Genetics of Carcass Composition in Irish Cattle Exploiting Carcass Video Image Analysis

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Doctoral Thesis
Swedish University of Agricultural Sciences
Uppsala 2012

Acta Universitatis agriculturae Sueciae

2012:5

Cover: 2D & 3D carcass pictures as taken by VBS2000 grading machine (E+V GmbH, Germany). (Photo design: T. Pabiou)

ISSN 1652-6880
ISBN 978-91-576-7689-4

Print: SLU Service/Repro, Uppsala 2012

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Abstract

In this thesis we investigated the feasibility of breeding for phenotypes predicted from video image analysis (VIA). In meat factories in Ireland, digital images are routinely taken after slaughter to derive EUROP conformation and fat grades. Two datasets (1,048 carcasses in total) on individual carcass dissections were made available for this study, one by a research center and the other by a commercial partner. Dissection data consisted of eight and six primal cuts taken in the hind- and fore-quarter, respectively, and analyses revealed significant genetic variations in these data. Heritabilities of primal cut weights ranged from 0.03 to 0.83 in the fore-quarter cuts, and from 0.14 to 0.86 in the hind-quarter cuts. Primal cut weights were subsequently grouped into four wholesale cut weights according to their retail values: lower value cuts, medium value cuts, high value cuts, and very high value cuts. Equations to predict wholesale cut weights were subsequently derived from VIA image parameters. Accuracy of prediction were >0.84 and >0.72 in the steer and heifer datasets, respectively.

Genetic analysis of the wholesale cut weights predicted in a large national dataset of steers and heifers revealed heritabilities of 0.18, 0.27, 0.40, and 0.17 for lower value cuts, medium value cuts, high value cuts, and very high value cuts, respectively. Genetic correlations among predicted wholesale cut weights ranged from 0.45 to 0.89 across genders. Predicted wholesale cut weights were also strongly genetically correlated with animal price at weaning age (0.37 to 0.66), as well as price at post-weaning age (0.50 to 0.67) suggesting a benefit of indirect selection especially where data on carcass cut weights were not yet available.

Including predicted wholesale cut weights in a selection criteria increased genetic gain for carcass traits over and above the current selection practice of selection on EUROP conformation score. Expanding knowledge on wholesale cut weights and extending it to meat quality traits is an attractive option for Ireland.

Keywords: beef cattle, genetic parameters, video image analysis, carcass cuts, regression, accuracy.

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Dedication

Cette thèse est entièrement dédicacée à mes parents, Jean-Julien et Marie-Louise Pabiou ♥

Contents

List of Publications

This thesis is based on the work contained in the following papers, referred to by Roman numerals in the text:

I Pabiou T., Fikse W.F., Näsholm A., Cromie A.R., Drennan M.J., Keane M.G., & Berry D. P. (2009). Genetic parameters for carcass cut weight in Irish beef cattle. *Journal of Animal Science,* 87:3865–3876.

II Pabiou T., Fikse W.F., Cromie A.R., Keane M.G., Näsholm A. & Berry D. P. (2010). Use of digital images to predict carcass cut yields in cattle. *Livestock Science,* 137: 130-140.

III Pabiou T., Fikse W.F., Amer P.R., Cromie A.R., Näsholm A. & Berry D. P. (2011). Genetic variation in wholesale carcass cuts predicted from digital images in cattle. *Animal,* 5(11): 1720-1727.

IV Pabiou T., Fikse W.F., Amer P.R., Cromie A.R., Näsholm A. & Berry D. P. (2011). Genetic relationships between carcass cut weights predicted from video image analysis and other performance traits in cattle (submitted manuscript).

Papers I-III are reproduced with the permission of the publishers.

Abbreviations

AI	Artificial Insemination
EU	European Union
HVC	High Value Cuts
ICBF	Irish Cattle Breeding Federation
LVC	Lower Value Cuts
MVC	Medium Value Cuts
REML	Restricted Maximum Likelihood
RMSE	Root Mean Square Error
VHVC	Very High Value Cuts
VIA	Video Image Analysis

1 Background

1.1 Appraising carcasses

Carcasses at slaughter differ greatly in both conformation and size, from emaciated cows at the end of lactation to double muscled specialised beef cattle. The necessity and ability to appraise carcass quality is the key to differentiating the product for different markets; some carcasses will yield more high priced joints while others will mostly yield minced meat.

1.1.1 Need of carcass classification

National initiatives to assess carcasses for fat cover and meat yield in Sweden, Germany, and the United States started in the 1970's (Riordan et al., 1978). In the same period, the Irish Department of Agriculture developed two 7-point scales to appraise conformation (i.e. carcass silhouette and compactness) and fat cover. Conformation was scored using the letters I. (excellent) R. E. L. A. N. D. (poor), while fat was scored on a 1 (very lean) to 7 (very fat) scale (Riordan et al., 1978). Carcass grading was undertaken by expert classifiers from the Irish Department of Agriculture.

Harmonised carcass classification became a requirement of the member states of the European Union (**EU**) in the early 1980's as the Common Agricultural Policy entered a system of subsidies and border tariffs, demanding a price reporting process (European Council regulation 1358/80 of 5 June 1980). European Council regulations 1208/81 of 28 April 1981 and 2930/81 of 12 October 1981 determined the Community scales for the classification of bovine carcasses. Notably amended in 1991 (European Council regulation 1026/91) with the introduction of gender categories (i.e. young bull, bull, steer, cow, heifer) and the addition of a superior class of conformation (class "S"), the classification of carcasses is currently widely used across slaughter houses in the EU as a basis for payment to producers. The appraisal of carcasses in the EU is currently based on scores given for both conformation and fat; these scores are usually referred to as the 'EUROP gradings' for conformation and fat. The aim of EUROP conformation grading is to give an appreciation of the carcass shape, in particular the round, back, and shoulder, using the letters S (superior), E, U, R, O, and P (poor) to describe the conformation of the carcass (Table 1).

Table 1. *Description of conformation classes in use in the European Union bovine classification system (European Council regulation 1183/06 of 24 July 2006)*

Conformation class	Description
S - Superior	All profiles extremely convex; exceptional muscle development (double-muscled carcass type)
E - Excellent	All profiles convex to super-convex; exceptional muscle development
U - Very good	Profiles on the whole convex; very good muscle development
R - Good	Profiles on the whole straight; good muscle development
O - Fair	Profiles straight to concave; average muscle development
P - Poor	All profiles concave to very concave; poor muscle development

The carcass fat classification system uses the scale 1 (low), 2, 3, 4 and 5 (very high) to measure the quantity of fat on the outside of the carcass and in the thoracic cavity (Table 2).

Table 2. *Description of fat classes in use in the European Union bovine classification system (European Council regulation 1183/06 of 24 July 2006)*

Fat class	Description
1 - Low	None up to low fat cover
2 - Slight	Slight fat cover, flesh visible almost everywhere
3 - Average	Flesh, with the exception of the round and shoulder, almost everywhere covered with fat, slight deposits of fat in the thoracic cavity
4 - High	Flesh covered with fat, but on the round and shoulder still partly visible, some distinctive fat deposits in the thoracic cavity
5 - Very high	Entire carcass covered with fat; heavy fat deposits in the thoracic cavity

EUROP gradings were based on subjective assessments by highly trained personnel. Boggaard et al. (1996) presented some limitations of European beef carcass grading operated by expert classifiers: bias can occur between groups of carcasses, classifiers' judgment can vary over time, and differences can be observed between classifiers. Objective carcass grading as operated by calibrated grading machines overcame these weaknesses. In Ireland, the accuracy (R^2) and fit (bias) of three classification machines (VIAscan, VBS2000, and BCC2) at predicting carcass classification in abattoir conditions for conformation and fat against a reference classification established by experts was documented by Allen et al. (2000).

1.1.2 Mechanical grading of carcasses in Ireland

The main technical challenges of mechanical grading systems are: i) to generate accurate predictions of carcass quality, and ii) to operate at line speed in slaughter houses. Allen (2005) detailed the technology available at the time to automatically predict the EUROP grades for conformation and fat. Three main steps exist in the mechanical grading process: 1) capture images of the carcass using camera(s), 2) estimate carcass measurements such as length, contour, angles, volumes, colour amongst others using image analysis, and 3) use an algorithm to predict the EUROP gradings from the collected data.

Three mechanical grading machines (VBS2000, VIAscan, BCC2) were evaluated using over 7,000 carcasses in Ireland and compared to three expert classifiers between 1999 and 2000. At the end of the trial, each of the three classification machines had the potential to be used for bovine classification purposes (Allen et al., 2000). A formal authorisation trial of the three systems was undertaken in Ireland in 2003 using 600 carcasses and each of the three mechanical grading systems exceeded the performance criteria laid down in the regulation 1215/03 of 7 July 2003 for authorisation. The use of the VBS2000 carcass grading machine was subsequently recommended by the Irish meat processing industry for EUROP mechanical grading in Irish slaughter houses. Since 2005, copies of the two pictures (tiff format) taken after slaughter by the VBS2000 mechanical grading machine (E+V GmbH, Germany) for each carcass to derive the EUROP conformation and fat grading have been stored in the Irish Cattle Breeding Federation (**ICBF**) database.

In practice, VBS200 mechanical grading machines use a one-angle colour camera, a holding frame, and a lighting system to create a two-dimensional (2D, in normal lighting) and a three-dimensional (3D, after changing the lighting to striped lighting) picture of the carcasses. Every day, before the slaughter line starts processing cattle, VBS2000 machines need to be calibrated to adjust mainly to the new light conditions and potential changes to the camera angle. To operate the calibration, the machine initialises itself by taking pictures of 2D and 3D template boards. After calibration, the slaughter line can start its daily work, and the right side of each carcass is photographed twice to create the 2D and 3D pictures. Both images are immediately broken down into 428 variables describing length, contour, angles, volumes, and colour of the carcasses. Using carcass weight, sex category (i.e. young bull, bull, steer, heifer, or cow) and the variables derived from the images, VBS2000 applies the relevant prediction equations to derive the EUROP gradings for conformation and fat (Figure 1).

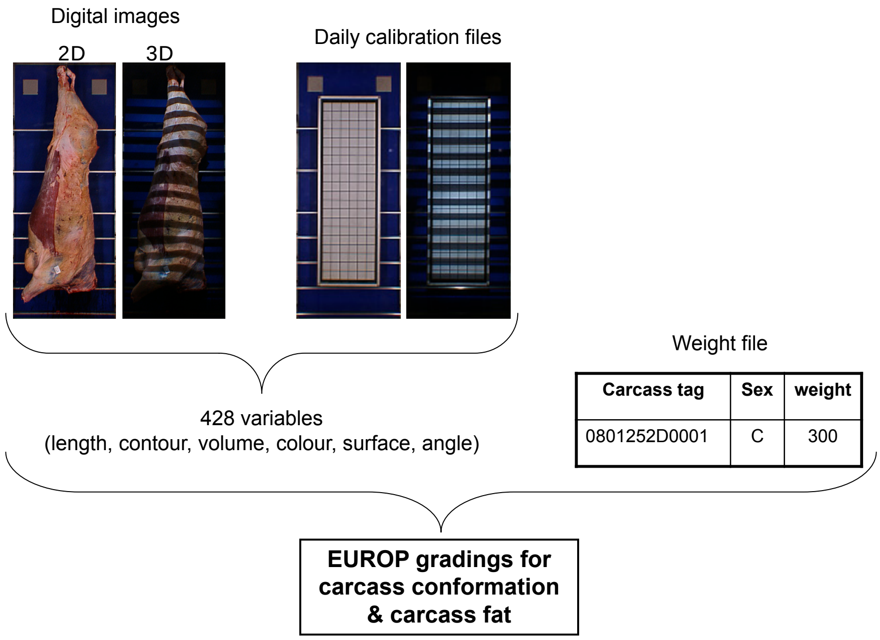


Figure 1. Overview of the mechanical grading process operated by VBS2000.

1.2 Beef breeding in Ireland

There were 5.93 million cattle in Ireland in 2009, of which 1.1 million were dairy cows and 1.12 million were beef cows (CSO, 2009). The average number of cows in Irish dairy and beef herds was 41 and 15 cows, respectively (CSO, 2007). The most common breeds in beef were Limousin, Charolais, Hereford and Simmental for beef cows, while Charolais, Limousin, and Angus were the common beef sire breeds mated to beef cows. Also, approximately 40% of dairy cows are mated to Angus, Hereford and the Limousin sires.

