Genetic Parameters for Carcass Cuts Yields in Beef Cattle

T. Pabiou,[a, c, d] F. Fikse[b], A. Näsholm[c], A.R. Cromie[a], M.D. Drennan[d], M.G. Keane[d] and D.P. Berry[e]

[a] The Irish Cattle Breeding Federation, Shinagh House, Bandon, Co. Cork, Ireland.
[b] Swedish University of Agricultural Sciences, Interbull Centre, Department of Animal Breeding and Genetics, Uppsala, Sweden.
[c] Swedish University of Agricultural Sciences, Department of Animal Breeding and Genetics, Uppsala, Sweden.
[d] Grange Research Center, Teagasc, Dunsany, Co. Meath, Ireland
[e] Moorepark Dairy Production Research Center, Teagasc, Fermoy, Co. Cork, Ireland.

1) Introduction

In Ireland, as in most other countries, the value farmers generally receive for each carcass is predominantly based on carcass weight, carcass conformation and carcass fat score. The EUROP conformation class describes the development of the carcass with particular emphasis on the round, back, and shoulder. However, differences in retail value exist between different parts of the carcass (Morris *et al.*, 1999). Farmers should logically be rewarded for producing larger quantity of these high value cuts, but the current EUROP grading system, measuring the overall conformation and fat, may not be reflecting these differences within carcasses. The objective of this study was to estimate genetic parameters for yields of different carcass cuts and to quantify the implications of selection for carcass weight, conformation and fat score on the individual cut yields.

2) Materiel and methods

Two databases on carcass cut yields were used in the present study. The first database originated from a series of experiments run at a research herd over recent years while the second database was made available by an Irish supermarket chain.

Experimental dataset

A total of 538 dissections were made available on crossbred animals from the Teagasc beef research center in Dunsany, co. Meath, Ireland. These data will hereon in be referred to as the "experimental data". All the animals were processed in the same factory and the cuttings were supervised by the same Teagasc researcher. Animals without a known sire (n=158) were iscarded from the analysis. Contemporary group was defined as experimental treatment by slaughter date. There were 11 contemporary groups with at least 6 animals; 7 animals were discarded as they were in small contemporary groups. The remaining animals were from across 11 different treatments that investigated the performance of different finishing diets as well as animals of divergent genetic merit for growth rate and on an economic index. The animals slaughtered were either bulls (n=73) or steers (n=300). The average slaughter ages of the bulls and steers were 458 and 756 days respectively. Heterosis and recombination loss was computed for each animal.

Cold carcass weight (hereon in referred to as carcass weight) as well as carcass conformation and carcass fat grade, scored using the EUROP classification system (Anon, 2004), is recorded for each animal slaughtered in Ireland. In the present study the EUROP classification grades were transformed to a 15-point scale as outlined by Hickey *et al.* (2007). The right side of each carcass was dissected into 23 different cuts: 11 taken in the forequarter and 12 in the hindquarter. Using the ratio of total carcass weight over the right side carcass weight, the weight of the cuts measured from the right side of the carcass was extrapolated to a weight taken from the whole carcass. The retail beef yield was defined as the sum of the all meat cuts. Only some of the different cuts recorded were retained for estimation of variance components and some were grouped together into primal cuts. Figure 1 illustrates the location of the retained cuts.

The retained forequarter cuts were the front shin, brisket, flank, ribs, shoulder, chuck, and neck. The 13 long ribs and the flank were summed as 'ribs'. The clod cut and the whole outside shoulder muscles (blade steak, braising muscle, chuck tender, and leg of mutton cut) were labelled 'shoulder'. The chuck was cut from the first to the sixth thoracic vertebrae. For

the analysis, the chuck and the neck cuts were grouped as 'chuck'. The total weight of the forequarter meat was labelled 'foremeat' The retained hindquarter cuts were the cap of ribs, cube roll, strip-loin, rump, tail of rump, round, heel, and back shin. The cube roll and the cap of ribs were cut between the fifth and the eleventh thoracic vertebrae and were summed as 'rib roast'. The strip-loin is part of the *longissimus* muscles cut between the 10th thoracic vertebrae and the rump. The sum of the rump and tail of rump cuts was labelled 'sirloin'. The fillet also known as the tenderloin, is the *psoas* muscles, in the loin area. The round is the main part of the back leg, summing the silverside, topside, knuckle, and salmon cuts. The back shin and heel cuts were grouped as 'back shin'. The total weight of the hindquarter meat was labelled 'hindmeat'. In addition, an overall sum 'total meat' was computed from the relevant cuts from the forequarter and hindquarter respectively.

