d</sup>	0.103	<0.001	23.27 <sup>a</sup>	24.26 <sup>b</sup>	25.11 <sup>c</sup>	26.20 <sup>d</sup>	0.066	<0.001
Silverside flat	16.02 <sup>a</sup>	17.33 <sup>b</sup>	18.52 <sup>c</sup>	19.76 <sup>d</sup>	0.094	<0.001	16.89 <sup>a</sup>	17.44 <sup>b</sup>	17.84 <sup>c</sup>	18.41 <sup>d</sup>	0.063	<0.001
Eye of round	6.37 <sup>a</sup>	6.91 <sup>b</sup>	7.47 <sup>c</sup>	8.23 <sup>d</sup>	0.043	<0.001	6.73 <sup>a</sup>	6.96 <sup>b</sup>	7.20 <sup>c</sup>	7.69 <sup>d</sup>	0.032	<0.001
Knuckle	13.87 <sup>a</sup>	14.95 <sup>b</sup>	15.97 <sup>c</sup>	16.89 <sup>d</sup>	0.065	<0.001	14.53 <sup>a</sup>	14.99 <sup>b</sup>	15.43 <sup>c</sup>	15.87 <sup>d</sup>	0.042	<0.001
Rump	18.75 <sup>a</sup>	19.50 <sup>b</sup>	20.31 <sup>c</sup>	21.11 <sup>d</sup>	0.099	<0.001	19.72 <sup>a</sup>	19.60 <sup>ab</sup>	19.55 <sup>b</sup>	19.62 <sup>ab</sup>	0.069	<0.001
Striploin	15.32 <sup>a</sup>	16.44 <sup>b</sup>	17.12 <sup>c</sup>	18.05 <sup>d</sup>	0.121	<0.001	16.21 <sup>a</sup>	16.55 <sup>b</sup>	16.56 <sup>b</sup>	16.82 <sup>b</sup>	0.098	<0.001
Fillet	6.73 <sup>a</sup>	7.32 <sup>b</sup>	7.80 <sup>c</sup>	8.29 <sup>d</sup>	0.044	<0.001	7.01 <sup>a</sup>	7.36 <sup>b</sup>	7.59 <sup>c</sup>	7.83 <sup>d</sup>	0.037	<0.001
Cuberoll	12.61 <sup>a</sup>	12.87 <sup>a</sup>	13.24 <sup>b</sup>	13.53 <sup>b</sup>	0.124	<0.001	13.13 <sup>a</sup>	12.97 <sup>ab</sup>	12.86 <sup>ab</sup>	12.74 <sup>b</sup>	0.109	<0.001
Bavette	13.86 <sup>a</sup>	14.39 <sup>b</sup>	14.50 <sup>b</sup>	14.61 <sup>b</sup>	0.126	<0.001	14.60 <sup>a</sup>	14.48 <sup>b</sup>	13.97 <sup>c</sup>	13.51 <sup>d</sup>	0.108	<0.001
Brisket	15.98 <sup>a</sup>	16.86 <sup>b</sup>	17.65 <sup>c</sup>	18.68 <sup>d</sup>	0.116	<0.001	16.99 <sup>a</sup>	17.01 <sup>ab</sup>	16.94 <sup>a</sup>	17.24 <sup>b</sup>	0.080	<0.001
Chuck tender	13.31 <sup>a</sup>	13.91 <sup>b</sup>	14.54 <sup>c</sup>	15.10 <sup>d</sup>	0.080	<0.001	14.06 <sup>a</sup>	13.95 <sup>b</sup>	13.98 <sup>ab</sup>	13.98 <sup>ab</sup>	0.049	<0.01
Leg of mutton and forequarter miscellaneous	26.83 <sup>a</sup>	28.06 <sup>b</sup>	29.51 <sup>c</sup>	30.91 <sup>d</sup>	0.126	<0.001	28.15 <sup>a</sup>	28.20 <sup>a</sup>	28.49 <sup>b</sup>	28.87 <sup>c</sup>	0.077	<0.001
Chuck and neck	36.61 <sup>a</sup>	38.99 <sup>b</sup>	41.18 <sup>c</sup>	43.10 <sup>d</sup>	0.190	<0.001	38.69 <sup>a</sup>	39.17 <sup>a</sup>	39.56 <sup>b</sup>	39.85 <sup>b</sup>	0.117	<0.001
Heel and shank	11.86 <sup>a</sup>	12.61 <sup>b</sup>	13.37 <sup>c</sup>	14.03 <sup>d</sup>	0.052	<0.001	12.45 <sup>a</sup>	12.67 <sup>b</sup>	12.95 <sup>c</sup>	13.19 <sup>d</sup>	0.035	<0.001
Frying	40.58 <sup>a</sup>	43.16 <sup>b</sup>	45.20 <sup>c</sup>	47.90 <sup>d</sup>	0.289	<0.001	42.89 <sup>a</sup>	43.40 <sup>ab</sup>	43.61 <sup>bc</sup>	44.41 <sup>c</sup>	0.178	<0.001
Roasting	58.46 <sup>a</sup>	63.27 <sup>b</sup>	68.04 <sup>c</sup>	72.99 <sup>d</sup>	0.329	<0.001	61.30 <sup>a</sup>	63.47 <sup>b</sup>	65.52 <sup>c</sup>	68.18 <sup>d</sup>	0.184	<0.001
Mincing	103.67 <sup>a</sup>	109.89 <sup>b</sup>	114.58 <sup>c</sup>	120.03 <sup>d</sup>	0.818	<0.001	109.48 <sup>a</sup>	109.65 <sup>ab</sup>	109.94 <sup>ab</sup>	110.27 <sup>c</sup>	0.334	<0.01