1.2.1 The cattle breeding database

Cattle breeding data in Ireland is recorded on two databases: i) the Centralised Movement and Monitoring System operated by the Irish Department of Agriculture in accordance with the relevant EU regulations for animal traceability, and ii) the cattle breeding database operated by ICBF. The ICBF database operates alongside the Centralised Movement and Monitoring System database, and stores additional data for the purpose of genetic evaluation

(Figure 2). 90% of calves born in Ireland annually are registered in the ICBF database.

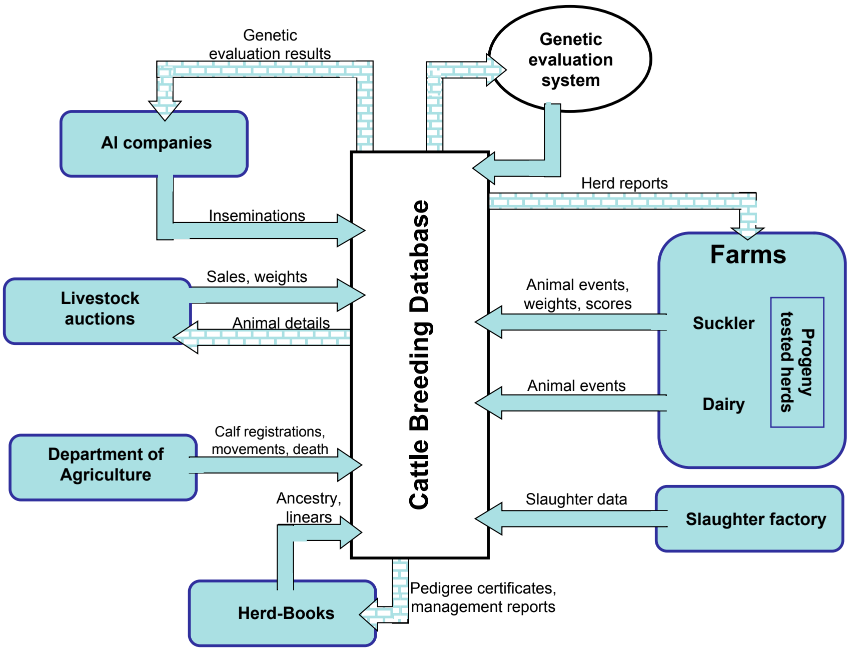


Figure 2. Data and information flow around the ICBF database.

1.2.2 Breeding objective in Ireland

The breeding objective for beef cattle in Ireland was originally described by Amer et al. (2001), acknowledging that use of beef germplasm in beef and dairy herds, as well as the different production systems (i.e. weanling and finishing cattle) found in Ireland.

Irish beef farming comprises of a small quantity of pedigree farms (approximately 3,300 in 2010; on average 4 pedigree cows per farm) and a large number of commercial (i.e. non-pedigree) farms (approximately 56,000 farms in 2010 with, on average, 17 cows per farm). Pedigree farms produce the next generation of superior bulls and commercial farmers source the best of these animals from the pedigree farms.

Of the 2.0 million calves born in 2009 in Ireland, 62% were from crossbreeding matings across dairy and beef breeds (DAFF, 2009). The most popular breed(s) is Holstein in dairy herds, and Charolais, Limousine, Angus, Simmental, Hereford, and Belgian Blue in beef herds. There is a seasonal aspect to calving in both dairy and beef production systems with 76% of calves born between January and May (DAFF, 2009). Of the calves born in Ireland, 69% were destined to be slaughtered, 16% were exported live, and the remaining 15% were used as replacements. Steers and heifers represented 70% of cattle slaughtered in Ireland in 2009 (DAFF, 2010; Figure 3).

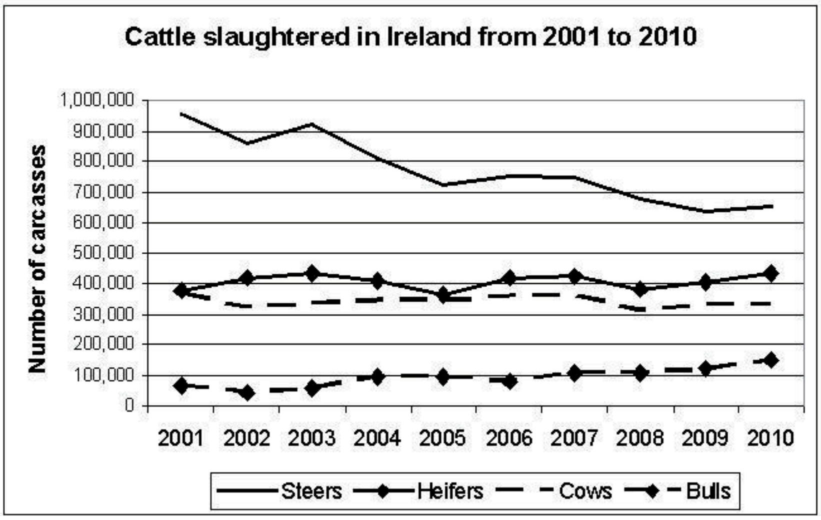


Figure 3. Evolution of cattle slaughtered in Ireland from 2001 to 2010.

The beef breeding goal is defined by 4 groups of economically weighted indexes:

- Calving index, by reflecting the cost of calving, gestation length, and calf mortality;
- Weanling production and live exports, by reflecting the value of weanlings (weight, price);
- Finished animals, by reflecting the value of slaughtered cattle (weight for age, carcass weight, carcass conformation, carcass fat, feed efficiency);
- Replacement animals, by reflecting the value of milk and fertility in females.

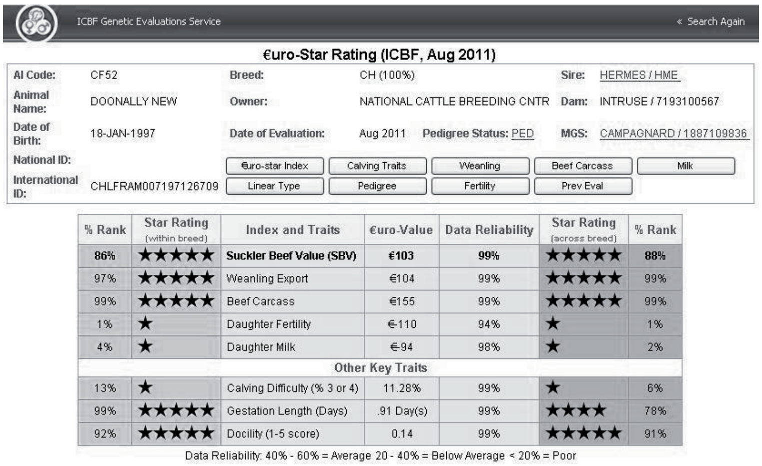
The Suckler Beef Value combines all 4 indexes to reflect the overall profit value of animals. Currently, calving index, weanling export index, carcass index, and replacement index represent 44%, 9%, 35%, and 13%, respectively of the Suckler Beef Value.

1.2.3 Genetic evaluation of beef cattle

Genetic evaluations are computed at ICBF on behalf of the Irish cattle breeding industry. The process involves extracting data (phenotypes and pedigree) from the ICBF database, computing the genetic evaluation, then loading this data back into the database for publication through a variety of mediums, including the ICBF website (www.icbf.com) and various breeding reports.

The genetic evaluation, operated by ICBF for dairy and beef cattle, is currently ran across breeds in several modules: calving (joint beef & dairy), milk production (dairy), maternal weaning weight (beef), fertility (distinct beef & dairy), carcass (joint beef & dairy), linear traits (distinct beef & dairy), and docility (beef). All genetic evaluations are undertaken in MixBlup (Mulder et al., 2010).

Breeding values are associated with a star-rating system equally based on percentile rank: for a given trait, animals ranking in the bottom 20% of the population are given 1 ★ ; whereas animals ranking in the top 20% of the population are given 5 ★. Figure 4 gives the example of a bull with excellent aptitudes for producing weanlings and finished cattle, but deficient at calving, and not a wise choice for breeding replacement heifers.


ICBF Genetic Evaluations Service « Search Again

€uro-Star Rating (ICBF, Aug 2011)

AI Code: CF52 Breed: CH (100%) Sire: HERMES / HME
Animal Name: DOONALLY NEW Owner: NATIONAL CATTLE BREEDING CNTR Dam: INTRUSE / 7193100567
Date of Birth: 18-JAN-1997 Date of Evaluation: Aug 2011 Pedigree Status: PED MGS: CAMPAGNARD / 1887109836
National ID:
International ID: CHLFRAM007197126709

€uro-star Index | Calving Traits | Weanling | Beef Carcass | Milk | Linear Type | Pedigree | Fertility | Prev Eval

% Rank	Star Rating (within breed)	Index and Traits	€uro-Value	Data Reliability	Star Rating (across breed)	% Rank
86%	★★★★★	Suckler Beef Value (SBV)	€103	99%	★★★★★	88%
97%	★★★★★	Weanling Export	€104	99%	★★★★★	99%
99%	★★★★★	Beef Carcass	€155	99%	★★★★★	99%
1%	★	Daughter Fertility	€-110	94%	★	1%
4%	★	Daughter Milk	€-94	98%	★	2%
		Other Key Traits				
13%	★	Calving Difficulty (% 3 or 4)	11.28%	99%	★	6%
99%	★★★★★	Gestation Length (Days)	.91 Day(s)	99%	★★★★	78%
92%	★★★★★	Docility (1-5 score)	0.14	99%	★★★★★	91%

Data Reliability: 40% - 60% = Average 20 - 40% = Below Average < 20% = Poor

Figure 4. August 2011 indexes of CF52 (Data were taken from the ICBF website on 03/11/2011)

The main source of revenue for beef farmers, either directly or indirectly, is carcass value which is currently derived across the EU with carcass weight and the EUROP gradings for conformation and fat. In Ireland, the beef breeding objective as well as the beef carcass selection index used by farmers are based on the overall scores given by the EUROP gradings for conformation and fat.

Based on the external appreciation of muscle and fat, EUROP grades are currently the only carcass phenotypes routinely collected in slaughter houses in Ireland to allow farmers to breed for carcass quality. New sources of reliable routinely collected carcass phenotypes needs now to be investigated to improve selection for finished cattle.

2 Aim of the thesis

The general aim of the thesis was to investigate the feasibility and potential benefit for the Irish industry, of including carcass cut weights predicted from video image analysis (**VIA**) in the Irish beef selection index. Specifically, the aims were:

- to estimate, using both an experimental and a commercial dataset, the genetic parameters and correlations for weight of different wholesale beef cuts (Paper I);

- to investigate the accuracy of VIA technology in predicting carcass cut yields using carcass images routinely taken at slaughter (Paper II);

- to estimate genetic parameters for wholesale carcass cut weights predicted from digital images using the prediction equations on a large population of commercial cattle (Paper III);

- to quantify the genetic associations between carcass cut weights predicted from video image analysis and a range of performance traits currently being recorded on Irish cattle such as live weight, animal price, linear scores, and farmer recorded performance scores (Paper IV).

3 Summary of investigations

3.1 Materials

Phenotypic data used in this thesis were obtained from pre-existing databases: Teagasc beef research center, a commercial partner, and ICBF database. Pedigree information was extracted from the ICBF database.

3.1.1 Carcass dissections

Teagasc Grange beef research center, located in Dunsany, Co. Meath, Ireland, is dedicated to providing research information on all aspects of beef production in Ireland (www.teagasc.ie). Since 2005, the center has raised steers and bulls on the experimental farm for numerous studies dedicated to carcass traits associated with different nutritional planes (e.g. Cummins et al., 2007), feed intake (e.g. Clarke et al., 2009), live measurements (e.g. Conroy et al., 2009) and genetic merit (e.g. Campion et al., 2009). For Paper I, carcass muscle dissection data collated from previous experiments on bull and steers collected between 2005 and 2008 (hereon in referred to as 'experimental' data) were made available. Carcasses (right side) were dissected into 23 different muscle cuts (11 taken in the forequarter and 12 in the hindquarter) using a controlled cutting procedure based on the Beef Cuts Code (Riordan et al., 1978).