Commercial dataset

A total of 3,501 carcass dissections from pure and cross bred animals were also made available by an Irish supermarket chain. This data will be hereon in referred to as the "commercial data". All the animals were processed through the same meat processing plant. Animals with no known sire (n=2,502) as well as animals without data on herd prior to slaughter (n=16) were removed. Additionally, animals slaughtered younger than 12 months of age (n=2) were discarded. Age of the dam was grouped into 4 categories: missing data, 2 to 3 years old, 4 to 7 years old and ≥8 years old. Heterosis and recombination loss was computed for each animal. Contemporary groups of slaughter were generated using the algorithm of Crump *et al.* (1997) using herd of origin immediately prior to slaughter and date of slaughter as the variables of interest. The optimal contemporary group size was set at 6 animals with a minimum size of 4 animals. Remaining animals consisted of either heifers (n=575), bulls (n=26) or steers (n=34).

Cold carcass weight and EUROP classification were recorded for each animal as described above for the experimental dataset. Additional to the routinely recorded carcass traits, information on individual cut yields were also made available. The system of dissection used on these animals composed of 16 different cuts, 6 taken in

the forequarter, 6 in the hindquarter, and 4 from both locations. The sum of the cuts was defined as the retail beef yield. Not all of the different cuts were retained for estimation of variance components. The location of the cuts is presented in Figure 1.

Cuts retained for the analysis from the forequarter were the chuck, flat ribs, brisket, and flank. Additionally, the clod was grouped with the braised muscle and the chuck tender into a primal cut labelled 'blade'. The flat rib cut was taken from the ribs 1 to 6. The retained hindquarter cuts were rib roast, strip-loin, sirloin, fillet, and round. Due to occasional retail demand of T-bones steaks, whole strip-loin and fillet weights were only available on a reduce amount of data; the T-bone steak being cut through the strip-loin and the fillet. Four cuts were generated from both the forequarter and the hindquarter: the beef trimmings, steak trimmings, diced beef, and stew beef cuts. Diced and stew beef have been summed as one diced and stewed beef trait hereon referred as 'Dice&Stew'. In addition, all cuts were summed within the forequarter and hindquarter and will be referred to as 'Foremeat' and 'Hindmeat', respectively. Within carcass trait, observations greater than ±4 standard deviations from the mean estimated within sex by breed groups were set to missing. In order to keep a consistent dataset, if the cold carcass weight or one of the following major cuts: boneless rib steak, brisket, blade, rib roast, round, or sirloin was missing, the animal was removed from the analysis (n=31).

Analysis

Model building for fixed effects was under taken using PROC GLM (SAS, 2007) for both set of data. For the experimental dataset, the fixed effects kept in the model were contemporary group, age of the dam at the birth of the animal, heterosis (continuous variable), age of the animal at slaughter (continuous variable) as well as interactions. (Co)variance components were estimated with ASREML (Gilmour *et al.,* 2007) using a linear animal mixed model where relationships between animals were accounted for using a relationship matrix. A total 8,300 animals were included in the pedigree file and unknown ancestors were included as phantom groups of the breeds Belgian Blue, Charolais,

Friesian, Holstein, Limousin, Angus, Simmental, and unknown breed.

For the commercial dataset, the fixed effects considered for inclusion in the model were contemporary group, sex of the animal, age of the animal at slaughter (continuous variable) as well as interactions. The effect of age at slaughter on the carcass traits differed by sex of the animal and thus a two-way interaction between animal sex and age at slaughter was also included in the model. (Co)variance components were estimated using a linear animal mixed model in ASREML (Gilmour *et al.,* 2007) where relationships between animals were accounted for using a relationship matrix. A total of 6,250 animals were included in the relationship matrix where unknown ancestors were included as phantom groups of breeds: Belgian Blue, Charolais, Friesian, Holstein, Limousin, and unknown breed.

Within both datasets a series of bivariate analyses were used to estimates correlations between the different traits. Only correlations among carcass weight, carcass conformation, carcass fat, shoulder, chuck, rib roast, strip-loin, sirloin, round, and fillet are presented in the tables.

