Potential exists to change, through breeding, the yield of individual primal carcass cuts in cattle without increasing overall carcass weight[1]

Michelle M. Judge,*[,2] Thierry Pabiou,† Jessica Murphy,‡ Stephen B. Conroy,† P. J. Hegarty,† and Donagh P. Berry*

*Teagasc, Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co., Cork, Ireland; †ICBF, Highfield House, Shinagh, Bandon, Co., Cork, Ireland; and ‡Slaney Foods International, Bunclody, Co., Wexford, Ireland

ABSTRACT: The ability to alter the morphology of cattle towards greater yields of higher value primal cuts has the potential to increase the value of animals at slaughter. Using weight records of 14 primal cuts from 31,827 cattle, the objective of the present study was to quantify the extent of genetic variability in these primal cuts; also of interest was the degree of genetic variability in the primal cuts adjusted to a common carcass weight. Variance components were estimated for each primal cut using animal linear mixed models. The coefficient of genetic variation in the different primal cuts ranged from 0.05 (bavette) to 0.10 (eye of round) with a mean coefficient of genetic variation of 0.07. When phenotypically adjusted to a common carcass weight, the coefficient of genetic variation of the primal cuts was lesser ranging from 0.02 to 0.07 with a mean of 0.04. The heritability of the 14 primal cuts ranged from 0.14 (bavette) to 0.75 (topside) with a mean heritability across all cuts of 0.48; the heritability estimates reduced, and ranged from 0.12 (bavette) to 0.56 (topside), when differences in carcass weight were accounted for in the statistical model. Genetic correlations between each primal cut and carcass weight were all ≥0.77; genetic correlations between each primal cut and carcass conformation score were, on average, 0.59 but when adjusted to a common carcass weight, the correlations weakened to, on average, 0.27. The genetic correlations among all 14 primal cut weights was, on average, strong (mean correlation of 0.72 with all correlations being ≥0.37); when adjusted to a common carcass weight, the mean of the genetic correlations among all primal cuts was 0.10. The ability of estimated breeding values for a selection of primal cuts to stratify animals phenotypically on the respective cut weight was demonstrated; the weight of the rump, striploin, and fillet of animals estimated to be in the top 25% genetically for the respective cut, were 10 to 24%, 12 to 24%, and 7 to 17% heavier than the weight of cuts from animals predicted to be in the worst 25% genetically for that cut. Significant exploitable genetic variability in primal carcass cuts was clearly evident even when adjusted to a common carcass weight. The high heritability of many of the primal cuts infers that large datasets are not actually required to achieve high accuracy of selection once the structure of the data and the number of progeny per sire is adequate.

Key words: beef, genetic parameters, heritability, retail cuts

J. Anim. Sci. 2019.97:2769–2779
doi: 10.1093/jas/skz152

INTRODUCTION

The desire to alter the characteristics of domesticated animals has been to the fore for centuries with Robert Bakewell's (1725–1795) ability to "*modify […] the forms and qualities of […] cattle*" recognized in Darwin's "On the Origin of

[1]This publication has emanated from research supported in part by a research grant from Science Foundation Ireland and the Department of Agriculture, Food and Marine on behalf of the Government of Ireland under the Grant 16/RC/3835 (VistaMilk) as well as funding from the Research Stimulus Fund (BreedQuality and GREENBREED)

[2]Corresponding author: michelle.judge@teagasc.ie

Received January 15, 2019.
Accepted May 3, 2019.

Species by Means of Natural Selection" (Darwin, 1859). Modern-day beef cattle breeding programs, like most breeding programs in meat-producing species, aim to alter the morphology of animals towards a greater quantity of value-added saleable product. Traditionally, such an objective was accomplished by selecting for heavier animals, but the impact of animal weight on production efficiency, especially in the mature herd (Ferrell and Jenkins, 1984; Montañdo-Bermudez et al., 1990), has questioned such a motive.

Many carcass payment systems in cattle are based on relatively crude estimates of carcass value. In Europe, for example, the value received by producers for a carcass generally reflects a 15-point classification system which attempts to describe the conformation of the animal based predominantly on the round, back, and shoulder; Conroy et al. (2010) using a population of 662 dissected beef carcasses reported a correlation of 0.85 between this classification system and carcass meat proportion. Hence, the European system of carcass classification explains only 73% of the variability in saleable meat yield. Because many national genetic evaluations for carcass merit are based on such relatively crude metrics (Pabiou et al., 2012), scope for improvement in the precision of the evaluations possibly exists. However, due to the large resource demand to generate detailed carcass cut data, few have embarked on generating large study populations with detailed primal cut weights from which to estimate the necessary genetic parameters for use in genetic evaluations.

The existence of genetic variability in the weight of primal cuts has been established previously; Short et al. (2002) demonstrated how a mutation in the myostatin gene can contribute to differences in the relative weights of different primal cuts in cattle. From a population of 842 Chianina cattle, Sarti et al. (2013) documented heritability estimates of between 0.21 and 0.74 for the weight of 7 different carcass cuts. In a population of 503 steers, Cundiff et al. (1969) reported heritability estimates of between 0.44 and 0.68 for the weight of the round, loin, rib, and chuck primal cuts. Based on 2 separate populations of Irish beef cattle comprised of 413 and 635 animals, Pabiou et al. (2009) documented heritability estimates for individual carcass cut weights of between 0.03 and 0.86 for 14 different primal cuts. Although they did not estimate the variance components for actual primal cut weights, Choi et al (2015) reported heritability estimates of between 0.19 and 0.83 for 10 different primal cuts expressed as a percentage of carcass weight from a population of 920 Hanwoo cattle. All 3 studies were based on relatively few animals contributing to relatively poor precision in the genetic parameter estimates documented; for example, the standard errors of the heritability estimates reported by Sarti et al. (2013) were between 0.13 and 0.27 while those of Pabiou et al. (2009) and Choi et al. (2015) were all ≥0.15 and ≥0.08, respectively.