Also included in Paper I were carcass muscle dissections collected from 1999 to 2005 by a commercial industry partner (hereon in referred to as 'commercial' data). Cutting procedures in the hindquarter were very similar to those used in the experimental dataset. However, in the forequarter dissections, the commercial cutting procedure applied more severe cutting procedures on the individual muscle cuts with the objective of neat presentation of the cut on the supermarket shelves. As a result, the number of muscle cuts available in the forequarter was lower in the commercial dataset compared to the experimental dataset, but also included heavier lean trimming weights. In both the experimental and the commercial datasets, muscle cuts were grouped into 14 primal cuts according to their location on the carcass (Table 3 & Figure 5). The primal cuts were used for analysis in Paper I and Paper II. Data used in Paper I comprised of 413 animals from the experimental center (340 steers and 73 bulls) and 635 animals from a commercial partner (575 heifers, 26 bulls, and 34 steers).

Table 3. *Summary of data used in Paper I*

	Experimental		Commercial	
	N	Mean	N	Mean
Cold carcass weight (kg)	413	337	635	290
Forequarter (kg)				
Fore shin	413	5		
Brisket	413	10	635	8
Ribs	413	35	628	5
Flank			451	2
Chuck	413	28	635	13
Shoulder	413	28	635	12
Hindquarter (kg)				
Rib Roast	413	10	635	8
Strip-loin	413	11	523	11
Sirloin	413	13	635	10
Round	413	48	635	43
Fillet	413	6	520	5
Hind shin	413	9		
Other weight (kg)s				
Total lean trimmings	413	27	635	82
Total carcass measures				
Total meat weight (kg)	413	230	635	192
Meat percentage (%)	413	68%	635	66%

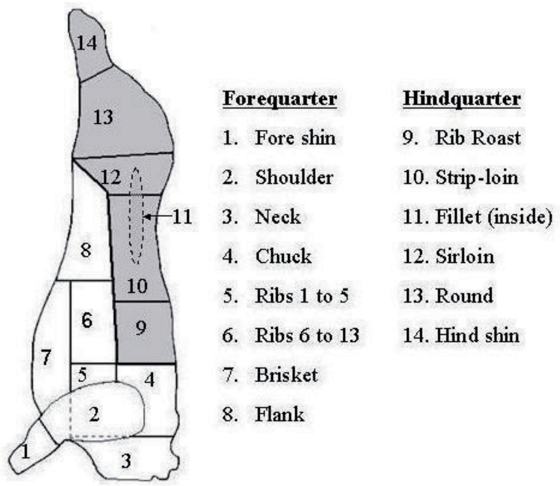


Figure 5. Location of the primal cuts used in Paper I & II.

In Paper II, the primal cut weights were assembled into four wholesale cut weights based on retail value: lower value cuts (**LVC**), medium value cuts (**MVC**), high value cuts (**HVC**), and very high value cuts (**VHVC**). This step was done with the support of meat experts (researchers and industry representatives). Wholesale cut weights were used for analysis in Papers II, III, and IV (Figure 6).

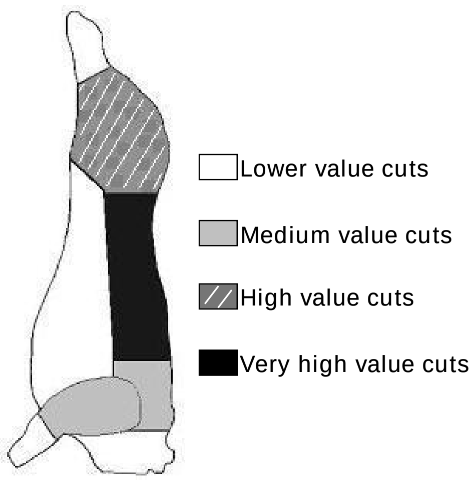


Figure 6. Location of the predicted wholesale cuts used in Papers II, III, & IV.

3.1.2 Carcass images

Digital images taken after slaughter for each carcass (2 images per carcass) were used in Paper II, III, and IV.

To fulfill the objective of Paper II of validation of carcass cut weights prediction equations, observed wholesale cut weights LVC, MVC, HVC, and VHVC needed to be accompanied by their relevant carcass digital images. However, the recording of carcass cut weight in the commercial partner started earlier than the introduction of mechanical gradings of carcasses (Figure 7), and a loss of commercial data was observed in Paper II compared to the previous paper.

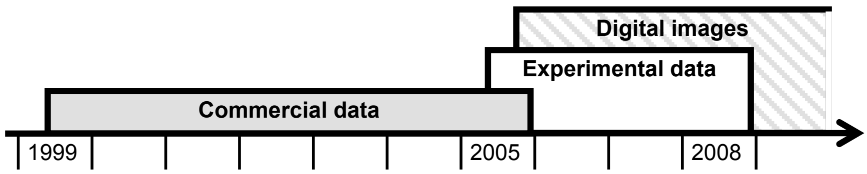


Figure 7. Different data recording periods for carcass cut data and digital images used in Paper II.

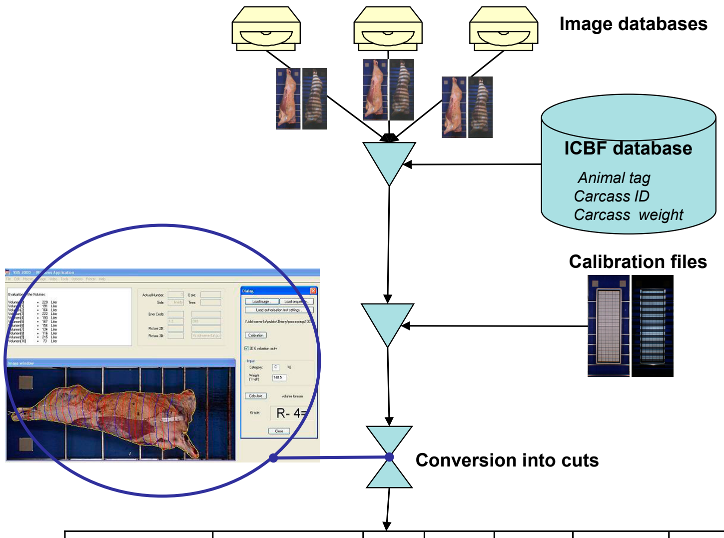
Multivariate analyses studied in Paper II were based on 281 heifers (commercial data), 346 steers, and 74 bulls (experimental data). Images have been collected by ICBF across 25 slaughter houses and stored on hard drives since July 2005. Images were recorded in *tif* format and the approximate size per individual image was 400Kb; total storage space used by images is around 6.5Tb to this date, amounting to approx. 15 million double images (i.e. 7.5 million carcasses). Images are not identified by the animal tag, but by a specific name containing the date of slaughter and the carcass number: for example image *1009292D3800.tif* relates to the two-dimensional image (2D) of carcass number 3800, slaughtered on 29/09/2010; and the 3D image of the same carcass is labeled *1009293D3800.tif* (Figure 8).

Figure 8. Digital images collected on carcass 3800 mechanically graded on 29/09/2010.

3.1.3 Predicted carcass cut weights

Data used in Papers III and IV were carcass cut weights predicted from images taken between the years 2005 and 2010. The first step prior to further genetic analysis was to convert the stored digital images into predicted cut weights; thus recreating the mechanical grading conditions (light, camera angle) for each day of slaughter. This was achievable by recovering the calibration files used daily within factories from 2005 to 2010.

The conversion of historical images into cut weights can be broken down into 2 major editing steps: 1) creating the carcass file (animal tag, carcass weight, sex) by linking carcass tags attached to each double image with animal tags present in the ICBF genetic database, 2) matching calibration files recovered from factories to their corresponding factory and date of slaughter. The edited datasets were converted into wholesale cut weights by applying the regression equations validated in Paper II. Figure 9 summarises the steps involved in the conversion of 2005-2010 data.



Carcass ID	Animal tag	Sex	CCW	LVC	MVC	HVC	VHVC
0801252D0001	IE1234567899	H	300	80	40	59	25
0801252D0002	IE1234567890	C	340	82	45	65	26
…		…	…	…	…	…	…

Figure 9. Converting historical stock of images into wholesale cut weights.

Paper III utilised datasets of carcass cut weights predicted from animals slaughtered between November 2006 and May 2009. For Paper IV, the dataset of predicted cut weights was expanded to animals slaughtered between July 2005 and December 2010.

3.1.4 Other data

Associated traits investigated in Paper IV comprised of live weights, auction prices, linear scoring, farmer scores, and slaughter traits.

Live weights were recorded on pedigree farms as well as in live-auction sales around Ireland. Prices per animal were collected from live-auction sale on calves, weanlings, and post-weanling animals. Linear scores for muscle (4 traits) and skeletal (7 traits) were collected on pedigree farms, whereas farmer scores of weanling quality (score from 1 (poor quality) to 5 (good quality)) were collected mainly on commercial farms. Slaughter records included carcass value (price per kilo x carcass weight).

Estimated genetic and phenotypic parameters from Papers III and IV were used in a genetic gain study (only presented in the thesis) designed to quantify the impact of including the four predicted cut weights (i.e. LVC, MVC, HVC, & VHVC) in the overall Irish beef breeding program. Heritability, phenotypic and genetic correlations from McHugh et al. (2011a, 2011b) and Crowley et al. (2010) were also used in the genetic gain predictions.

3.2 Methods

Three distinctive methods were used in this thesis: 1) Restricted Maximum Likelihood (**REML**) in Papers I, III and IV, 2) multivariate analysis (Paper II), and 3) selection index theory and gene flow principles in the genetic gain study.

3.2.1 Genetic analysis using REML

The majority of the research in this thesis focused on the estimation of genetic parameters. Variance and covariance components were estimated using the average information algorithm for restricted maximum likelihood included in the ASreml (Gilmour et al., 2006) and DMU (Madsen et al., 2007) packages.

Linear animal (Paper I) and sire (Papers III & IV) models were used for all traits. Pedigree phantom groups of breed were also used. Phenotypic and genetic correlations were estimates by series of bivariate analyses, and the general model can be summarised as:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{ZQg} + \mathbf{e} \qquad \text{(Quaas et al., 1981)}$$

where y is the vector of records, b is the vector of fixed effects, u is the vector of random effects, g is the vector of breed groups, e is the vector of residual effects and the X, Z, and Q matrices are the respective design matrices.

For carcass cut traits and other pre-slaughter traits in Paper IV, contemporary groups were created using the algorithm described by Crump et al. (1997). The algorithm is parameterised initially by the minimum (e.g. 30 days) and maximum (e.g. 120 days) group span, as well as a minimum number of records (e.g. n = 4) per group. First, consecutive animals are put into groups according to a specific date (e.g. date of slaughter) and the minimum span of days defined in the parameter file. This step is then repeated considering the start and end date of the groups and the minimum span defined in the parameter file. Second, contemporary groups are created by reading the groups created previously and clustering consecutive groups according to the maximum span and the minimum records required per group. This step is then repeated considering the maximum span and the minimum records required per group in the parameter file.

3.2.2 Multivariate analysis

Paper II used multivariate analysis and validated the equations used to predict wholesale cut weights. The general purpose of multivariate analysis is to learn more about the relationship between independent (or predictor) variables and dependent (or predicted) variables. Several statistical approaches were evaluated: stepwise regression, partial least square regression, least absolute shrinkage and selection operator, principal component analysis, and canonical correlation analysis.

Statistics used to quantify the robustness of predictions included the mean bias, the Root Mean Square Error (**RMSE**), the accuracy of prediction ($\mathbf{R^2}$), and the correlation between the predicted values and the residuals ($\mathbf{r_e}$) to investigate the presence of systematic bias. For each trait under investigation, the prediction equations were calibrated on 66% of the data and validated on the remaining 33%. Prediction equations were developed separately in the experimental and commercial datasets. The accuracy of prediction was based on the validation dataset.

Three different sets of models based on the predictors used were also tested: 1) carcass weight only, 2) carcass weight plus EUROP carcass classification, and 3) carcass weight plus VIA parameters.