Results

Experimental data

Descriptive statistics and heritability estimates for carcass weight, carcass conformation, carcass fat grade, retail yield, and the meat cuts are presented in Table 1. The average cold carcass weight was 339 kg and the average retail cut yield was 193 kg (57% of the total cold carcass weight). The average EUROP conformation and fat grades in the animals in the present study corresponded approximately to "R=" and "3=", respectively. The forequarter represented on average 54% of the carcass weight and the major cut of the forequarter was the ribs (35 kg – 18% of the retail cut weight). The round cut was the biggest cut in the hindquarter (48 kg – 25% of the retail cut weight), and the smallest was the tenderloin averaging 6 kg (3% of the retail cut weight).

Heritability of carcass weight and retail cut weight was 0.32 and 0.68, respectively. In the

forequarter, the shoulder and the chuck primal cuts had the highest heritability (0.61 and 0.69, respectively). Low heritability estimates were obtained for the brisket and ribs cuts (≤0.07). The heritability for the total forequarter meat was 0.49. In the hindquarter, the round cut was most heritable (0.79) while the lowest heritability estimates were for the rib roast (0.12) and the fillet (0.28). The heritability for the total hindquarter meat was 0.60. The coefficient of genetic variation of the cuts varied from 1.8% (ribs) to 13.0% (chuck).

Phenotypic and genetic correlations between the major cuts (blade, chuck, brisket, rib roast, strip-loin, sirloin, round, fillet) and carcass weight, conformation and fat score are detailed in Table 2. Phenotypically carcass weight and conformation were positively associated with the different carcass cut yields; the phenotypic correlations between carcass fat and the carcass cut yields were all close to zero. Few genetic correlations with carcass weight, conformation and fat score were more than twice their respective standard error. However, carcass weight was positively genetically correlated with the different carcass cut yields while carcass fat score was negatively genetically correlated with the different cuts. The genetic correlations among the different carcass cuts were all strongly positive (≥0.73)

Commercial data

Descriptive statistics and heritability estimates for carcass weight, retail yield, carcass conformation, carcass fat grade, and the meat cuts are presented in Table 1. Average cold carcass weight was 290 kg and the retail cut yield averaged 196 kg (68% of the total cold carcass weight). The average EUROP conformation and fat grades in the animals in the present study corresponded approximately to "R+" and "3", respectively. Only 3 carcass conformation classes (conformation 5, 8, and 11) were represented in the dataset with 69% of the animals graded as class "8". Six carcass fat classes were represented (class 3, 4.5, 6, 8.25, 9, and 9.75) with 63% of the animals residing in class "6". Within the forequarter cuts, the chuck and the blade muscles equally made up 33% of the total forequarter meat weight (average 38 kg - 19% of retail cut weight). The round cut made up the major proportion (56%) of the hindquarter

cut weight, while the tenderloin averaged 5 kg (6% of total weight the back part of the carcass) represented the smallest proportion of the hindquarter.

Heritability of cold carcass weight and retail cut weight were 0.59 and 0.52, respectively. Carcass conformation and fat grading data were available for only a limited number of animals; the heritability estimates were high (0.79 and 0.63 for carcass conformation and fat grade, respectively). In general, heritability estimates of the different cuts in both the forequarter and hindquarter were all moderate ranging from 0.28 (flat ribs) to 0.62 (tenderloin). The coefficient of genetic variation of the cuts varied from 5.9% (round) to 10.0% (brisket, flank).

Phenotypic and genetic correlations between the major cuts (blade, chuck, brisket, rib roast, strip-loin, sirloin, round, fillet) and carcass weight, conformation and fat score are summarized in Table 3. Both the phenotypic and the genetic correlations between the cold carcass weight and across all the cuts were moderate to strongly positive; the phenotypic correlations ranged from 0.48 (brisket) to 0.77 (round and blade) while the genetic correlations ranged from 0.47 (chuck) to 0.75 (tenderloin). The phenotypic and genetic correlations between carcass conformation and the different guts were all positive. The phenotypic correlations between carcass fat and the different cuts tended to be negative or close to zero while the genetic correlations were mostly negative but not different from zero. Among the different carcass cuts, all phenotypic correlations were positive and moderate ranging from 0.48 to 0.76. The genetic correlations between the cuts were also positive but stronger than their respective genetic correlations, ranging from 0.36 to 0.99.

Discussion

Differences in carcass weight across the two datasets were observed: 339 kg and 290 kg in the experimental and commercial data set, respectively. The heritability observed from both the experimental and the commercial dataset for cold carcass weight is in accordance with the mean estimate of 0.40 reported by Rios Utrera and Van Vleck (2004) following an extensive review of heritability estimates for carcass traits in 56 studies.