<sup>a-d</sup>Least squares means differing in superscripts differ ( $P < 0.05$ ) from each other.

between adjacent genetic merit strata would be equal. This was true for most of the cuts evaluated. The coefficient of variation of the pairwise difference in means between adjacent strata was less than 20% for all cuts with the exception of the rump and bavette signifying a close to similar difference between the least squares means in adjacent genetic merit strata. For example, the mean difference in topside cut weight between the very low and low stratum, between the low and high stratum, and between the high and very high stratum was 2.03, 1.84, and 1.92 kg indicating an almost consistent difference between adjacent strata. For both the rump and bavette, however, the difference in mean cut weight between the very low and low strata was greater than the difference between the remaining adjacent strata. The difference in mean cut weight between the very low and very high genetic merit strata as a proportion of the overall mean weight of that cut in the data set varied from 0.05 (bavette) to 0.28 (eye of round); the average was 0.17.

A trend in consistently greater primal cut weight with increasing genetic merit stratum was not always obvious following adjustment to a common carcass weight (Table 2); no consistent increase was detected for the 5 primal cuts of rump, cuberoll, bavette, brisket, and chuck tender. The weight of both

the cuberoll and bavette reduced consistently with increasing genetic index with the animals in the very high genetic merit stratum yielding, on average, 0.40 and 1.09 kg lighter ( $P < 0.05$ ; Table 2) cuberoll and bavette, respectively, than the very low genetic merit index stratum representing a respective 3% and 8% of the mean of the population. Nonetheless, the difference in weight of striploin and fillet between the very high and very low index strata represented 4% and 11% of the population mean in favor of the higher index animals. The difference in primal cut weight between adjacent genetic merit strata was generally not consistent once adjusted to a common carcass weight; the coefficient of variation in the difference in primal cut mean weights between adjacent strata was less than 20% for only the topside, silverside flat, knuckle, heel and shank, and the cut group of roasting.

The least squares means for the primal (group) cuts by strata of genetic merit when adjusted to both a common carcass weight and fat score are in Table 3. After adjustment for differences in both carcass weight and fat score, the weight of the different primal cuts increased consistently with increasing genetic index stratum for 10 of the 17 primal cuts (groups) evaluated. The weight of the cuberoll consistently reduced within increasing genetic index

**Table 3.** Least squares means (kg) and weighted pooled standard error (SE) for the yields of different carcass primal cuts following adjustment to a common carcass weight and fat score in animals stratified as very low, low, high, and very high on genetic merit index