3.2.3 Genetic gain

The breeding goal for carcass traits was comprised of carcass weight, LVC, MVC, HVC, VHVC, weaning weight, and residual feed intake; economic weights are presented in Table 4. The overall breeding goal was modeled by including sub-indexes for calving, maternal and milk trait categories as both selection criteria and breeding objective traits. This circumvented the need to model a very large number of non-carcass traits using selection index theory (Hazel, 1943), while still allowing the importance of these non-carcass traits in selection decisions to be taken into account. Thus, the overall breeding objective modeled closely represents the industry breeding index known as Suckler Beef Value. The main difference is that the current industry Suckler Beef Value has carcass fat score and carcass conformation in the breeding goal, whereas the breeding goal modeled in this study includes the traits LVC, MVC, HVC, and VHVC instead.

Five selection indexes were derived (Table 4) and evaluated against the common breeding goal described above: scenario 1 was based on live recordings (i.e. no slaughter predictors), scenario 2 added carcass weight to scenario 1, scenario 3 added EUROP grades to scenario 2, and scenario 4 added the predicted carcass cut weights to scenario 3. Additionally, a scenario 5, based on scenario 4, mimicked the use of better accuracy of carcass cut prediction by increasing the heritability of each predicted carcass cut by 0.10 to maximum heritability of 0.38 (heritability of total meat weight for steers in Paper III).

Heritabilities (Table 4), phenotypic and genetic correlations were taken from Papers III & IV results and from McHugh et al. (2011a, 2011b) and Crowley et al. (2010).

Table 4. *Heritability (h^2), phenotype variance (σ^2_P), economic weight (EW) of traits as well as the different scenari used in the genetic gain study*

Trait	h^2	σ^2_P	EW (€/unit)	Selection index 1	2	3	4
Calving sub-index[1]	0.10	1022	1.63	✓	✓	✓	✓
Maternal sub-index[2]	0.10	19389	0.23	✓	✓	✓	✓
Milk sub-index[3]	0.14	1606	0.23	✓	✓	✓	✓
Weaning weight	0.27	1606	2.24	✓	✓	✓	✓
Weaning price	0.49	3692	0.41	✓	✓	✓	✓
Carcass weight	0.48	756	1.47		✓	✓	✓
Residual feed intake	0.45	19044	-0.12	✓	✓	✓	✓
LVC	0.22	16.56	1.72				✓
MVC	0.26	3.17	2.59				✓
HVC	0.39	11.09	3.45				✓
VHVC	0.21	2.07	6.90				✓
Weanling quality	0.32	0.37		✓	✓	✓	✓
Weaning muscle score	0.22	1.11		✓	✓	✓	✓
Weaning skeletal score	0.26	1		✓	✓	✓	✓
Post-weaning weight	0.25	4069		✓	✓	✓	✓
Calf price	0.43	935		✓	✓	✓	✓
Post-weaning price	0.38	3259		✓	✓	✓	✓
Carcass EUROP conformation	0.40	1.21				✓	✓
Carcass EUROP fat	0.30	1.69				✓	✓

[1] *Calving subindex : calving ease, calf mortality, and gestation length.*

[2] *Maternal subindex: maternal calving ease, age at 1st calving, calving interval, and survival.*

[3] *Milk subindex: maternal weaning weight.*

Phenotypic variances and heritability estimates were adjusted for reduction of the genetic variance due to selection (Rutten et al., 2002).

The dissemination of genetics on beef farms uses 3 major pathways: i) artificial insemination (**AI**) accounts for approximately 15% of the calvings, ii) pedigree natural mating bulls (i.e. non AI bulls from a pedigree farm) account for 50% of the calves born annually, and iii) commercial stock bulls (i.e. non AI bulls from a non pedigree farm) account for 35% of calving annually (Figure 10). Additionally, an industry-based progeny testing program evaluates 15 to 20 beef bulls every year, and importation of foreign genetics (AI and live bulls) mainly from France and the United Kingdom, accounted for 25% of the AI bulls used in 2010.

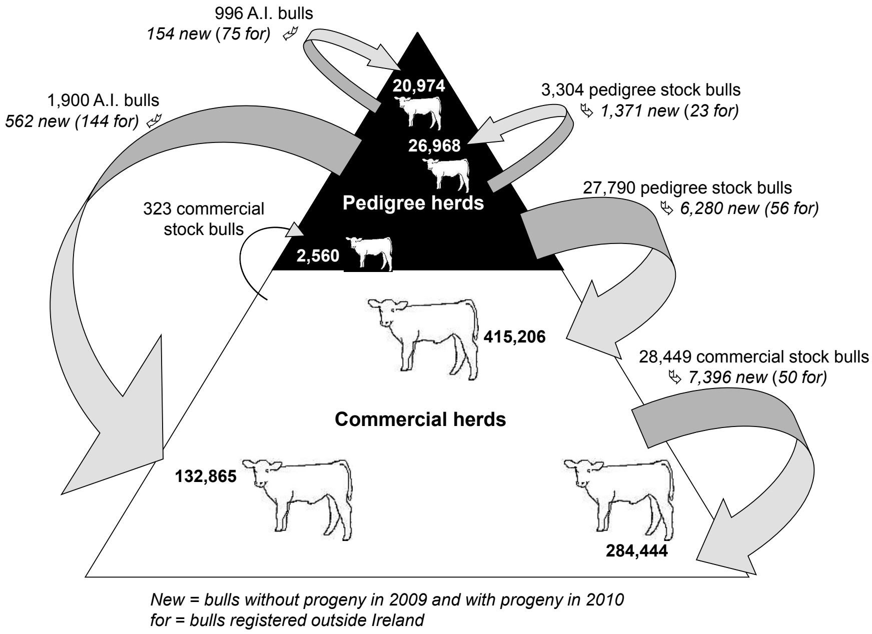


Figure 10. Paternal origin of calves born in Ireland in 2010.

Four types of selection candidate were established according to the current industry gene flow (Table 5):

- AI: Bulls already used widely in artificial inseminations: males purchased by AI stations after weaning and set to have relatively large number of daughters with records, as well as slaughtered progeny;
- PT: Progeny tested bulls; approximately 15 to 20 bulls were annually chosen by the industry; bulls have 700 straws of semen collected which are dispersed on selected beef farms by AI companies; at the time of selection, PT bulls have recorded progeny for a wide range of selection criteria, but across less progeny than AI bulls;
- PED: Pedigree stock bulls were purchased any time after weaning from a pedigree farm, and benefit from performance recording undertaken by pedigree farmers on the bulls themselves, and on half sibs;

- STK: Non-pedigree stock bulls were purchased from commercial farmers at weaning and have limited records available for their selection

Genetic (Table 6) and phenotypic correlation matrices were bent to insure they were positive definite using procedure from Jorjani et al. (2003).

Accuracy of selection was computed as

$$r_{IH} = \frac{\sigma_I}{\sigma_H};$$

Response to selection per generation were $R = i \times \sigma_H \times r_{HI}$;

Annual genetic gain were calculated as

$$\delta G = \frac{i_m \times \sigma_{H(m)} \times r_{IH(m)}}{L_m + L_f} + \frac{i_f \times \sigma_{H(f)} \times r_{IH(f)}}{L_m + L_f}$$

where σ_I =standard deviation in the selection criteria, σ_H =standard deviation in the selection objective, i_m, i_f = selection intensity for males and females, respectively (i_f = 0), and L is the generation interval for males (L_m) and females (L_{fe}).

Table 5. *Records at time of selection for the selection candidates*

Traits / Selection candidates	AI bulls (AI)	Progeny tested bulls (PT)	Pedigree stock bulls (PED)	Non-pedigree stock bulls (STK)
Records on self				
Calving	1	1	1	1
Weaning quality	1	1	1	1
Weaning weight	1	1	1	
Muscle linear scores at weaning	1	1	1	
Skeletal linear scores at weaning	1	1	1	
Residual Feed Intake	1	1		
Records on paternal half-sibs				
Calving	25	20	15	
Weaning quality	15	10	8	
Weaning weight	15	10	8	
Muscle linear scores at weaning	15	10	8	
Skeletal linear scores at weaning	15	10	8	
Price at weaning	15	10	8	
Post-weaning weight	10	5	5	
Price at post-weaning	10	5	5	
Carcass traits[1]	5	3	3	
Records on progeny				
Calving	1000	300		
Weaning quality	400	100		
Weaning weight	400	100		
Muscle linear scores at weaning	100	50		
Skeletal linear scores at weaning	100	50		
Price at weaning	200	100		
Residual Feed Intake	10	10		
Post-weaning weight	140	10		
Price at post-weaning	100	10		
Carcass traits[1]	400	100		
Maternal records				
Maternal traits dam	1	1	1	1
Maternal traits daughters	200	100		

[1] *Carcass traits =carcass weight, LVC, MVC, HVC, VHVC, EUROP grades for conformation and fat.*

Table 6. *Genetic correlation matrix used in the calculation of genetic gains*

	[1]	[2]	[3]	[4]	[5]	[6]	[7]	[8]	[9]	[10]	[11]	[12]	[13]	[14]	[15]	[16]	[17]	[18]
[1] Calving SI[1]	1																	
[2] Maternal SI[1]	0	1																
[3] Milk SI[1]	0	0	1															
[4] Weaning weight	-0.20	0	0	1														
[5] Weanling quality	-0.10	-0.20	-0.20	0.30	1													
[6] Carcass weight	-0.20	-0.15	-0.15	0.31	0.30	1												
[7] Res. feed intake[2]	0	0	0	-0.10	0	-0.29	1											
[8] LVC	-0.20	-0.18	-0.18	0.10	0.29	0.36	-0.30	1										
[9] MVC	-0.20	-0.18	-0.18	0.10	0.29	0.27	-0.30	0.46	1									
[10] HVC	-0.20	-0.18	-0.18	0.10	0.28	0.40	-0.30	0.68	0.79	1								
[11] VHVC	-0.20	-0.17	-0.17	0.10	0.30	0.41	-0.30	0.58	0.83	0.88	1							
[12] Muscle score[3]	-0.20	0	0	0.36	0.46	0.20	-0.19	0.24	0.17	0.22	0.34	1						
[13] Skeletal score[3]	-0.20	0	0	0.46	0.09	0.20	0	-0.07	-0.09	-0.10	-0.08	0.30	1					
[14] P. wean. weight[4]	-0.10	0	0	0.50	0.21	0.50	-0.10	0.10	0.10	0.10	0.10	0.32	0.30	1				
[15] Weanling price	-0.30	-0.10	-0.10	0.55	0.60	0.40	0	0.37	0.55	0.36	0.47	0.48	0.21	0.39	1			
[16] P. wean. price[4]	-0.30	-0.11	-0.11	0.25	0.24	0.50	0	0.57	0.47	0.61	0.60	0.24	0.11	0.40	0.56	1		
[17] EUROP conf. [5]	-0.20	-0.10	-0.10	0.21	0.30	0.40	-0.29	0.38	0.46	0.58	0.72	0.37	0	0.19	0.36	0.51	1	
[18] EUROP fat[5]	0	0	0	0.05	0	0.10	-0.28	-0.20	-0.30	-0.33	-0.19	-0.20	-0.16	0.10	-0.34	-0.28	-0.05	1

[1] SI = sub-index; [2] Residual feed intake; [3] linear score at weaning; [4] records at post-weaning; [5] EUROP gradings

A cost and benefit analysis was also conducted to quantify differences in average Suckler Beef value per annum between selection criteria scenari (i.e. scenario 1 to 5) while accounting for time delay in genetic improvement due to different generation intervals across bull candidates. Several steps have been followed to compute the cost and benefit analysis:

- Assuming a rate of genetic progress of €3 Suckler Beef Value /year over the first 10 years (current rate of genetic progress in pedigree herds);
- Computing the Suckler Beef value of cows (SBV_{cows}), bred to produce replacement heifers, assuming the following age distribution in an average herd:

$$(SBV_{cows})_t = \sum_{2}^{k} a_k \times SBV_{calves}^{t-k}$$

where$(SBV_{cows})_t$ = SBV_{cowss} computed at year t

k = age of cows

a_k= proportion of cows of age k in average herd: a = 0.25, 0.20, 0.18, 0.16, 0.13, 0.08 at age 2,3,4,5,6,7, respectively.