The objective of the present study was to use carcass primal cut weights from a relatively large population of 31,827 beef cattle to estimate the necessary genetic parameters and quantify the gains that can be achieved in increasing the weight of individual primal cuts; of particular interest was the capacity for breeding programs to increase the weight of individual primal cuts without necessarily increasing overall carcass weight.

MATERIALS AND METHODS

The data used in the present study were obtained from a pre-existing 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.

Data

Carcass weight, as well as primal cut weights, were available on 127,635 steers and 64,606 heifers slaughtered in a single abattoir between the years 2013 to 2017, inclusive. Carcass conformation and fat score were also available and were measured on a 15-point scale where a score of 1 for conformation and fat represented poor and lean, respectively while a score of 15 represented the opposite. The vast majority of the data were some form of crossbred animal with Angus, Charolais, Belgian Blue, Limousin, Holstein-Friesian, Hereford, and Simmental. 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 days in the herd from which they were slaughtered from. The sire and dam had to be known for all animals. For consideration in the present study, all animals had to be slaughtered between 16 and 36 mo of age. Only data from animals with carcass weight records between 200 and 550 kg were retained for steers, while carcass weight limits of between 180 and 550 kg was imposed for heifers.

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 customers. For the present study, only primal cuts with the same cut specification from a large number of carcasses in the

dataset were considered; the cut weights used in the present study had not yet been trimmed for excessive fat cover. 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 cut weights ±4 standard deviations 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 hindquarter 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 (**LMC**), 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 dataset; the cuberoll was not included because of a fewer number of records 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.

A general heterosis coefficient for each animal was categorized into 0%, >0 and ≤10%, >10% and ≤20%, …. >90% and <100%, and 100%. A 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 days) 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 dataset consisted for 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.

(Co)variance Component Estimation

Residual and genetic variance components for all primal cut weights as well as the macro-carcass traits of carcass weight, conformation, and fat score were estimated using a series of univariate animal linear mixed models in AsReml (Gilmour et al., 2009). The fitted model was:

$$y_{ijklmno} = HYSG_n + gender_m|age_l + heterosis_k + recombination_j + animal_i + e_{ijklmno}$$

where HYSG represents the fixed effect of herd–year–season–gender of slaughter, gender|age is the fixed effect of the interaction between animal gender (m = steer or heifer) and age_l, in months, at slaughter, heterosis is the fixed effect of heterosis coefficient (k = 0%, >0 and ≤10%, >10% and ≤20%, …. >90% and <100%, and 100%) of the animal, recombination is the fixed effect of recombination coefficient (0%, >0 and ≤10%, >10% and ≤20%, >20% and ≤30%, >30% and ≤40%, >40% and ≤50%, and >50%) of the animal, animal is the random direct additive genetic component for the animal $N(0,\mathbf{A}\sigma_a^2)$, and e is the random residual term $N(0,\mathbf{I}\sigma_e^2)$ where σ_a^2 is the additive genetic variance, σ_e^2 is the residual variance, **A** is the numerator relationship matrix, and **I** is an identity matrix. To construct the numerator relationship matrix, the pedigree of all animals was traced back to their respective founder generations which were in turn allocated to genetic groups of breed.

In a separate series of univariate analyses, carcass weight was also included as a linear covariate in the model and, in a further series of analyses, both carcass weight and carcass fat score were together included in the model. The pairwise correlations among all primal cuts and between the primal cuts and all of carcass weight, conformation and fat score were estimated using bivariate sire linear mixed models; the fixed effects included in the model were those of the univariate models.

Genetic Evaluation

To assess the ability of parental average estimated breeding values (**EBV**) for a given primal cut in stratifying animals on the weight of that primal cut, genetic evaluation for the 3 frying

Table 1. Number of records (N), mean (μ; kg), genetic standard deviation (σ_g; kg), and heritability (h^2; standard error in parenthesis) for the different cut traits analyzed as raw data (i.e., no adjustment), or where adjusted via inclusion of covariates in the statistical model for carcass weight, or carcass weight plus fat score

			No adjustment		Adjustment for carcass weight		Adjustment for carcass weight and fat score	
Cut[1]	*N*	μ	σ_g	h^2 (SE)	σ_g	h^2 (SE)	σ_g	h^2 (SE)
Topside	29,822	23.56	2.01	0.75 (0.03)	1.10	0.58 (0.03)	0.93	0.48 (0.03)
Silverside	23,281	16.64	1.35	0.58 (0.03)	0.58	0.27 (0.03)	0.56	0.26 (0.03)
Eye of round	22,107	6.67	0.67	0.68 (0.04)	0.45	0.56 (0.04)	0.43	0.54 (0.04)
Knuckle	26,632	14.46	1.12	0.68 (0.03)	0.58	0.45 (0.03)	0.50	0.38 (0.03)
Rump	28,602	19.28	1.31	0.45 (0.03)	0.69	0.26 (0.03)	0.69	0.26 (0.03)
Striploin	15,707	16.35	0.97	0.30 (0.04)	0.59	0.17 (0.03)	0.56	0.16 (0.03)
Fillet	19,943	7.23	0.46	0.37 (0.04)	0.29	0.22 (0.03)	0.27	0.20 (0.03)
Cuberoll	10,955	12.52	0.66	0.23 (0.05)	0.53	0.19 (0.04)	0.54	0.20 (0.04)
Bavette	16,192	13.76	0.66	0.14 (0.03)	0.54	0.12 (0.03)	0.41	0.07 (0.03)
Brisket	20,251	16.56	1.22	0.39 (0.03)	0.72	0.28 (0.03)	0.71	0.28 (0.03)
Chuck Tender	17,751	13.48	0.88	0.48 (0.04)	0.45	0.32 (0.03)	0.44	0.32 (0.03)
LMC[1]	27,800	26.98	1.81	0.54 (0.03)	0.66	0.22 (0.02)	0.61	0.20 (0.02)
Chuck and Neck	29,172	37.44	2.79	0.51 (0.03)	1.40	0.34 (0.03)	1.38	0.33 (0.03)
Heel & shank	28,379	12.16	0.92	0.68 (0.03)	0.50	0.49 (0.03)	0.45	0.42 (0.03)
Frying	11,350	43.28	2.36	0.42 (0.05)	1.10	0.25 (0.05)	1.10	0.25 (0.05)
Roasting	18,560	60.94	4.91	0.73 (0.04)	2.22	0.51 (0.04)	1.85	0.40 (0.04)
Mince	7,333	104.10	5.56	0.46 (0.07)	1.98	0.35 (0.07)	2.00	0.36 (0.07)