Large differences in heritability were observed between the experimental and the commercial datasets for the certain traits. These observed discrepancies may be due to factors such as i) population specific genetic parameters, and ii) some possible differences in the cutting method even for well located cuts such as the chuck or the brisket. Additionally relatively large standard errors were observed for the heritability estimates of most traits. Heritability estimates observed for the forequarter and the hindquarter were consistent with the literature (e.g., Brackelsberg et al.,1971; Cundiff et al., 1969; Cantet et al., 2003.)

The phenotypic correlations between carcass conformation, carcass fat and carcass weight across the two datasets are consistent with those cited by Hickey et al. (2007), ranging from 0.17 to 0.38. The genetic correlations observed in the experimental dataset between carcass weight and EUROP conformation and fat grading are negative (-0.06 and -0.19) and different to the positive, albeit weak genetic correlations (0.11 and 0.26) reported by Hickey et al. (2007); the genetic correlation between carcass weight and conformation and fat score estimated from the commercial dataset was -0.27 and 0.42, respectively. Coupled with the heritability estimates reported in the present study being within the range of heritability estimates reported by Hickey et al. (2007) in a large database on Irish cattle, this suggests that the variance components estimated from the sample population in the present study are similar to those estimated using national data.

Strydom and Smith (2005) observed that, phenotypically, carcass visual conformation and weight of the beef cuts were positively associated. This association was also observed in both our datasets where the phenotypic correlations between carcass weight and carcass conformation was positive and moderate (0.38 in the experimental study, and 0.17 in the commercial study). In both datasets, carcass weight was moderate to strongly positively correlated, both phenotypically and genetically, with the various carcass cuts; genetic correlations ranged from 0.54 (strip-loin) to 0.99 (fillet) in the experimental dataset, and from 0.47 (chuck) to 0.75 (fillet) in the commercial study. This is not unexpected given the part whole relationship between the different cuts and carcass weight. The genetic correlations between

the cuts were positive and large in the experimental dataset (minimum 0.78), and also positive but moderate to large in the commercial dataset (minimum 0.35). These results show that direct selection on a primal beef cut would result in indirect positive selection on all the cuts although some of the correlations were less than unity, albeit with large standard errors.

Implications

The existence of moderate to large heritability estimates, albeit with large standard errors, and large coefficients of genetic variation suggest that genetic selection for individual carcass cut yields may be fruitful. Genetic correlations among all carcass cuts were moderate to strongly positive although some were less than unity, albeit with sometimes large standard errors, indicating a potential benefit of placing more emphasis on some higher value cuts to increase carcass value. This is further substantiated by the genetic correlations with carcass weight, that although positive, implying that selection for increased carcass weight will, on average increase the weight of each cut, the correlations were less than unity suggesting a benefit of more direct selection on high value cuts. Further research is to be undertaken on the feasibility of using routinely collected carcass digital images to predict individual carcass cut yields and to subsequently investigate the feasibility of genetic selecting for these traits.

Acknowledgements

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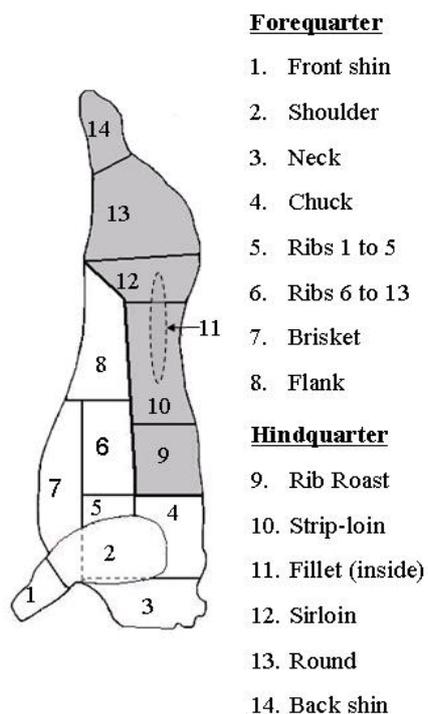**Figure 1.** Location of the different cuts (Gerrard and Mallion, 1977).