- Computing the Suckler Beef value of bull candidates (SBV_{bulls}) using parameters described in Table 7 and the following formulae:

$$(SBV_{bulls})_t = p_k \times \sum_{k} (SBV_{calves}^{t-a_k} + R_k)$$

where$(SBV_{bulls})_t$ = SBV_{bulls} computed at year t

k = bull candidates for selection: AI, PT, PED, and STK

a_k = age of candidates at birth of their progeny

R_k = response to selection per generation for candidate k

p_k = proportion of usage of candidate k

- Computing the Suckler Beef value of calves (SBV_{calves}) as parent averages: $(SBV_{calves})_t = ½(SBV_{bulls})_t + ½(SBV_{cows})_t$

  where$(SBV_{calves})_t$ = SBV_{calves} computed at year t
- Computing yearly differential benefits in SBV_{calves} between 2 scenarios: scenarios 2 and 1; scenarios 3 and 2; scenarios 4 and 3; scenarios 5 and 4.
- Discounting yearly differential benefits in SBV_{calves} between scenarios assuming a discount rate of 5% per annum to recognise that a significant amount of time may occur between the selection of candidates and the expression of the Suckler Beef Value within generations.

Table 7. *Parameters of age, selection intensity, and proportion of selected candidates used in the computation of* SBV_{bulls}

Selection candidate	Average age of candidate[1]	Selection intensity	Proportion selected
AI bulls (AI)	8	1.8	0.15
Progeny tested bulls (PT)	6	2.0	0.05
Pedigree bulls (PED)	4	1.4	0.40
Stock bulls (STK)	3	1.0	0.40

[1] *At birth of progeny*

Costs associated with scenarios 1 to 3 were considered negligible as the processes considered in those scenarios are currently in place (collection of live records, EUROP grades). Improving the accuracy of the current prediction equations for carcass cut weights requires the dissection of extra carcasses. A goal would be to reach 500 steers and heifers carcasses (L. Keuchwig, E+V, personal communication). The cost associated with the dissections of 150 steers and 250 heifers can be broken down as follows:

- time required = 4 hours / carcass
- labour cost = 15 €/hour
- carcass = €500

A total cost of the upgrading operation would require €224,000.

3.3 Main findings

3.3.1 Genetic variation in primal cut weight

Analysis conducted in Paper I showed the existence of genetic variation in primal cut weights; heritabilities were on the whole high, and genetic correlations between primal cuts ranged between 0.44 and 0.93 across experimental and commercial datasets (Table 8).

Table 8. Average weight (Mean), heritability, standard error of heritability (s.e.) for primal cut weights in the experimental and the commercial datasets in Paper I

	Primal cut weight (kg)	Experimental data		Commercial data	
		Mean	Heritability (s.e.)	Mean	Heritability (s.e.)
Hindquarter	Rib-roast	10	0.14 (0.16)	8	0.40 (0.19)
	Striploin	11	0.49 (0.22)	11	0.41 (0.22)
	Sirloin	13	0.67 (0.22)	10	0.55 (0.20)
	Round	48	0.86 (0.23)	43	0.42 (0.19)
	Fillet	6	0.29 (0.20)	5	0.62 (0.20)
Forequarter	Brisket	10	0.25 (0.19)	8	0.47 (0.18)
	Chuck	28	0.83 (0.24)	13	0.41 (0.20)
	Shoulder	28	0.79 (0.23)	12	0.61 (0.20)
	Ribs	35	0.03 (0.15)	5	0.28 (0.15)

3.3.2 Accurate predictions of carcass cut using VIA

Across the five multivariate methods tested in Paper II, stepwise regression methods gave the best results in terms of maximising R^2 and minimising bias. Across the three models tested (i.e. carcass weight; carcass weight + EUROP gradings, carcass weight + VIA variables), the model that included VIA variables topped the other models in terms of accuracy of prediction across traits (lowest RMSE, highest R^2); mean bias and correlations between the residuals and predicted values were generally not different from zero (Table 9).

Table 9. *Mean bias (kg), residual root mean square error (RMSE; kg), coefficient of determination (R^2), and correlation between residuals and predicted weights (r_e) in the validation dataset of wholesale cut weights and overall weights from 114 steers (experimental dataset) and 92 heifers (commercial dataset) using models including carcass weight and VIA variables developed in the calibration dataset of 232 steers (experimental dataset) and 189 heifers (commercial dataset), respectively*

	Trait (kg)	Bias (s.e)	RMSE	R^2	r_e
STEERS	Total meat	-0.74 (0.63)	6.77	0.97	-0.02
	Total fat	-0.58 (0.60)	6.38	0.77	-0.13
	Total bone	0.32 (0.30)	3.22	0.81	-0.12
	LVC	0.15 (0.52)	5.60	0.92	-0.08
	MVC	0.13 (0.26)	2.73	0.86	-0.10
	HVC	1.18 (0.31)**	3.27	0.93	0.05
	VHVC	-0.11 (0.16)	1.75	0.84	-0.01
HEIFERS	Total meat	-0.24 (0.83)	8	0.84	0.06
	LVC	-0.01 (0.69)	6.62	0.65	0.07
	MVC	-0.12 (0.14)	1.37	0.70	-0.03
	HVC	0.01 (0.23)	2.16	0.85	-0.01
	VHVC	0.04 (0.13)	1.24	0.72	-0.44**

Bias / Correlation different from zero at $P < 0.01$ (**)

3.3.3 Genetics of predicted carcass weights

Heritability for predicted carcass cut weights were estimated twice using large datasets of converted images, Paper IV dataset (n = 110,308 observations) being an extension of Paper III dataset (n = 52,722 observations). Heritability estimates for predicted carcass cut weights were very consistent across both studies. Genetic correlations between predicted carcass cut weights were estimated in Paper III, and as expected were strong and positive (Table 10).

Table 10. Heritability in a combined population of steers and heifers (on diagonal), genetic correlations in steers (above diagonal) and heifers (below diagonal)

	Total meat	Total fat	Total bone	LVC	MVC	HVC	VHVC
Total meat	**0.44**	-0.61	-0.24	0.71	0.78	0.93	0.80
Total fat	*n/a*	**0.14**	0.13	-0.50	-0.56	-0.58	-0.54
Total bone	*n/a*	*n/a*	**0.49**	-0.22	-0.23	-0.35	-0.62
LVC	0.87	*n/a*	*n/a*	**0.18**	0.45	0.66	0.57
MVC	0.75	*n/a*	*n/a*	0.47	**0.27**	0.79	0.86
HVC	0.89	*n/a*	*n/a*	0.80	0.82	**0.40**	0.89
VHVC	0.82	*n/a*	*n/a*	0.69	0.82	0.82	**0.17**

3.3.4 Genetic association with predicted carcass cut weights

Strongest genetic correlations were obtained between predicted carcass cut weights and carcass value (min $r_{g(MVC)} = 0.35$; max $r_{g(VHVC)} = 0.69$), and animal price at both weaning (min $r_{g(MVC)} = 0.37$; max $r_{g(VHVC)} = 0.66$) and post-weaning (min $r_{g(MVC)} = 0.50$; max $r_{g(VHVC)} = 0.67$).

Moderate genetic correlations existed between carcass cut weights and weanling quality (min $r_{g(MVC)} = 0.12$; max $r_{g(VHVC)} = 0.49$), and linear scores for muscularity at both weaning (hindquarter development: min $r_{g(MVC)} = -0.06$; max $r_{g(VHVC)} = 0.49$), and post-weaning (hindquarter development: min $r_{g(MVC)} = 0.23$; max $r_{g(VHVC)} = 0.44$).

3.3.5 Genetic gain

Overall economic responses to selection

Response to selection per generation increased from scenario 1 to scenario 5 across AI, progeny tested, and pedigree bulls. Comparing scenario 4 to scenario 3 gave the effect of adding predicted carcass cut weights (scenario 4) to the current selection index (scenario 3), and the increased response to selection in the Suckler Beef Value were +1.1%, +1,4%, and +0.7% for AI bulls, progeny tested bulls, pedigree stock bulls, respectively. Non pedigree stock bulls were negligibly affected by the different selection index scenario as they only have records on weaning quality at the time of selection (Table 11).

Table 11. *Response to selection per generation on Suckler Beef Value (€) for 5 scenarios of selection criteria*

	Scenario 1	Scenario 2	Scenario 3	Scenario 4	Scenario 5
Traits used in selection index	*Live traits*	*Scenario 1 + carcass weight*	*Scenario 2 + EUROP grades*	*Scenario 3 + predicted carcass cuts*	*Scenario 4 + more accurate prediction equations of carcass cuts*
AI bulls	106.72	111.96	112.26	113.45	113.52
PT bulls	111.47	119.52	119.98	121.64	121.77
PED bulls	40.93	41.10	41.18	41.49	41.74
STK bulls	13.32	13.32	13.32	13.32	13.33

Annual gains on profit traits

Annual gains on goal traits (δG) were computed across all scenarios and candidates for five groups of traits: Calving, Maternal (maternal cow sub-index, and maternal milk), Growth (weaning weight, and weaning price), Residual Feed Intake, and Carcass (LVC, MVC, HVC, VHVC, and carcass weight) (Figure 11).

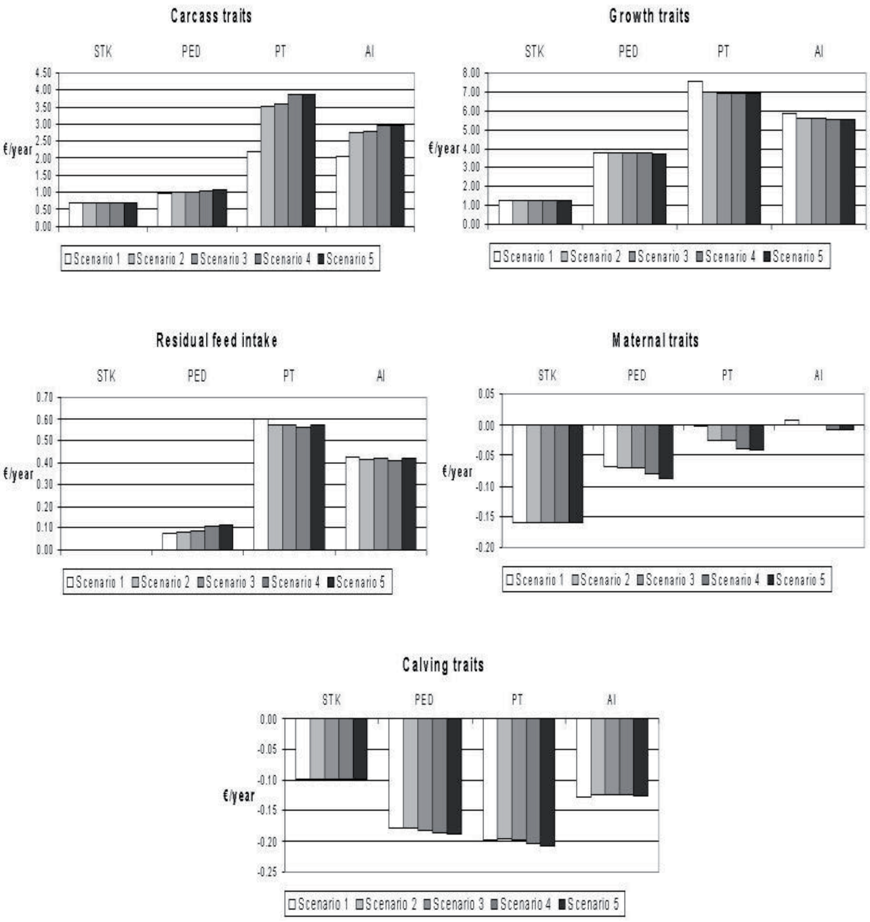


Figure 11. Annual gains in calving, maternal, growth, residual feed intake, and carcass traits calculated across the different candidates, traits, and scenario explored.

Adding predicted cut weights (scenario 4) to the selection index including EUROP grades (scenario 3) increased the annual gain on carcass traits by 6%, 7%, 4%, and 0% for AI, PT, PED, and STK candidates, respectively. Modifying the selection indexes by including more detailed information on slaughter traits gradually increased the annual gains on the carcass sub-index. Growth gets the highest positive annual response to selection on Suckler Beef Value compared to the other traits. More accurate prediction equations for wholesale cut weights will increase the annual gain on RFI. Although minor, there is an increase in the negative response on maternal traits when slaughter data (i.e. EUROP grades or predicted wholesale cut weights) were part of the selection criteria. Small negative gains were also observed for calving traits whatever the selection criteria applied.