[1]LMC is the leg of mutton cuts plus miscellaneous.

cut traits of striploin, rump, and fillet were undertaken separately in Mix99 (Strandén and Lidauer, 1999). While the final specification of each primal cut differed per customer, a total of 10,934 animals had recorded striploin weights from both sides of the carcass which were destined for the same customer with the same recorded specification (i.e., achieving the desired specification was mainly through trimming of excess fat cover). Similarly, rump weights and fillet weights were available on 24,730 and 15,681 animals, respectively. All data from these animals were masked and their EBVs for each primal cut estimated through their relationships, via the numerator relationship matrix with phenotyped animals. All genetic evaluations were univariate and based on the untrimmed weights of the respective primal cut. The model used was as described for the estimation of variance components without any adjustment for carcass weight or fat and then separately with adjustment for both carcass weight and fat. The variance components used were those estimated in the present study. The animals with the masked phenotypes were stratified into 4 equal groups per primal cut based on the respective EBV; only animals with a reliability for the primal cut under investigation of >0.01 were retained.

The association between stratum of genetic merit for each individual primal cut and the phenotypic trimmed primal cut weight was estimated using a linear mixed model that accounted for an interaction between gender and age, in months, at slaughter, as well as the heterosis and recombination coefficient of the animal; herd–year–season–gender of slaughter was included as a random effect. A variable with 4 levels representing EBV stratum for each primal cut (estimated from the model without an adjustment for carcass weight and fat score) was included as a fixed effect and the least square means estimated. This effect was then replaced by the 4-level EBV stratum for the primal cut estimated from the model with an adjustment for both carcass weight and fat score; in the association analyses, phenotypic carcass weight was also included in the mixed model.

RESULTS

Genetic Parameters

The heritability (standard error in parenthesis) and genetic standard deviation for carcass weight was 0.62 (0.03) and 21.5 kg, respectively, for carcass fat score was 0.56 (0.03) and 1.02 units, respectively, and for carcass conformation was 0.78 (0.03)

and 0.96 units, respectively. Mean carcass weight was 348.5 kg. Summary statistics for the individual primal cuts and groups of cuts are given in Table 1. The coefficient of genetic variation for the individual primal cuts without adjustment for carcass weight or carcass fat varied from 0.05 (Bavette) to 0.10 (eye of round); the mean coefficient of genetic variation for the primal cuts was 0.07. The coefficient of genetic variation for the groups of cuts (i.e., frying, roasting, mince) ranged from 0.05 to 0.08 (Table 1). Following phenotypic adjustment to a common carcass weight via the inclusion of carcass weight as a covariate in the statistical model, the genetic standard deviation was 0.36 (LMC) to 0.82 (Bavette) times that of the original unadjusted genetic standard deviation; the genetic standard deviation for the group of cuts more than halved when adjusted to a common carcass weight (Table 1). Further adjustment to a common fat score had minimal additional impact on the genetic standard deviation of the primal cuts with the greatest relative impact being on the bavette cut (76% of the genetic standard deviation prior to adjusting for carcass weight).

The heritability of the different primal cuts without adjustment for either carcass weight or fat score varied from 0.14 (bavette) to 0.75 (topside) with the mean heritability across all cuts being 0.49 (Table 1); the heritability of the groups of cuts was 0.42 (frying), 0.46 (mince), and 0.73 (roasting). The heritability estimates of the cuts all reduced (the mean heritability reduced to 0.33) when the cut weights were adjusted statistically to a common carcass weight and, with the exception of the rump and cuberoll, the heritability estimates reduced further when also adjusted to a common fat score.

Genetic Correlations Between the Cut Traits and Carcass Weight, Fat, and Conformation

The genetic correlations between the individual primal cuts and groups of primal cuts with the macro-carcass traits of carcass weight, fat score, and conformation are in Table 2. Little variability existed in the genetic correlations between the individual primal cuts with carcass weight although this is not unexpected given the part-whole relationship that exists between carcass weight and each of the retail cuts; the standard deviation of the correlations was only 0.05 with the correlations varying from 0.77 (cuberoll with carcass weight) to 0.93 (LMC with carcass weight). All 3 groups of primal cuts were very strongly genetically correlated (i.e., ≥0.92) with carcass weight. The genetic correlations between the individual carcass cuts with carcass fat varied more per trait (Table 2) ranging from −0.30 (knuckle with carcass fat) to 0.54 (bavette with carcass fat).