Primal cut	Very low	Low	High	Very high	SE	P-value
Topside	23.69 <sup>a</sup>	24.44 <sup>b</sup>	24.98 <sup>c</sup>	25.83 <sup>d</sup>	0.064	<0.001
Silverside flat	17.01 <sup>a</sup>	17.49 <sup>b</sup>	17.80 <sup>c</sup>	18.30 <sup>d</sup>	0.063	<0.001
Eye of round	6.81 <sup>a</sup>	6.99 <sup>b</sup>	7.17 <sup>c</sup>	7.62 <sup>d</sup>	0.032	<0.001
Knuckle	14.78 <sup>a</sup>	15.11 <sup>b</sup>	15.35 <sup>c</sup>	15.65 <sup>d</sup>	0.041	<0.001
Rump	19.55 <sup>a</sup>	19.52 <sup>a</sup>	19.60 <sup>ab</sup>	19.77 <sup>b</sup>	0.069	<0.001
Striploin	15.99 <sup>a</sup>	16.45 <sup>b</sup>	16.67 <sup>c</sup>	17.01 <sup>d</sup>	0.097	<0.001
Fillet	7.10 <sup>a</sup>	7.40 <sup>b</sup>	7.56 <sup>c</sup>	7.76 <sup>d</sup>	0.037	<0.001
Cuberoll	13.01	12.92	12.90	12.84	0.109	0.471
Bavette	14.23 <sup>a</sup>	14.30 <sup>a</sup>	14.07 <sup>ab</sup>	13.80 <sup>b</sup>	0.107	<0.001
Brisket	16.71 <sup>a</sup>	16.88 <sup>ab</sup>	17.03 <sup>b</sup>	17.49 <sup>c</sup>	0.079	<0.001
Chuck tender	14.12 <sup>a</sup>	13.98 <sup>ab</sup>	13.96 <sup>bc</sup>	13.92 <sup>c</sup>	0.049	<0.001
Leg of mutton and forequarter miscellaneous	28.37 <sup>a</sup>	28.29 <sup>a</sup>	28.43 <sup>a</sup>	28.68 <sup>b</sup>	0.077	<0.001
Chuck and neck	38.97 <sup>a</sup>	39.30 <sup>ab</sup>	39.48 <sup>ac</sup>	39.62 <sup>c</sup>	0.117	<0.001
Heel and shank	12.65 <sup>a</sup>	12.76 <sup>b</sup>	12.89 <sup>c</sup>	13.02 <sup>d</sup>	0.034	<0.001
Frying	42.58 <sup>a</sup>	43.26 <sup>b</sup>	43.77 <sup>c</sup>	44.78 <sup>d</sup>	0.177	<0.001
Roasting	62.16 <sup>a</sup>	63.85 <sup>b</sup>	65.22 <sup>c</sup>	67.38 <sup>d</sup>	0.180	<0.001
Mincing	109.86	109.80	109.80	109.93	0.334	0.902

<sup>a-d</sup>Least squares means differing in superscripts differ ( $P < 0.05$ ) from each other.

**Table 4.** Linear regression coefficients (SE in parenthesis) of the weight (kg  $\times 100$ ) of the different carcass primal cuts on carcass weight in the genetic merit categories very low, low, high, and very high