Adding the predicted wholesale cuts to the selection index (i.e. comparing scenario 4 to scenario 3) gave the largest changes in carcass composition in kg/year (Table 12). However, changes varied with the type of candidate: no effects were observed for STK bulls, and relatively constant increases (~ 14%) were calculated for PED bulls. In PT bulls, the biggest changes in carcass composition were observed for LVC, MVC, and HVC (~30%), while change in VHVC was lower at around 23%. A trend similar to PT bulls was observed for AI bulls: changes in LVC, MVC, and HVC were around 28%, while change in VHVC was approximately 21%.

Table 12. *Annual gains for LVC, MVC, HVC, and VHVC in kg/year*

		Scenario 1	Scenario 2	Scenario 3	Scenario 4	Scenario 5
Lower value cuts	AI	0.47	0.47	0.46	0.58	0.58
	PT	0.42	0.44	0.43	0.59	0.60
	PED	0.17	0.18	0.17	0.20	0.22
	STK	0.22	0.22	0.22	0.22	0.22
Medium value cuts	AI	0.31	0.28	0.29	0.38	0.38
	PT	0.33	0.29	0.30	0.39	0.39
	PED	0.12	0.12	0.12	0.14	0.15
	STK	0.13	0.13	0.13	0.13	0.13
High value cuts	AI	0.54	0.55	0.59	0.75	0.75
	PT	0.47	0.52	0.55	0.75	0.75
	PED	0.19	0.19	0.18	0.21	0.23
	STK	0.23	0.23	0.23	0.23	0.23
Very high value cuts	AI	0.19	0.19	0.21	0.26	0.26
	PT	0.18	0.20	0.22	0.27	0.27
	PED	0.07	0.07	0.07	0.08	0.09
	STK	0.08	0.08	0.08	0.08	0.08

Benefit for the Irish industry

Cumulating the yearly differential benefits of adding predicted cut weights (scenario 4) to the current Irish selection index (scenario 3) over 10 years will bring an extra €2.4 million to the Irish beef industry (Table 13). No extra costs were associated with the upgrade of the selection criteria to predicted carcass cut weights (scenario 4) as a process of collecting and converting images is already active.

Table 13. *Expected benefit for including carcass cut weights in the selection index*

	(million of Euros)			
Scenari tested	Adding carcass weight	Adding EUROP grades	Adding predicted carcass cuts	Using more accurate prediction of carcass cuts
Comparison of	*Scenario 1*	*Scenario 2*	*Scenario 3*	*Scenario 4*
with	*Scenario 2*	*Scenario 3*	*Scenario 4*	*Scenario5*
10 years	+ € 7.3	+ € 0.6	+ € 2.4	+ € 0.6
20 years	+ € 17.5	+ € 1.5	+ € 5.7	+ € 1.8
30 years	+ € 27.4	+ € 2.3	+ € 8.9	+ € 2.9

Using more accurate prediction equations to derive predicted cut weights (scenario 5) has the potential to add €0.6 million over a 10 year horizon to the industry in Ireland. An initial cost of €224,000 associated with the upgrade of the accuracy of prediction of carcass cut weight was taken out of the cumulative benefits.

4 General discussion

4.1 Working with beef carcass cuts

Beef carcass cuts are expensive traits to generate recordings routinely because of the intense labour requirement to undertake the dissections. Few studies have attempted to quantify the genetic variation in beef carcass cut yields, and where undertaken the populations studied were of limited size: Brackelsberg et al. (1971) used 257 Hereford- and Angus-sired animals, Cundiff et al. (1969) studied 287 Hereford-, Angus, and Shorthorn-sired animals, Cantet et al. (2003) studied 474 Angus animals. The present research had access to more individual carcass dissections than any previous study as it gathered two existing databases from a series of research projects and from a commercial partner (Paper I).

Carcass cutting methods vary across the world (Gerrard et al., 1977); nonetheless, some groups of joints were commonly identified: back leg (round), hip (sirloin), full loin (striploin, Tbone, porterhouse, rib-roast), ribs (short ribs, plate, rib steak), shoulder, and chuck. Within the cutting procedure used across this research project (i.e. UK 8-ribs hindquarter and 5-ribs forequarter; Gerrard et al., 1977), dissimilar ways of cutting the muscle were observed between the experimental and the commercial datasets (Paper I). This yielded differences in fore-quarter primal weights and heritability differences (e.g. chuck, shoulder). Identical cutting procedures across carcasses would have been desirable as it would yield more accurate wholesale cut grouping, and therefore better prediction equations (Paper II).

The quantity of dissected primal cuts used in Paper I was sufficient to estimate genetic parameters clearly showing evidence of genetic variation in the different cuts, albeit with relatively large associated standard errors. Results from Paper I were published from models adjusting the traits for age at slaughter. Berg et al. (1968) studied growth patterns of bovine muscle, fat, and bones, and showed, across ages, linear growth for bone weight, but sigmoidal growth patterns for muscle and fat. Results from Teuscher et al. (2006) on changes in muscle structure with breed and age also suggested that differences in muscle size (defined by the muscle cross-sectional area) within and between breeds (Angus, Galloway, Holstein-Friesian, and Belgian Blue) become significantly more apparent after 12 months of age. Adjusting genetic models for age at slaughter and carcass weight to account for differences in growth as well as carcass composition seems especially advisable in a multi-breed context.

4.2 Predicting beef carcass composition

Predicting carcass composition while preserving carcass integrity remains an attractive prospect for the beef industry. Carcass composition is the amount of meat, fat and bones present in a carcass, and can be expressed in weights or as proportions of the carcass weight. Prediction of carcass composition can be made from live animals or from carcass records.

Ultrasound scanning on live animals was largely used to appreciate carcass composition. May et al. (2000) reported accuracy of prediction of 0.31 for the prediction of the 12^{th} rib fat thickness using ultrasound scanning carried out on live animals. Conroy et al. (2009) observed accuracy of prediction for proportion of meat of 0.31 using ultrasound technology at weaning age. Greiner et al. (2003) insisted on the importance of the technician's expertise in getting accurate ultrasound measurements.

Linear scoring implied a visual assessment of animals morphology at a specific age by a trained expert. Conroy et al. (2009) reported larger R^2 when predicting carcass composition proportions from muscular linear score measurements taken at pre-slaughter age ($R^2 \sim 0.50$) compared to muscle linear scores taken at weaning age ($R^2 \sim 0.30$).

Paper IV results reported that routinely collected phenotypes such as animal price at weaning or post-weaning age showed positive and strong genetic correlations with wholesale carcass cuts (0.35 – 0.67). These results indicate that animal price can be used as early predictors of carcass cuts.

In Ireland, Conroy et al. (2009) have described regression equations from EUROP gradings for conformation and fat scores to proportions of meat, fat, and bones and reported accuracy of predictions of 0.63, 0.54, and 0.76 for meat, fat, and bone proportions, respectively.

Predicting carcass composition gets more accurate as predictors are recorded closer to slaughter age or post slaughter. This is demonstrated in

Paper IV, where genetic correlations between wholesale carcass cuts and animal price were higher at post-weaning than at weaning, and also in the study by Conroy et al. (2009).

Prediction of carcass composition on a routine basis has to explore fast and non-invasive methods of predictions, and several methods of predicting carcass composition have been investigated. Shackelford et al. (1995) have developed accurate equations to predict yields of retail product (R^2 = 0.87), fat (R^2 = 0.88), and bones (R^2 = 0.77) from rib dissections in a procedure that can be done in factory. Griffin et al. (1999) acknowledged the limitations of using ultrasound scanning of carcasses to sort carcasses before chilling in high speed lines. X-ray tomography or CT scan uses attenuation of X-ray through tissues to create an internal image of the scanned product. Navajas et al. (2010) and Prieto et al. (2010) used X-ray tomography of primals and found an accurate method of predicting carcass composition without damaging or depreciating the beef cuts, particularly suitable for research and breeding programs. Bioelectrical impedance conducted by positioning electrodes on chilled carcasses gave accuracy (R^2) of 0.81 and 0.84 for percentage of sealable meat and fat, respectively (Zollinger et al., 2010). However, the bioelectrical impedance process tested on chilled carcasses does allow factories to sort carcasses before chilling, and the authors acknowledge that more research may be necessary.

Video image analysers were introduced in slaughter houses to objectively grade beef carcasses (Cross et al., 1983, 1992; Boggaard et al., 1996; Vote et al., 2009, Polkinghorne et al. (2010). The VIA methods developed in the present research (Paper II) have the advantages of being fast (working at speed line), non-invasive (does not require any extra manipulation of carcasses), and offers predictions on the slaughter floor (i.e. allowing factories to sort and stratify carcasses before chilling). The same process was also applied with success on sheep carcasses by Ruis-Vilaressa et al. (2009).

At present, the image conversion process in Ireland is not streamlined as images are collected on external drives from the different factories in batches three or four times annually and are then processed at ICBF. This set-up leads to two levels of data loss: i) when the finishing herd is not present in the genetic database, and ii) when the image cannot be converted. Missing herds can be contacted individually only if the amount of extra data justifies it. The non-conversion of images mainly occurred when the calibration files could not be recovered or could only be recovered partially; to a much lesser extent, conversions could not be done if carcasses were not positioned properly on the board. One way of improving image conversion rates is to operate the predictions for carcass cut weights directly in the factories, thus avoiding any loss of data due to misplaced or faulty calibration files. Technically, the process is straightforward as the VBS2000 grading machine grading for EUROP conformation and fat supports the software necessary for the conversions. This has the potential to double the amount of predicted carcass cut weights available for genetic evaluation purposes.

Accuracy of prediction equations for heifers were lower across all traits compared to steers (Paper II). The probable causes for this difference in accuracy between steers and heifers were related to the characteristics of the heifer dataset: lower number of heifers compared to steers, over-representation of 'R' conformed animals, and to a lesser extent the less controlled cutting procedures for the commercial in comparison with the experimental setups. More dissections following a consistent cutting procedure of heifers would provide more accurate prediction equations of carcass cut weights, and thus better genetic gain responses.

4.3 New opportunities for the beef industry

Among the worldwide carcass classifications and grading schemes presented by Polkinghorne et al. (2010), the European and South African grading systems appear to be the most simplistic as they only classify carcasses based on overall external carcass appreciation. In the US, carcasses are graded for quality and yield. Quality grading based on marbling and maturity of the animal is an appreciation of factors that affect palatability (tenderness, juiciness and flavour) of meat. Yield grades gives an appreciation of the retail cuts on the carcass using regression equations built with carcass weight, fat appreciation, and rib-eye area. At industry level, the EUROP grading system is the simplest to manage, and industry professionals in Europe can be reluctant to move to other more sophisticated grading schemes (Hocquette et al., 2011). The national acceptance of mechanical gradings in Ireland in 2003 eliminated the uncertainty linked to human judgment (Boggaard et al. 1996), but carcass composition has still no part in carcass payment. Hocquette et al. (2011) acknowledged that the EUROP gradings as a basis for payment for carcasses tend to be less and less adequate with a more and more demanding consumer exigency on meat quality.

Using VIA predicted wholesale cuts would provide meat retailers with a more detailed management of carcasses towards their specific markets while avoiding extra costs for machinery (i.e. the EUROP mechanical grading machine supports the carcass cut prediction software). By applying price differentials based on predicted wholesale cuts, meat industrials would encourage producers to raise cattle that meet their markets. In Germany, Brinkman et al. (2007, 2008) devised a method based index points per kilo of sub-primal cuts to reward farmers on predicted cut yields, thus showing the possibility for factories to move to a meat yield payment. Farmers would welcome the extra information on predicted wholesale cut weights as it would provide more transparency in carcass payment. Nonetheless, factories and farmers alike will need access to predicted wholesale cuts for each type of cattle slaughtered, and no predictions of wholesale cut weights are yet available for bulls and cows which represent 30% of cattle slaughtered in Ireland in 2009 (DAFF, 2010). Muscle dissections or wholesale cut dissections need to be recorded on cows and bulls to satisfy industry needs and also to account for production variation over time (Figure3).