Forequarter
1. Front shin
2. Shoulder
3. Neck
4. Chuck
5. Ribs 1 to 5
6. Ribs 6 to 13
7. Brisket
8. Flank

Hindquarter
9. Rib Roast
10. Strip-loin
11. Fillet (inside)
12. Sirloin
13. Round
14. Back shin

Table 1. Number of animals (N), raw mean, phenotypic standard deviation (σ_p), and heritability (h^2) for carcass traits common to the experimental and the experimental dataset.

Trait	Experimental dataset				Commercial dataset			
	N	Mean	σ_p	h^2 (s.e.)	N	Mean	σ_p	h^2 (s.e.)
Carcass weight (kg)	373	339.3	55.9	0.42 (0.216)	635	290	30.9	0.59 (0.200)
Carcass conformation (scale 1-15)	373	7.4	2.7	0.44 (0.224)	345	9	1.5	0.78 (0.265)
Carcass fat (scale 1-15)	373	6.9	1.5	0.31 (0.189)	345	6	1.2	0.63 (0.264)
Retail cut weight (kg)	373	193.3	38.1	0.76 (0.248)	635	196	23.6	0.52 (0.191)
Shoulder (kg)	373	27.8	5.7	0.75 (0.238)	635	12	1.5	0.61 (0.195)
Strip-loin (kg)	373	11.2	2.7	0.45 (0.231)	523	11	1.4	0.41 (0.217)
Sirloin (kg)	373	13.3	3.5	0.61 (0.227)	635	10	1.2	0.55 (0.199)
Round (kg)	373	48.1	10.9	0.84 (0.247)	635	43	5.6	0.42 (0.193)
Fillet (kg)	373	5.8	1.2	0.32 (0.214)	520	5	0.6	0.62 (0.204)

Table 2. Genetic (above the diagonal) and phenotypic* (below the diagonal) correlations between different carcass cuts estimated from the experimental dataset.

	Cc weight	Cc conf.	Cc fat	Shoulder	Strip-loin	Sirloin	Round	Fillet
Carcass weight		-0.06 (0.414)	-0.19 (0.466)	0.7 (0.153)	0.54 (0.258)	0.86 (0.130)	0.93 (0.082)	0.99 (0.135)
Carcass conformation	0.38		0.40 (0.377)	0.16 (0.303)	0.23 (0.09)	0.48 (0.172)	0.33 (0.265)	0.19 (0.416)
Carcass fat	0.20	0.05		-0.35 (0.348)	-0.50 (0.419)	-0.34 (0.359)	-0.50 (0.340)	-0.04 (0.468)
Shoulder	0.62	0.34	-0.06		0.82 (0.163)	0.98 (0.085)	0.86 (0.090)	0.84 (0.102)
Strip-loin	0.66	0.42	0.00	0.57		0.92 (0.118)	0.84 (0.126)	0.86 (0.223)
Sirloin	0.72	0.42	-0.12	0.63	0.60		0.99 (0.056)	0.78 (0.103)
Round	0.77	0.45	-0.07	0.70	0.66	0.72		0.98 (0.116)
Fillet	0.67	0.35	-0.06	0.61	0.56	0.66	0.74	

Maximum phenotypic standard error of correlation was 0.075.

Table 3. Genetic (above the diagonal) and phenotypic (below the diagonal) correlations between different carcass cuts estimated from the commercial dataset.

	Cc weight	Cc conf.	Cc fat	Blade	Strip-loin	Sirloin	Round	Fillet
Carcass weight		-0.27 (0.107)	0.42 (0.273)	0.63 (0.144)	0.59 (0.214)	0.67 (0.148)	0.62 (0.173)	0.75 (0.135)
Carcass conformation	0.17		-0.25 (0.307)	0.17 (0.293)	0.69 (0.246)	0.31 (0.277)	0.21 (0.337)	0.13 (0.292)
Carcass fat	0.22	-0.16		-0.18 (0.333)	-0.21 (0.445)	-0.09 (0.347)	-0.34 (0.389)	-0.32 (0.346)
Blade	0.77	0.30	-0.06		0.49 (0.259)	0.91 (0.081)	0.86 (0.096)	0.96 (0.069)
Strip-loin	0.68	0.36	0.07	0.57		0.39 (0.295)	0.35 (0.316)	0.46 (0.264)
Sirloin	0.71	0.36	-0.02	0.69	0.57)		0.81 (0.117)	0.74 (0.138)
Round	0.77	0.42	-0.16	0.76	0.65	0.73		0.83 (0.119)
Fillet	0.68	0.24	-0.12	0.67	0.53	0.68	0.74	

Maximum phenotypic standard error of correlation was 0.074.