The genetic correlations between the individual primal cuts and unadjusted carcass conformation

Table 2. Genetic correlations (SE) between the different carcass cuts with carcass weight (weight) carcass fat score (fat) and finally carcass conformation without any adjustment for the other carcass traits, with adjustment for carcass weight, or with adjustment for carcass weight and fat

			Conformation		
Cut[1]	Weight	Fat	No adjustment	Adjustment for carcass weight	Adjustment for carcass weight and fat
Topside	0.88 (0.01)	−0.29 (0.04)	0.73 (0.02)	0.63 (0.03)	0.64 (0.03)
Silverside	0.92 (0.01)	−0.17 (0.05)	0.70 (0.03)	0.52 (0.05)	0.49 (0.05)
Eye of round	0.79 (0.02)	−0.17 (0.05)	0.73 (0.02)	0.57 (0.03)	0.56 (0.03)
Knuckle	0.88 (0.01)	−0.30 (0.04)	0.65 (0.03)	0.43 (0.04)	0.41 (0.04)
Rump	0.86 (0.02)	−0.04 (0.05)	0.65 (0.03)	0.39 (0.05)	0.41 (0.05)
Striploin	0.88 (0.02)	0.20 (0.07)	0.70 (0.04)	0.48 (0.07)	0.56 (0.07)
Fillet	0.84 (0.02)	−0.24 (0.06)	0.63 (0.04)	0.34 (0.06)	0.30 (0.07)
Cuberoll	0.77 (0.05)	0.07 (0.10)	0.44 (0.08)	0.03 (0.10)	0.07 (0.10)
Bavette	0.78 (0.05)	0.54 (0.07)	0.34 (0.08)	−0.19 (0.09)	−0.08 (0.12)
Brisket	0.84 (0.02)	0.10 (0.06)	0.58 (0.04)	0.18 (0.06)	0.23 (0.06)
Chuck Tender	0.86 (0.02)	−0.11 (0.06)	0.43 (0.04)	−0.25 (0.06)	−0.27 (0.00)
LMC	0.93 (0.01)	−0.20 (0.05)	0.58 (0.03)	0.19 (0.05)	0.14 (0.06)
Chuck and Neck	0.87 (0.01)	−0.16 (0.05)	0.53 (0.03)	0.10 (0.05)	0.07 (0.05)
Heel and shank	0.89 (0.01)	−0.22 (0.04)	0.62 (0.03)	0.39 (0.04)	0.35 (0.04)
Frying	0.94 (0.01)	0.07 (0.07)	0.75 (0.04)	0.64 (0.07)	0.65 (0.07)
Roasting	0.92 (0.01)	−0.26 (0.05)	0.73 (0.02)	0.63 (0.04)	0.64 (0.04)
Mince	0.96 (0.01)	−0.06 (0.09)	0.62 (0.06)	0.06 (0.08)	0.03 (0.08)

[1]LMC is the leg of mutton cuts plus miscellaneous.

varied from 0.34 (bavette with carcass conformation) to 0.73 (both eye of the round and topside with carcass conformation). The mean of the genetic correlations between the primal cuts in the forequarter with carcass conformation was 0.47 while the mean of the genetic correlations between the primal cuts in the hindquarter with carcass conformation was 0.65. Adjusting phenotypically for differences in carcass weight had more of an impact on the genetic correlations with carcass conformation for cuts in the forequarter than for cuts in the hindquarter; the genetic correlations between the hindquarter carcass cuts and carcass conformation were, on average, 0.62 times as strong when differences in carcass weight were adjusted for. Once adjusted for differences in carcass weight, the correlations with carcass conformation for both the bavette and the chuck tender were actually negative (Table 2). Adjustment for differences in carcass fat (additional to adjustment for differences in carcass weight) had minimal impact on the genetic correlations with conformation; the exception was the bavette (Table 2). The genetic correlations between the groups of cuts (i.e., frying, roasting, mince) and unadjusted carcass conformation varied from 0.62 to 0.75 and did not change much when adjusted to a common carcass weight (Table 2).

Genetic Correlations Among the Carcass Cuts

The mean of the genetic correlations among all 14 primal cuts was 0.72 (Table 3) varying from 0.37 (between the knuckle and bavette) to 0.91 (between the knuckle and topside). When not adjusted to a common carcass weight, the mean of the genetic correlations among the hindquarter cuts was 0.76 while the mean of the genetic correlations among the forequarter cuts was 0.68. The mean of the genetic correlations between all forequarter cuts with all hindquarter cuts was 0.69. When adjusted to a common carcass weight, the mean of the genetic correlations among all 14 primal cuts was 0.10 varying from −0.60 (between the bavette and knuckle) to 0.64 (between the topside and knuckle). When adjusted to a common carcass weight, the mean of the genetic correlations among the hindquarter cuts was 0.28 while the mean of the genetic correlations among the forequarter cuts was 0.03 with the mean of the genetic correlations between all forequarter cuts with all hindquarter cuts being −0.01 (Table 3). The residual correlations among traits, with and without adjustment for carcass weight, are given in Supplementary Appendix 1.