Cut	Very low	Low	High	Very high	P-value
Topside	5.41 (0.0758) <sup>a</sup>	5.72 (0.0356) <sup>b</sup>	6.12 (0.0367) <sup>c</sup>	6.31 (0.0689) <sup>d</sup>	<0.001
Silverside flat	4.40 (0.0717) <sup>a</sup>	4.60 (0.0345) <sup>a</sup>	4.90 (0.0356) <sup>b</sup>	5.00 (0.0642) <sup>c</sup>	<0.001
Eye of round	1.75 (0.0366) <sup>a</sup>	1.75 (0.0174) <sup>a</sup>	1.94 (0.0179) <sup>b</sup>	1.97 (0.0331) <sup>b</sup>	<0.001
Knuckle	3.16 (0.0471) <sup>a</sup>	3.36 (0.0224) <sup>a</sup>	3.60 (0.0235) <sup>b</sup>	3.67 (0.0442) <sup>c</sup>	<0.001
Rump	5.25 (0.0800)	5.19 (0.0377)	5.28 (0.0389)	5.29 (0.0714)	0.176
Striploin	4.14 (0.1870)	4.10 (0.0564)	4.06 (0.0538)	4.09 (0.0985)	0.933
Fillet	1.41 (0.0442) <sup>a</sup>	1.58 (0.0209) <sup>a</sup>	1.62 (0.0218) <sup>a</sup>	1.58 (0.0408) <sup>b</sup>	<0.001
Cuberoll	2.38 (0.1873) <sup>a</sup>	2.78 (0.0613) <sup>bc</sup>	2.89 (0.0582) <sup>bc</sup>	2.60 (0.1069) <sup>a</sup>	0.003
Bavette	4.04 (0.1371) <sup>a</sup>	3.95 (0.0618) <sup>a</sup>	3.68 (0.0620) <sup>b</sup>	3.44 (0.1146) <sup>b</sup>	<0.001
Brisket	5.38 (0.0932)	5.41 (0.0443)	5.29 (0.0452)	5.35 (0.0845)	0.150
Chuck tender	3.65 (0.0595) <sup>a</sup>	3.66 (0.0263) <sup>b</sup>	3.71 (0.0274) <sup>ab</sup>	3.81 (0.0523) <sup>bc</sup>	0.047
Leg of mutton and forequarter miscellaneous	7.13 (0.0870) <sup>a</sup>	7.29 (0.0413) <sup>a</sup>	7.45 (0.0430) <sup>b</sup>	7.51 (0.0805) <sup>b</sup>	<0.001
Chuck and neck	10.78 (0.1379) <sup>a</sup>	11.22 (0.0643) <sup>a</sup>	11.37 (0.0664) <sup>a</sup>	11.25 (0.1229) <sup>b</sup>	<0.001
Heel and shank	2.81 (0.0412) <sup>a</sup>	2.83 (0.0192) <sup>a</sup>	2.99 (0.0202) <sup>b</sup>	2.96 (0.0380) <sup>b</sup>	<0.001
Frying	11.20 (0.3177)	11.22 (0.1033)	11.17 (0.0996)	11.27 (0.1853)	0.946
Roasting	14.88 (0.2054) <sup>a</sup>	15.52 (0.0983) <sup>a</sup>	16.73 (0.1026) <sup>b</sup>	17.01 (0.1908) <sup>c</sup>	<0.001
Mincing	30.54 (0.4313)	29.89 (0.1894)	29.99 (0.2014)	29.54 (0.3993)	0.335

<sup>a-d</sup>Solutions with different superscripts differ ( $P < 0.05$ ) from each other.

The significance value represented the significance of the 2-way interaction between carcass weight and genetic merit stratum.

stratum once differences in carcass weight and fat score were accounted for in the statistical model, although this was not significant.

#### **Association Between Primal Cut Weight and Carcass Weight by Genetic Merit Strata**

The regression coefficients of each cut weight on carcass weight by genetic merit stratum are in

Table 4. The association between carcass weight and the weight of each of the evaluated cuts differed ( $P < 0.05$ ) by genetic merit stratum for all traits evaluated with the exception of the rump, striploin, and brisket as well as the group cuts of frying and mincing. With the exception of the aforementioned 5 primal (group) cuts, the regression coefficients of primal cut weight on carcass weight increased with increasing genetic merit stratum for all traits except

the fillet, cuberoll, bavette, chuck and neck, and heel and shank (Table 4). For the 7 remaining primal (group) cuts, the regression coefficient on carcass weight in the very high index stratum was, on average, 12% greater (varying from 4% for chuck tender to 16% for topside), than the respective regression coefficient in the very low index stratum.

## DISCUSSION

The contribution of artificial selection to changing animal characteristics (e.g., height), as well as improving performance, is well recognized internationally across species (Chen et al., 2002; Havenstein et al., 2003; García-Ruiz et al., 2016). Breeding, however, has also (rightfully) been criticized for causing unwanted changes in animal characteristics and key performance indicators (Berry et al., 2016b). Agriculture, and in particular ruminant production systems, is often heavily condemned for its contribution to climate change (Opio et al., 2013) but also the efficiency of food utilization relative to many domesticated monogastrics (Wilkinson and Lee, 2018). Although saleable meat yield affects processor revenue, being able to alter the carcass morphology of an animal toward a greater quantity of higher-value primal cuts is also advantageous, especially if achieved without increasing animal size (where carcass weight may be used as a proxy). The desire for a more valuable carcass was the motivation for the present study, which attempts to quantify whether readily available breeding tools (i.e., genetic merit for often routinely available carcass weight, conformation, and fat score) can alter the partitioning of the carcass into more saleable yield. Although for most cuts, the very high genetic merit animals in the present study generated proportionally more primal cut yield, it is likely that more granular phenotyping strategies of carcass characteristics could further improve the efficacy.