This research has shown a positive benefit of selecting for predicted wholesale cut weights for the Irish beef industry. Nonetheless, accuracy of selection and genetic gains can be improved as they are linked to the accuracy of the wholesale cut prediction equations: the stronger the accuracy of prediction is, the closer predicted carcass cut weights used in the selection criteria will be to true carcass cut weights used in the selection objective. At present, accuracy of predictions are lower in heifers compared to steers, the need of collecting more carcass dissection phenotypes is therefore stronger for heifer carcasses. Scenario 5 developed in this thesis showed additional benefit for the Irish industry if a project to improve the accuracy of prediction equations was developed.

A program could be initiated in Ireland to organise the collection of more carcass cut as well as meat quality phenotypes. A regular supply of predicted carcass cut weights would i) enable the industry to validate the accuracy of the current predictions, and ii) build up a database of carcass cut weight which can be used when re-training of the equations is necessary. Such a program would imply extra costs, and lower benefits as predicted in this thesis since no costs associated with the routine collection of wholesale cut weights has been considered in those calculations.

Enhancing the beef breeding scheme by rapidly providing carcass breeding values to (especially) non-AI bulls can now be explored with the advent of genomic selection. Research and implementation of genomic selection in dairy cattle has been very successful in Ireland since 2009 (Kearney et al., 2010). Traits now included in the dairy genomic selection program include production, fertility, as well as beef (carcass weight, EUROP gradings, live weight) traits. The beef genomic selection program started in 2010 and targets six main breeds (Charolais, Limousin, Angus, Hereford, Simmental, and

Belgian Blue) in Ireland and in other countries. This program could provide extra data not yet available to the bull candidates at the time of selection.

Changes in carcass composition when selection is based on growth remain small. Baeza et al. (2002) observed that 25 years of selection on growth traits produced only moderate changes in fillet muscle size of ducks. Koch (1978) studied the correlated response on carcass composition in beef cattle when selection was on live weights or muscling score. The authors reported small variations in proportion of product after selection on muscling score: +0.6%, -0.7%, +0.2%, for meat, fat, and bone, respectively, and also reflected that selection on growth over an eight year period produced only small changes in rib-eye area, fat thickness, and marbling. In the present research, the changes in wholesale cut weight observed for the first year of selection in scenario 4 compared to scenario 3 were less than 1% of the average steer composition, thus agreeing with the literature that relative changes in carcass composition will be slow.

Selection for better carcass composition may have a favourable impact on high value retail cut prices to consumers as these cuts will be selected upon. Nonetheless, upgrading the selection criteria with predicted carcass cut weights may not be sufficient to satisfy the consumer's palate. The perception of meat quality involves price, but also revolves around intrinsic and extrinsic cues that can occur prior to the purchase, at the time of purchase, and upon consumption (Issanchou, 1996).

4.4 Investigating meat quality

The evaluation of meat quality plays a major role for consumers in determining meat purchases. The definition of meat quality may not be easy to describe by consumers (Grunert et al., 2004) as there are multiple factors involved in the definition of meat quality.

Animal breeders and geneticists are directly interested in factors acting at the moment of purchase and at the time of consumption because they relate to animal performances. The other factors influencing meat quality perception include branding, beliefs (include cultural, social, personal and psychological factors), country of origin, animal welfare, and traceability of the meat products. At the moment of purchase, visual assessment of beef meat is highly driven by the importance of internal and external fat (linked to healthiness) and the colour of the cut (linked to freshness). When the meat is being consumed, gustative indicators for quality develop in the consumer's mind: flavour, juiciness, tenderness, and texture. Tenderness is generally considered the most important property of beef cuts (Glitsch, 2000; Becker, 2000, Miller et al., 1995), and is closely correlated with the other meat quality indicators at consumption (Kogel, 2005).

Methods used in collecting phenotypes for genetic analysis of meat quality revolve around the post-slaughter process of carcasses, the dissection of the sample of interest (e.g. *M. Longissimus dorsi* at the 6^{th} rib), and the sample treatments: preparation of samples (e.g. extraction, cooking), and measurement of phenotypes. Further details of protocols can be found in Perry et al. (2001) and Renand et al. (2001).

Video image analysers are now capable of recording phenotypes other than carcass grades: marbling, colour score, skeletal maturity, tenderness (Tan., 2004), and water holding capacity (Irie et al., 1996). As technology is already present in meat factories across the country, the potential of VIA should be exploited further in Ireland. Outside VIA, other technologies have been researched to assess meat quality: X-ray computer tomography provides a fast and accurate access to carcass composition (e.g. Prieto et al., 2010); beef tenderness was positively evaluated by near infra-red spectroscopy (e.g. Bowling et al., 2009); or hyper-spectral imaging techniques (Wu et al., 2011). As meat markets are increasingly driven by consumers, investigations are needed to assess the impact of the current selection on meat quality traits of interest for consumers.

5 Conclusion

This research project clearly showed the feasibility of using video image analysis of digital carcass images to predict wholesale cut weights, to be used in a breeding program.

The research added new references to the paucity of studies carried out on carcass primal cuts. Accurate prediction equations were derived from digital images of carcasses taken after slaughter enabling the prediction of wholesale carcass cut weights in a population of steers and heifers. Heritabilities of predicted carcass cuts from commercial cattle in Ireland were medium high to high, and genetic correlations among predicted carcass cut weights were strong across steers and heifers.

Weaning or post-weaning animal auction prices showed strong genetic correlations with predicted carcass cuts. Farmer score weanling quality and linear scores for muscle at weaning and post-weaning age were moderately correlated with the predicted carcass cuts.

Including the predicted carcass cut weight in a selection index gives out a positive gain for the whole Irish beef industry. Attention needs to be drawn to calving and maternal traits as they tend to respond negatively to selection for growth or carcass traits. The Irish industry could investigate the feasibility of collecting more carcass and meat quality phenotypes to further improve the efficiency of the beef breeding scheme and its return to farmers, retailers, and consumers.

6 Future research

As data from video image analysis are potentially available on all animals slaughtered in Ireland as well as other countries that use VIA, the ability to collect phenotypes, measurable or predictable from VIA and other in-line technologies is immense. Further knowledge would, however, be appreciated in the following areas:

- Strengthening the current prediction equations more particularly for heifers requires more carcass dissections. The prediction of carcass cut weights for cows and bulls will also be needed to get a full picture of the cattle slaughtered in Ireland.
- Meat quality traits need to be investigated in Ireland in order to fulfil consumer expectations of meat: tenderness is a popular quality sought by consumers. VIA parameters not investigated in the present research like muscle and fat colour will be worth researching in the future.
- Research on meat quality will probably require the expansion of current knowledge to other imaging technologies.
- The beef genomic selection research program will need, in time, to be expanded to carcass cut weights predicted from VIA.
- Research in VIA technology also needs to be investigated for sheep production in Ireland.
- Options to collect more phenotypes on wholesale cuts as well as meat quality traits have to be explored.

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8 Sammanfattning

Genetiska aspekter på slaktkroppens sammansättning hos irländska nötkreatur med utnyttjande av bildanalys

Vid uppfödning av nötkreatur till slakt varierar värdet på slaktkroppen beroende på djurets ålder och kön samt slaktkroppens vikt, muskelmängd och fettinnehåll. I detaljhandeln varierar också värdet mellan olika styckningsdelar. Slaktkroppens pris bygger i många EU-länder på ett gemensamt system för klassificering, den så kallade EUROP-bedömningen, Det är välutbildad personal på slakteriet som gör en subjektiv bedömning av slaktkroppens form och fettinnehåll, enligt en 15-gradig skala. Tidigare studier har visat att det är svårt att göra rättvisande bedömningar av slaktkropparna. Klassificerarnas bedömningar varierar över tid och de skiljer sig mellan klassificerare. Vid irländska slakterier används därför sedan 2005 bildanalys, så kallad ”Video Image Analysis” (VIA). Det är en objektiv mekanisk bedömning av slaktkroppens form och fettinnehåll. Mekaniska bedömningar eliminerar de nackdelar som finns med subjektiva bedömningar, dock kvarstår problemet att EUROP-bedömningen inte reflekterar hela skillnaden i värdet mellan olika styckningsdetaljer.

I avelsindexet för nötkreatur av köttras i Irland ingår egenskaper som kalvningsförmåga, dräktighetens längd, kalvdödlighet, fruktsamhet, mjölk till kalven, foderutnyttjande, kalvens vikt och pris vid avvänjning samt slaktvikt. Vikten av värdefulla styckningsdetaljer ingår inte i avelsmålet, delvis på grund av att det hittills har varit omöjligt att skatta dessa vikter för alla slaktade djur. Syftet med detta doktorandprojekt var att undersöka möjligheterna att använda de digitala bilderna, som tas på slaktkropparna vid de irländska slakterierna, för att skatta vikten av olika styckningsdetaljer och inkludera avelsvärden för de skattade vikterna i avelsindexet.

Information för stutar och kvigor om vikter av enskilda styckningsdetaljer vägda med vanlig våg och skattade med VIA samt slaktvikt, form och fettinnehåll från EUROP-bedömningen ingick i analyserna. Ett mindre dataset med uppgifter från totalt 1048 slaktkroppar från flera kommersiella besättningar och en försöksbesättning användes för att skatta genetiska parametrar för enskilda styckningsdetaljer. Arvbarheterna för vikten av olika detaljer var övervägande höga men varierade mellan 0.0 och 0.9. De enskilda styckningsdetaljerna delades upp i fyra grupper med lågt, medelhögt, högt och mycket högt ekonomiskt värde. Vikten av dessa fyra olika detaljgrupper kunde med hjälp av VIA skattas med hög säkerhet. Säkerheten i skattningen var högre än 0,7 och något högre för stutar än för kvigor.

Med ledning av resultaten från det mindre datasetet skattades vikter för de fyra olika detaljgrupperna i ett dataset med mer än 50 tusen slaktkroppar från både stutar och kvigor. Arvbarheten för vikten av detaljer med lågt värde skattades till 0,2, för de med medelhögt värde till 0,3, för de med högt värde till 0,4 och för detaljer med mycket högt värde till 0,2. De genetiska sambanden mellan dessa vikter och auktionspriset för kalven vid och efter avvänjning var starka (genetisk korrelation 0,4 - 0,7). Det betyder att kalvarnas pris kan användas som en selektionsegenskap för ökad andel värdefulla styckningsdetaljer. Detta indirekta sätt att mäta slaktkroppens kvalitet är värdefullt när man vill göra en tidig selektion och inte vänta tills det finns tillräckligt många släktingar med information om styckningsdetaljer. Att ta med information om slaktkroppsegenskapar påverkade det genetiska framsteget för funktionella egenskaper som fruktsamhet och kalvningsförmåga endast marginellt. Studierna visade dock att med det nuvarande avelsmålet för köttproduktion i Irland finns, på grund av negativa genetiska samband, en risk att ekonomiskt och etiskt betydelsefulla egenskaper som fruktsamhet och kalvningsförmåga försämras.

Studierna i detta doktorandprojekt visade att vikten av olika styckningsdetaljer kan skattas med god säkerhet med hjälp av bildanalys och att arvbarheten för dessa vikter är medelhög till hög. Genom att inkludera vikten av styckningsdetaljer, skattade med bildanalys, i avelsindex blir det genetiska framsteget i slaktkroppens kvalitet större, jämfört med att använda EUROP-bedömningen av slaktkroppens form. I Irland kan därför bildanalys i avelsarbetet användas för att förbättra slaktkroppens kvalitet. För att inte djurens fruktsamhet eller kalvningsförmåga ska försämras är det viktigt att på ett kraftfullt sätt också beakta dessa egenskaper i avelsarbetet.