Genetic Correlations with and Among the Primal Cut Groups

The genetic correlations between the individual primal cuts with the groups of cuts with or without adjustment for differences in carcass weight are given in Table 4. As expected, the genetic correlations between a given primal group of cuts with its component individual cuts were strong and, on average, were >0.83. The genetic correlation between striploin, rump and fillet with the frying group of cuts was 0.85, 0.91, and 0.98, respectively. Once, however, differences in carcass weight were adjusted for, the average of the genetic correlations for a group of cuts with its respective component cuts weakened and was, on average, 0.68 for frying, 0.84 for roasting, and 0.31 for mince. Interestingly, after accounting for differences in carcass weight, the correlation between some individual retail cuts with the groups of cuts changed from positive to negative. For example, the correlation between topside, silverside, eye of round, rump, and fillet with the mince group of cuts changed from, on average, 0.77 to an average of −0.14. The genetic correlations among the groups of cuts themselves were all strong (i.e., ≥ 0.79) with the strongest correlation existing between frying and roasting (0.91). The correlations among the groups of cuts weakened following adjustment to a common carcass weight.

Ability of Genetic Evaluation for Primal Cuts to Discriminate Animals on Primal Cut Weight

Table 5 outlines the mean weights of individual trimmed primal cuts stratified on EBV for the untrimmed weight of that cut. Irrespective of primal cut, and whether or not the EBV was adjusted for carcass weight or not, the mean phenotypic weight of the primal cuts were progressively lighter ($P < 0.001$) with each incremental reduction in the associated EBVs (Table 5). The differential in primal cut weights between extreme EBV groups was less when carcass weight was adjusted for (both in the estimation of the EBV but also in the subsequent phenotypic analyses). Nonetheless, relative to the weight of the primal cuts in the poorest EBV stratum, the mean weight of the primal cut in the highest EBV stratum was up to 24% heavier (i.e., rump weight). The regression of phenotypic carcass weight (with all fixed effects considered in the model) on rump, striploin, and fillet EBV not adjusted for carcass weight was 1.19 (0.04), 1.39 (0.04), and 1.36 (0.05), respectively. The regression of phenotypic carcass weight (with all fixed effects

Table 3. Genetic correlations (SE) among the raw carcass cuts (below diagonal) or following phenotypic adjustment for carcass weight (above diagonal)

	Topside	Silver-side	Eye of round	Knuckle	Rump	Striploin	Fillet	Cuberoll	Bavette	Brisket	Chuck Tender	LMC	Chuck & Neck	Heel & shank
Topside		0.57 (0.05)	0.61 (0.03)	0.64 (0.03)	0.30 (0.06)	0.24 (0.09)	0.28 (0.07)	0.06 (0.11)	−0.46 (0.10)	−0.10 (0.07)	−0.23 (0.06)	0.22 (0.06)	−0.02 (0.05)	0.38 (0.04)
Silverside	0.90 (0.01)		0.62 (0.05)	0.48 (0.03)	0.25 (0.08)	0.36 (0.11)	0.44 (0.03)	0.04 (0.14)	−0.24 (0.13)	−0.10 (0.09)	−0.14 (0.09)	−0.04 (0.09)	−0.03 (0.07)	0.33 (0.06)
Eye of round	0.86 (0.01)	0.88 (0.01)		0.47 (0.03)	0.19 (0.06)	0.41 (0.09)	0.20 (0.08)	0.12 (0.12)	−0.14 (0.11)	0.12 (0.07)	−0.21 (0.07)	0.22 (0.07)	0.01 (0.06)	0.29 (0.05)
Knuckle	0.91 (0.01)	0.88 (0.01)	0.80 (0.02)		0.25 (0.06)	0.43 (0.04)	0.44 (0.03)	0.09 (0.12)	−0.60 (0.09)	−0.21 (0.07)	0.43 (0.03)	0.21 (0.07)	0.03 (0.06)	0.50 (0.02)
Rump	0.82 (0.02)	0.85 (0.02)	0.74 (0.03)	0.83 (0.02)		0.42 (0.1)	0.12 (0.09)	−0.04 (0.14)	−0.08 (0.13)	0.01 (0.08)	0.43 (0.03)	−0.11 (0.08)	−0.32 (0.06)	0.12 (0.06)
Striploin	0.81 (0.03)	0.85 (0.04)	0.79 (0.04)	0.74 (0.04)	0.84 (0.03)		−0.01 (0.13)	−0.12 (0.17)	0.58 (0.17)	0.04 (0.12)	−0.25 (0.12)	−0.04 (0.11)	−0.10 (0.10)	−0.02 (0.10)
Fillet	0.80 (0.03)	0.82 (0.03)	0.68 (0.04)	0.80 (0.03)	0.73 (0.04)	0.71 (0.05)		−0.28 (0.16)	−0.41 (0.15)	−0.04 (0.10)	0.09 (0.10)	0.11 (0.09)	0.21 (0.08)	0.08 (0.08)
Cuberoll	0.65 (0.07)	0.69 (0.07)	0.62 (0.08)	0.73 (0.07)	0.61 (0.08)	0.54 (0.10)	0.51 (0.09)		0.14 (0.20)	0.23 (0.14)	0.07 (0.14)	−0.11 (0.13)	−0.13 (0.12)	−0.08 (0.12)
Bavette	0.52 (0.07)	0.50 (0.08)	0.48 (0.09)	0.37 (0.08)	0.57 (0.07)	0.75 (0.09)	0.45 (0.10)	0.58 (0.15)		0.25 (0.13)	−0.33 (0.14)	−0.66 (0.11)	0.17 (0.11)	−0.61 (0.09)
Brisket	0.73 (0.03)	0.72 (0.03)	0.70 (0.04)	0.69 (0.03)	0.72 (0.04)	0.74 (0.05)	0.66 (0.05)	0.72 (0.08)	0.71 (0.08)		−0.19 (0.09)	0.16 (0.08)	0.06 (0.07)	−0.24 (0.07)
Chuck Tender	0.69 (0.03)	0.75 (0.03)	0.59 (0.04)	0.75 (0.03)	0.69 (0.04)	0.63 (0.06)	0.75 (0.05)	0.68 (0.09)	0.45 (0.10)	0.63 (0.05)		0.28 (0.08)	0.24 (0.07)	0.01 (0.07)
LMC	0.85 (0.02)	0.84 (0.02)	0.78 (0.02)	0.84 (0.02)	0.76 (0.03)	0.81 (0.04)	0.81 (0.03)	0.73 (0.07)	0.49 (0.08)	0.79 (0.03)	0.83 (0.02)		0.18 (0.07)	0.30 (0.06)
Chuck and Neck	0.75 (0.02)	0.80 (0.02)	0.69 (0.03)	0.76 (0.02)	0.65 (0.03)	0.73 (0.04)	0.78 (0.03)	0.72 (0.07)	0.53 (0.08)	0.74 (0.03)	0.81 (0.02)	0.82 (0.02)		−0.15 (0.06)
Heel and shank	0.84 (0.01)	0.85 (0.02)	0.74 (0.03)	0.62 (0.02)	0.77 (0.02)	0.74 (0.04)	0.72 (0.03)	0.65 (0.07)	0.47 (0.08)	0.71 (0.03)	0.74 (0.03)	0.88 (0.02)	0.74 (0.02)	