Breeding is cumulative and permanent implying that the genetic merit of an individual is a function of past selection decisions. In fact, traditional rates of genetic gain achievable in a well-structured breeding program are approximately 0.215 genetic standard deviations annually (Schaeffer, 2006); this can be accelerated with genomic selection (Meuwissen et al., 2001). Assuming an infinitesimal model, there is no rationale to expect a deceleration in genetic gain achievable (Berry, 2018). Based on the genetic parameters used in the national genetic evaluation for carcass weight, carcass conformation, and carcass fat score, the expected response

to selection per generation for each trait (assuming equal weight per trait within the index as per the current study) is +0.65, +0.68, and -0.54 for carcass weight, conformation, and fat score, respectively; this translates to a 1.862 unit expected improvement per generation in the generated carcass merit index in the present study. The mean difference in index value between adjacent genetic merit strata in the present study was 2.073, thus implying that a population could, in theory, shift one whole stratum, on average, every 1.1 generations; the average generation interval in beef is 6.31 (McParland et al., 2007). The actual gains achieved, however, are likely to be (far) less for numerous reasons such as 1) achieving high accuracy of selection for all 3 traits may not always be possible, 2) breeding objectives are likely to include more traits than just the 3 carcass traits which will reduce the trait-specific selection intensity and thus genetic gain, especially if antagonistically correlated with the other goal traits, and 3) penetrance of the achievable genetic gain into the wider population will not be fully realized, especially in beef production systems where the usage of artificial insemination is traditionally low. Nonetheless, the mathematics does illustrate that, if the willingness is there, the potential for performance gains is certainly achievable.

The ability of genetic merit estimates of animals to relate to actual phenotypic performance has been well proven in cattle at both the individual trait level (Campion et al., 2009; McHugh et al., 2014; Connolly et al., 2016) and the index level (Clarke et al., 2009a). Connolly et al. (2016) documented that animals excelling in the Irish terminal index produced heavier carcasses with superior conformation, were slaughtered younger, and commanded a greater price per kilogram and overall carcass value. In a controlled study of 107 male progeny from beef cows stratified into 2 groups on genetic merit for an overall index, Clarke et al. (2009b) reported that the genetically superior animals produced heavier carcasses of greater overall value, although no significant difference in the proportion of the carcass that was high-value cuts was detected. Although the observed differences in many of the cut yields between divergent genetic merit strata in the present study may seem small, the benefit is cumulative across the entire carcass.

### *Where to From Here?*

Genetic gain per generation is a function of the intensity of selection, the accuracy with

which genetically elite from inferior animals can be identified, and the extent of genetic variability (Rendel and Robertson, 1950). Genetic gain, however, is also a function of how the trait being selected reflects the true goal trait desired by the end user. For example, in the present study, phenotypic information (and associated pedigree information as well as data on contributing systematic environmental effects) was assumed available for the macro-level measures of carcass attributes (i.e., carcass weight, conformation, and fat score) from which to generate accurate genetic evaluations. Considerable genetic variability for such traits is known to exist (Crowley et al., 2011; Englishby et al., 2016) and intense selection is possible; therefore, rapid genetic gain is achievable. Nonetheless, such relatively crude macro-level traits are not necessarily the most relevant to the end user; in this case, the end user (here the meat processor) would prefer more saleable meat yield per animal but also a greater quantity of this saleable yield originating from higher-value primal cuts. Although for most cuts in the present study, the genetically elite animals on a simple carcass merit index yielded a heavier weight of primal cuts (even for the same carcass weight and fat score), the benefits were suboptimal in that first not all cuts improved (especially the higher-value cuts) and second the difference between adjacent genetic merit strata was not consistent. The ability of the macro carcass metrics used in the present study to differentiate the weight of individual cuts was largely reflective of the genetic correlations reported between these carcass metrics and individual primal cuts reported by Judge et al. (2019) using the same data set as used in the present study. For example, cuberoll weight did not differ by genetic merit stratum when adjusted to a common carcass weight in the present study; Judge et al. (2019) reported a near zero genetic correlation (0.03) between cuberoll weight and carcass conformation adjusted to a common carcass weight which was less than the mean of the absolute genetic correlations of 0.36 between all other cuts and carcass weight.