considered in the model including carcass weight) on rump, striploin, and fillet EBV adjusted for carcass weight was 1.16 (0.06), 1.14 (0.06), and 1.40 (0.10), respectively.

DISCUSSION

Genetic gain has been well-proven to be successful once both genetic variability exists and data are available from which to aid selection decisions (Berry et al., 2014; García-Ruiz et al., 2016). Nonetheless, routine access to data can often be a stumbling block to achieving genetic gain, especially for difficult to measure traits such as primal carcass cut weights. Compiling a business case to justify phenotyping strategies, however, requires knowledge of the potential gains achievable. The extent of genetic variability in a trait determines its evolvability (Houle, 1992) and thus the capacity to alter the trait through breeding. Nonetheless, genetic covariances with other traits can also impact the potential for change through breeding, especially if there is a desire to change positively correlated traits in opposite directions (or even halt genetic change in one trait), or change negatively correlated traits in the same direction. Hence, knowledge of the genetic variability in traits independent of their association with other important traits under (proposed) selection is a cornerstone to the optimal design of breeding schemes. While the boning out (and subsequent collation of the resulting data) of individual carcasses is currently not routine, the present study attempted to quantify the potential of breeding to alter the morphology of an animal; of greatest interest was the ability to increase the proportion of valuable cuts in a carcass without any consequences for carcass size (i.e., reflected by carcass weight in the present study). Clear genetic variability in the weight of high value primal carcass cuts was evident in the present study, even when adjusted phenotypically to a common carcass weight. Moreover, the ability of parental average measures of genetic merit to stratify carcasses on primal cut weight was also illustrated.

Potential Genetic Gain Achievable in Cut Weights

A relatively simple approach to increasing the value of a carcass is to select for heavier carcasses; carcass weight is measured on almost all slaughtered animals globally and, in many cases, these data are available for genetic evaluations (Pabiou et al., 2012; Englishby et al., 2017). Based on the genetic parameters estimates for carcass weight,

Table 4. Genetic correlations (standard errors in parenthesis) between the individual cuts with groups of cuts without any adjustment for carcass weight (unadjusted) or with phenotypic adjustment for carcass weight (adjusted to a common carcass weight)

	Unadjusted			Adjusted to a common carcass weight		
Cut[1]	Frying	Roasting	Mince	Frying	Roasting	Mince
Topside	0.91 (0.02)	0.98 (0.00)	0.81 (0.03)	0.49 (0.08)	0.92 (0.01)	−0.15 (0.09)
Silverside	0.94 (0.02)	0.96 (0.01)	0.86 (0.03)	0.54 (0.11)	0.75 (0.03)	−0.14 (0.12)
Eye of round	0.86 (0.03)	0.91 (0.01)	0.73 (0.05)	0.51 (0.09)	0.92 (0.01)	−0.20 (0.10)
Knuckle	0.85 (0.03)	0.95 (0.01)	0.85 (0.03)	0.23 (0.10)	0.78 (0.03)	0.01 (0.10)
Rump	0.98 (0.01)	0.87 (0.02)	0.76 (0.04)	0.89 (0.04)	0.25 (0.07)	−0.22 (0.11)
Striploin	0.91 (0.02)	0.82 (0.04)	0.64 (0.08)	0.68 (0.08)	0.27 (0.10)	0.09 (0.15)
Fillet	0.85 (0.03)	0.83 (0.03)	0.69 (0.07)	0.47 (0.09)	0.43 (0.08)	−0.01 (0.13)
Cuberoll	0.51 (0.10)	0.74 (0.07)	0.90 (0.11)	−0.43 (0.17)	0.09 (0.13)	0.06 (0.18)
Bavette	0.69 (0.09)	0.43 (0.09)	0.58 (0.10)	0.15 (0.18)	−0.51 (0.11)	−0.11 (0.17)
Brisket	0.78 (0.04)	0.77 (0.03)	0.81 (0.05)	−0.12 (0.12)	−0.05 (0.08)	0.21 (0.12)
Chuck Tender	0.73 (0.05)	0.73 (0.03)	0.91 (0.02)	−0.09 (0.12)	−0.23 (0.08)	0.42 (0.09)
LMC	0.87 (0.03)	0.87 (0.02)	0.91 (0.01)	−0.10 (0.12)	0.19 (0.07)	0.47 (0.09)
Chuck and Neck	0.80 (0.03)	0.80 (0.02)	0.94 (0.01)	−0.11 (0.10)	−0.04 (0.07)	0.82 (0.05)
Heel and shank	0.83 (0.03)	0.88 (0.01)	0.85 (0.03)	0.18 (0.10)	0.46 (0.05)	0.02 (0.10)
Frying						
Roasting	0.91 (0.02)			0.48 (0.10)		
Mince	0.79 (0.06)	0.85 (0.03)		0.12 (0.16)	−0.23 (0.11)	

[1]LMC is the leg of mutton cuts plus miscellaneous.