Two possible solutions exist to improve the differentiative ability of genetic merit estimates, namely to undertake genetic evaluations directly for the weight of each primal cut, or second undertake genetic evaluations for predictor traits more closely aligned to the desired traits. Although capturing the weight of individual carcass cuts may appear resource intensive, technologies (e.g., Marel) do exist that can provide the weights of different primal cuts even when

trimmed to a given retail customer specification. Given the reported relatively high heritability estimates of many primal cut weights in cattle (Pabiou et al., 2009), vast quantities of individual animal data (and ancillary information including pedigree) are not actually required, although it would be important to have a good representation of the germplasm in the data set. For example, assuming a heritability of 0.25 (brisket; Pabiou et al., 2009), 0.49 (striploin; Pabiou et al., 2009), and 0.62 (fillet; Pabiou et al., 2009) for a primal cut, to achieve an accuracy of selection of 0.70 (based solely on progeny information), records from approximately 15, 7, and 6 carcasses would be required. Because the recorded weight is that of the actual primal cut itself, then the genetic evaluation for that cut weight should relate closely (dependent on the heritability; Berry et al., 2017a) to the actual phenotype.

The second tactic to improve the efficacy of segregating carcasses on primal yields or breeding more valuable carcasses relative to the approach adopted in the present study would be to use available technologies to predict, more accurately, the weight of individual primal cuts. Pabiou et al. (2011) proposed such a strategy using video image analysis of cattle carcasses and reported a correlation of up to 0.96 between groups of primal carcass yields (i.e., very high-value cuts, high-value cuts, medium value cuts, and low value cuts) and the respective yield predictions from video image analyses. Using a population of 217 commercial Bradford Brazilian steers, Cardoso et al. (2019) documented the ability of ultrasound measures of longissimus thoracic muscle area and/or subcutaneous fat thickness on live animals immediately prior to slaughter to predict pistol hindquarter cut weights. Other technologies to predict carcass characteristics also exist, each with differing levels of prediction accuracy and cost (Scholz et al., 2015). Although errors in predicting individual primal cut weights undoubtedly exist for such strategies, they should be better than simply using the 15-point macro-level assessment of carcass conformation and fat score; Pabiou et al. (2011) reported that the accuracy of predicting groups of primal carcass cut yields was almost always superior when using video image analyses relative to when using the 15-point carcass conformation and fat score. Moreover, such noninvasive systems of predicting cut yields may be more amenable to routine implementation in more abattoirs thus helping achieve a very high accuracy of selection for the predicted trait. Pabiou et al. (2011) reported

heritability estimates of 0.13 to 0.47 for predicted groups of wholesale cuts in cattle. Using a data set of 17,765 carcass records from UK cattle with video image analysis-predicted weight of 6 primal cut traits, Moore et al. (2017) also documented heritability estimates of between 0.23 and 0.29 from the different cut weights when adjusted to a common carcass weight. A more logical strategy for generating genetic evaluations, however, would be to combine both data sources in a multitrait genetic evaluation where the goal trait is the actual primal cut weight (on fewer records) and the predicted cut weight as a correlated trait (from a larger population of animals).

### CONCLUSIONS

There is a clear ability of genetic merit of measures of carcass merit to identify carcasses with, on average, heavier primal cut yields. Although a clear potential exists, the efficacy of such a strategy could possibly be improved by either basing the genetic evaluations themselves on the actual primal cut weights or exploiting phenotypes more closely reflective of the primal cut weights.

### SUPPLEMENTARY DATA

Supplementary data are available at *Translational Animal Science* online.

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