Table 5. Least squares means (standard error in parenthesis) for the trimmed weights of rump, striploin and fillet cuts by stratum of parental average genetic merit for each cut weight (unadjusted) as well as when adjusted to a common carcass weight both in the genetic evaluation but also in the association analyses; also included is the number of records (N) and mean (standard deviation) of the entire validation dataset

	Rump		Strip Loin		Fillet	
N	3,745		4,237		3,804	
Mean (SD)	13.22 (2.37)		13.74 (2.55)		6.33 (0.90)	
Stratum	Unadjusted	Adjusted	Unadjusted	Adjusted	Unadjusted	Adjusted
Very light	11.23 (0.16)	12.79 (0.10)	11.91 (0.16)	13.28 (0.12)	5.52 (0.05)	6.12 (0.04)
Light	12.46 (0.15)	13.36 (0.10)	12.82 (0.16)	13.89 (0.12)	5.94 (0.04)	6.32 (0.04)
Heavy	13.61 (0.15)	13.79 (0.10)	14.42 (0.16)	14.53 (0.12)	6.27 (0.04)	6.46 (0.04)
Very heavy	13.92 (0.15)	14.07 (0.10)	14.71 (0.16)	14.87 (0.12)	6.46 (0.04)	6.56 (0.04)

and between carcass weight and the individual primal cuts, a 10 kg increase in genetic merit for carcass weight is expected to increase the weight of the frying cuts by 1.03 kg with the roasting cuts expected, on average, to increase by 2.10 kg. Carcass conformation is also clearly a useful predictor of several primal cut traits (Table 2). The strongest genetic correlations with carcass conformation were detected for the primal cuts, visible from the outside of the carcass, and located near the rump of the animal (i.e., topside, silverside, eye of the round, knuckle), and, to a lesser extent, from the loin area (i.e., striploin and rump). These genetic correlations remained relatively moderately strong (i.e., ≥0.39) even when adjusted to a common carcass weight. Based on the genetic parameters from the present study, for the same carcass weight, a one unit increase in genetic merit for carcass conformation (scale of 1 to 15) is expected to result in a 1.44 kg increase in the weight of the roasting group of cuts but only a 0.70 kg increase in the weight of the frying group of cuts and just a 0.15 kg increase in the weight of the mince cuts.

Even if carcass weight or conformation data were not routinely available or useful to genetic evaluations on all animals (e.g., due to missing parentage), the large heritability of carcass weight and conformation documented in the present study and elsewhere (Ríos Utrera and van Vleck, 2004) imply that massive quantities of carcass data are not actually required to achieve a high accuracy of selection, once of course, the structure of the data is appropriate. Considerable genetic variability is also known to exist for carcass weight and conformation

with reported coefficients of genetic variation for carcass weight of between 0.05 and 0.08 (the present study; Pabiou et al., 2009; Kause et al., 2015). Hence, great scope exists to increase carcass weight, and therefore carcass value. Animal size, however, relates to animal efficiency with heavier animals, on average, requiring more feed (Crowley et al., 2010); this greater feed demand, especially for the mature herd, has implications for feed availability for growing animals but also for the environmental footprint of the production system. Such a paradox therefore necessitates evaluation of the capacity to alter the value of a carcass without necessarily (or at least proportionally) increasing carcass weight.

While the coefficient of genetic variation is a useful statistic to quantify the potential to alter a trait genetically (Houle, 1992), in this instance, it is the coefficient of genetic variation in primal cut weight, adjusted to a common carcass weight which is mainly of interest. Although presented in Table 1 is the coefficient of genetic variation adjusted phenotypically to a common carcass weight, little difference was evident when the primal cut weights were adjusted genetically to a common carcass weight based on the genetic correlations with carcass weight presented in Table 2. Clearly, given the strong genetic (Table 2) correlations between the individual primal cuts and carcass weight, the genetic standard deviation, on average, more than halved once adjusted to a common carcass weight. Nonetheless, the coefficient of genetic variability was still, on average, 0.04, even after adjusting to a common carcass weight. This coefficient of genetic variation is similar, albeit slightly less, than traits such as milk yield in dairy cows (0.062 to 0.067; Berry et al., 2003) which are known to have improved rapidly through breeding. Hence, genetic change in individual primal carcass cut weights, without necessarily changing carcass weight, is indeed possible. The frying group of cuts comprised of the rump, striploin and fillet constitute, for most part, the most valuable fraction of the carcass. The genetic standard deviation for the frying cuts adjusted phenotypically to a common carcass weight was 1.1 kg in the present study. Therefore, the mean expected difference in the weight of frying cuts for the same carcass weight between the top 10% and bottom 10% of animals genetically divergent for adjusted frying cut weight is expected to be 3.86 kg. Relative to the mean frying weight in the present study of 43.28 kg (Table 1), this represents a 9% difference.

While knowledge of the extent of genetic variability independent of carcass weight is important, the extent of genetic independence of individual cuts from other individual cuts is also informative. Consistent with the results from the present study, strong genetic correlations have been reported between raw primal cut weights in cattle; from a population of 842 Chianina cattle, Sarti et al. (2013) reported genetic correlations varying from 0.66 to 0.95 between the 7 primal cuts of brisket, fore shank, chuck, rib, short plate, round, and loin. When Sarti et al. (2013) expressed the primal cut weights as a percentage of carcass weight, the genetic correlations among the traits all weakened with some even being negative; this was consistent with the trends also observed in the present study for the partial genetic correlations (adjusted for differences in carcass weight) among the primal cut weights.

Achieving Genetic Change in Primal Carcass Cut Weights

Given that the results from the present study clearly demonstrate the existence of exploitable genetic variability in both individual primal cuts and group of cuts, routine access to data from which to generate accurate genetic evaluations is likely to then be the biggest limiting factor to achieving genetic gain. The accuracy of selection, irrespective of whether based on traditional pedigree-based genetic evaluations (Cameron, 1997) or genomic evaluations (Daetwyler et al., 2008), is a function of both the heritability of the trait and the quantity of phenotypic data available. Although the correlations between carcass conformation and some of the primal cuts was moderate, the accuracy of the genetic evaluations for the individual primal cuts reaches an asymptote at this correlation, and thus actual phenotypic data on the primal cut itself (or another predictor trait weakly correlated with carcass conformation) would be required. Nonetheless, while accuracy of selection is important, the accuracy of predicting the phenotypic value, even if the true breeding value is known, is capped by the square root of the heritability. The expectation is that a one unit difference among animals in EBV should translate to a one unit difference in phenotype; the regression coefficients in the present study for the EBV of primal cuts on the respective phenotypic primal cut were all greater ($P < 0.05$) than one; this implies that the heritability estimate may in fact be an underestimate. While being able to predict the future phenotypic value of individual animals would be ideal, this is unlikely to be possible given the influences of nongenetic effects. Berry et al. (2017a), however, in the review

of breeding for improved meat sensory characteristics proposed that being able to stratify groups of animals on futuristic meat sensory characteristics could be useful. Results from the present study (Table 5) clearly show that phenotypic differentiation of groups of animal through EBVs is possible for the primal cuts of rump, striploin, and fillet. In fact, large differences were detected between groups of animals extreme for EBVs, despite the mean reliability for the EBVs of the rump, striploin, and fillet cuts being between 0.07 and 0.11. Improving the reliability of the genetic evaluations through either more phenotypic primal cut data, more phenotypic data on correlated traits (e.g., linear scores), or through genomic information, should lead to a greater discriminative ability of the genetic evaluations. It is worth noting however, that the reliability based solely on parentage information can never be greater than 0.49 (i.e., one quarter of the reliability of the sire plus one quarter the reliability of the dam).

Using frying cuts as an example, the genetic standard deviation for frying cuts (not adjusted to a common carcass weight) was 2.36 kg with a genetic correlation with carcass weight of 0.94. Therefore selection for heavier carcass weight, even with no data on frying cuts will lead to heavier frying cuts; the rate of genetic change per generation interval per selection intensity unit could be as high as 2.22 kg with this strategy (compared to the equivalent statistic of 2.36 kg if selection was on frying cuts alone). This strategy, however, would also result in heavier carcasses. If selection for heavier frying cuts was desired, without a concomitant increase in genetic merit for carcass weight, the maximum genetic gain achievable would be $\sqrt{1-0.94^2} \cdot 2.36 = 0.81$ kg. Therefore, genetic gain on the weights of individual primal cuts is achievable while holding genetic merit for carcass weight constant, albeit at a slower rate than selecting on the trait alone or through indirect selection via heavier overall carcasses.

While heritability estimates in the present study differed by primal cut (from 0.14 to 0.75 with a mean of 0.48), the estimates are relatively consistent with previously documented heritability estimates for carcass cut weights in cattle of between 0.21 and 0.74 (Sarti et al., 2013) and between 0.03 and 0.86 (Pabiou et al., 2009). The relatively high heritability estimates for many of the primal cut traits in the present study, and elsewhere (Pabiou et al., 2009; Sarti et al., 2013), implies that vast quantities of data are not required and, in fact, high accuracy could be achieved from the boning out of cattle from specialized "phenotyping herds" which record deep phenotypes on animals representative of the germplasm being used commercially (Banks, 2011). Moreover, the use of sensor and image analyses technology is intensifying in agriculture (Scholz et al., 2015; Rutten et al., 2018) thus providing an alternative solution to procuring (primal cut) data on a larger population of animals for use in genetic evaluations. Pabiou et al. (2011a) used video image analyses of cattle carcasses to predict groups of primal cuts based on their retail value; Pabiou et al. (2011a) reported an accuracy of prediction (i.e., correlation) of up to 0.96 between groups of primal carcass weights (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. Pabiou et al. (2011b) subsequently estimated genetic parameters for these predicted cut groups, reporting heritability estimates of between 0.13 and 0.47 for the 4 groups of retail cut yields predicted. Therefore, should the boning out of a relatively small number of genetically diverse carcasses still not be possible, alternatives to predict these cut yields also exist.

CONCLUSIONS

Analysis of the largest database with individual primal cut weights in cattle clearly demonstrate the existence of significant exploitable genetic variability even when the desire is to increase primal cut weight without an associated increase in carcass weight. The high heritability of many of the primal cuts infers that large datasets are not actually required to achieve high accuracy of selection and thus genetic gain. Based on the average heritability of the primal cuts of 0.48, only 7 progeny would be required to achieve an accuracy of selection of 0.70 from progeny records only. Even in the absence of recorded pedigree information, low-cost genomic tools can be used to reconstruct the relationships among animals (VanRaden, 2008), thus facilitating genetic evaluations for individual cut traits.

SUPPLEMENTARY DATA

Supplementary data are available at *Journal of Animal Science* online.

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