Nyckelord: nötkreatur, genetiska parametrar, bildanalys, slaktkropp, säkerhet

9 Résumé

Dans cette thèse, nous avons étudié les possibilités d'utiliser des phénotypes prédits à partir d'analyse d'images numériques à des fins de sélection animales. En abattoirs en Irlande, les procédés d'imagerie numérique sont utilisés après abattage pour dériver les notes de conformation et de gras des carcasses bovines (grille EUROP). Deux bases de données totalisant 1,048 dissections de carcasses bovines étaient disponibles afin d'établir des équations permettant de prédire le poids des différentes pièces de viande à partir de variables tirées des images numériques des carcasses. Les analyses génétiques ont révélé d'importantes variations génétiques dans le poids des différentes pièces de viande (huit pièces de quartier arrière et six pièces de quartier avant): les héritabilités estimées variaient de 0,03 à 0,83 pour les pièces de quartier avant, et de 0,14 à 0,86 pour les pièces de quartier arrière. Les différentes pièces de viande ont été ensuite regroupées en quatre coupes grossiste en fonction de leur valeur au détail: les coupes de moindre valeur, des coupes de valeur moyenne, les coupes de valeur élevée, et les coupes de très grande valeur. Ces quatres coupes grossiste réparties en deux fichiers (mâles castrés et génisses) ont été ensuite prédites par analyses multivariées utilisant les variables des images numériques comme prédicteurs. Les coefficients de détermination minimum étaient 0,84 pour les mâles castrés et et 0,72 pour les génisses.

Les analyses génétiques des coupes grossiste prédites ont révélé une héritabilité de 0,18, 0,27, 0,40 et 0,17 pour les coupes de moindre valeur, les coupes de valeur moyenne, les coupes de valeur élevée, et les coupes de très grande valeur, respectivement. Les corrélations génétiques entre les coupes grossiste prédites variaient de 0,45 à 0,89. Les poids des coupes grossiste étaient aussi fortement génétiquement corrélées avec le prix des animaux à l'âge de sevrage (0,37 à 0,66), et à l'âge post-sevrage (0,50 à 0,67) suggérant un bénéfice de sélection indirecte; ce bénéfice de sélection indirecte est d'autant plus intéressant lorsque les données carcasses ne sont pas encore disponibles.

Inclure les coupes grossiste prédites à partir d'images numériques prises en abattoir dans un des critères de sélection a augmenté les gains génétiques pour les qualités de carcasse au-delà de la pratique actuelle de la sélection sur les classifications EUROP. Élargir les connaissances sur les coupes grossiste de carcasses et les étendre à des caractères de qualité de viande devient une option attrayante pour l'Irlande.

Mots-clés: bovin, paramètres génétiques, images numériques, carcasse, régression, précision, pièces de viande.

10 Acknowledgements

The Irish Cattle Breeding Federation is a great place to work! Intimately connected to the Irish farming industry and the Irish research, the Irish Cattle Breeding Federation is also closely linked to the international scientific community, thus offering great potential for research and exchanges. Not to forget the very friendly atmosphere in the office! Throughout my PhD, I wish to particularly thank:

The persons directly responsible for opening this research opportunity to me: Brian Wickham, Andrew Cromie, and Donagh Berry. You all have a knack for making things happen! and I'm very grateful. Thanks a million.

The Swedish University of Agricultural Sciences in Uppsala, especially, the Department of Animal Breeding and Genetics lead by Erling Strandberg, for including me in their research staff. I always felt very very welcome every time I worked at your Department. Tack en miljon!

My advisors, Anna Näsholm, Freddy Fikse, Andrew Cromie, & Donagh Berry. Thanks for spending all this time and effort on my project: I always got constructive and valuable comments from you all. You got me thinking all right!

All the other advisors (not all volunteers): the ICBF team (IT, database, genetic, HerdPlus): I'm pretty sure I covered all ICBF sections with my image-related questions and queries; the Interbull team lead by Joao: great work atmosphere! great friends!; the SLU-Hgen students and researchers from dairy, pig, dog [...] breeding background that provided me with hints and ideas; Teagasc Moorepark PhD student with whom I great exchanges, and last but not least, the AbacusBio team down-under, where I did some serious brain-picking! Many thanks to all!

Mohammad Nilforooshan: my friend from Iran/Scandinavia/USA! Matrices, Music, and Indian Meals. Wish you well in the future my friend!

Finally, to my wife, Heather ♥ for her constant support and patience, and kids, James ♥, Lily ♥ & Eloïse ♥ for forcing me to go out in the fresh air,play football, war, farmer, monsters, building site, shop, burglar, art-attack, sharks, paint, chase... All kinds of support vitally important to complete my PhD project without losing too much hair.

I

Genetic parameters for carcass cut weight in Irish beef cattle[1]

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ABSTRACT: The objective of this study was to estimate genetic parameters for the weights of different wholesale cuts, using an experimental and a commercial data set. The experimental and commercial data sets included 413 and 635 crossbred Belgian Blue, Charolais, Limousin, Angus, Holstein, and Simmental animals, respectively. Univariate analyses using a mixed linear animal model with relationships were undertaken to estimate the heritability of cold carcass weight, carcass conformation and fat, and the cut weights, whereas a series of bivariate analyses was used to estimate the phenotypic and genetic correlations between carcass weight, carcass conformation, carcass fat, and the major primal cuts. Heritability estimates for cold carcass weight in both data sets were moderate (>0.48), whereas heritability estimates for carcass conformation and fat grading were greater in the commercial data set (>0.63) than in the experimental study (>0.33). Across both data sets, heritability estimates for wholesale cut weight in the forequarter varied from 0.03 to 0.79, whereas heritability estimates of carcass cut weight in the hindquarter varied from 0.14 to 0.86. Heritability estimates for cut weights expressed as a proportion of the entire carcass weight varied from 0.04 to 0.91. Genetic correlations were strong among the different carcass cut weights within the experimental and the commercial studies. Genetic correlations between the weights of selected carcass cuts and carcass weight were moderate to high (minimum 0.45; maximum 0.88) in both data sets. Positive genetic correlations were observed in the commercial data set between the different wholesale cut weights and carcass conformation, whereas these were positive and negative in the experimental data set. Selection for increased carcass weight will, on average, increase the weight of each cut. However, the genetic correlations were less than unity, suggesting a benefit of more direct selection on high value cuts.

Key words: beef, carcass, genetic, heritability, primal, wholesale

J. Anim. Sci. 2009. 87:3865–3876
doi:10.2527/jas.2008-1510

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. In the European Union, the EUROP classification system, as implemented by the European Council regulations 1208/81 and 2930/81, is currently used to assign a conformation and fat grade to each carcass (Department of Agriculture and Food, 2004). The conformation classification system uses the letters E (excellent), U, R, O, P (poor) to describe the development of the carcass profiles with particular emphasis on the round, back, and shoulder. The carcass fat classification system uses the scale 1 (low), 2, 3, 4, and 5 (very high) to measure the amount of fat on the outside of the carcass and in the thoracic cavity. Three subdivisions (+, =, −) can be accounted for in each carcass conformation or fat class. Differences in retail value exist between different parts of the carcass (Morris et al., 1999). Farmers should logically be rewarded for producing a larger quantity of these high value cuts, and the current EUROP grading system, measuring the overall conformation and fat, may not be reflecting these differences within carcasses.

Active selection for individual wholesale cut weight is currently limited by a lack of routinely collected phenotypic data to estimate breeding values, a lack of sufficient studies on the genetic parameters for carcass

[1]The authors gratefully acknowledge access by the Irish supermarket chain to their database on carcass cut weight, as well as the Walsh Fellowship finance granted by the Irish Ministry of Fishery and Food to this project.

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Received September 24, 2008.
Accepted August 26, 2009.

cut weights, as well as a lack of knowledge on the phenotypic and genetic correlations between carcass cut weights and other routinely measured traits. Cundiff et al. (1969) published moderate to high heritability estimates for some wholesale cut weights such as round (0.68), loin (0.48), rib (0.44), and chuck (0.49). Brackelsberg et al. (1971) reported similar heritability estimates. Despite most Irish farmers not currently being paid for individual primal weight, advances in technologies such as mechanical grading may facilitate future estimation of primal weight, which may subsequently lead to payment on these estimates. Therefore, to be proactive, as well as to ensure that the quality of Irish beef carcasses does not deteriorate, it is important that the effect of current selection practices on individual cut weights, especially high value cut weights, is quantified.

The objective of this study was to estimate, in the Irish context of across breed genetic evaluation, genetic parameters for weight of different wholesale beef cuts and to determine their correlations with the currently recorded traits of carcass weight, carcass conformation, and carcass fat. Carcass cut data used in the present study originated from 2 sources, which included an experimental herd and a commercial retailer.

MATERIALS AND METHODS

Data used in the present study were obtained from pre-existing databases. Hence, animal care and use committee approval was not necessary for this study. Two databases on carcass cut weight were used in the present study. The first database originated from a series of experiments conducted using a research herd during recent years, and the second database was made available by an Irish supermarket chain. Pedigree information was extracted from the Irish Cattle Breeding Federation database.

Experimental Data Set

Data from 578 carcasses cut into primal weights from animals slaughtered between 2005 and 2008 were made available from the Teagasc beef research center in Dunsany, Co. Meath, Ireland. These data will be referred to as the experimental data. All of the animals were processed in the same factory and the cutting methods were supervised by the same Teagasc researcher. Animals without a known sire (n = 158) were detected and discarded from the analysis. Within the remaining data set, 94% of animals were crossbred (26 were purebred animals; i.e., at least 28/32 purebred). Almost all of the sires (n = 411) were purebred males (Holstein: n = 89; Belgian Blue: n = 85; Charolais: n = 72; Angus: n = 62; Friesian: n = 41; Limousin: n = 34; Simmental: n = 28), and 84% of dams (n = 346) were crossbred females, where the most prevalent breeds represented were Holstein (n = 161), Limousin (n = 59), and Simmental (n = 37).

The animals originated from 7 different experiments that investigated the performance of different finishing diets, as well as animals of divergent genetic merit for growth rate and of different genetic backgrounds (Table 1). Contemporary group was defined as experimental treatment (n = 8) by slaughter date (n = 11). There were 12 contemporary groups with at least 6 animals; the data for 7 animals were discarded because they were in small contemporary groups. Contemporary groups were composed of steers or bulls. The animals slaughtered were bulls (n = 73) or steers (n = 340). The average slaughter age of the bulls and steers was 459 and 762 d, respectively. Age of the dam was grouped into 6 categories: 2 to 4.5 yr old (n = 53), 4.5 to 6 yr old (n = 62), 6 to 7.5 yr old (n = 90), 7.5 to 9 yr old (n = 51), ≥9 yr old (n = 68), and missing data (n = 49). Heterosis and recombination loss coefficients were computed using the formula of Van der Werf and De Boer (1989):

$$\text{heterozygosis} = \text{Pd}\ (1 - \text{Ps}) + \text{Ps}\ (1 - \text{Pd});$$

$$\text{recombination loss} = \text{Ps}\ (1 - \text{Ps}) + \text{Pd}\ (1 - \text{Pd}),$$

where Ps and Pd are the proportions of genes of the primary breed (most prevalent breed) in the sire and dam, respectively. Recombination loss was derived from the heterozygosity of the parental gametes, representing a within-gamete epistatic loss effect (Van der Werf and De Boer, 1989).

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 (Department of Agriculture and Food, 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). Each carcass was cut into forequarter and hindquarter by a section between the 5th and 6th ribs, giving an 8-rib hindquarter and a 5-rib forequarter (Gerrard and Mallion, 1977). The right side of each carcass was cut into 23 different primal cuts: 11 taken in the forequarter and 12 in the hindquarter. The fat trimming procedure aimed to remove all possible fat from the cuts. 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 kidney and pelvic fat were removed before carcass weighing. The total meat weight was defined as the sum of the primal cuts and lean trimmings weights, and the proportion of the total meat weight over the cold carcass weight defined the meat percentage. The total fat and total bone weights were created to respectively sum the carcass fat and bones. Not all of the different cuts recorded were retained for estimation of variance components, and some were grouped together into combined primal cuts. Figure 1 illustrates the location of the retained cuts.

Table 1. Description of the different experiments used in the experimental data set

Exp.	n[1]	Sex[2]	DOS[3]	Sire breed[4]	Dam breed[4]	Description
A	43	S	Feb. 7, 2005	BB, CH, HO, LM, SI	FR, HO, LM, SI	The spring-born animals spent their first winter indoors on a grass-silage and barley-based concentrate. These animals then grazed on a rotational grazing, paddock-based system before being housed indoors for the second winter where they were fed on ad libitum grass silage and 6 kg of barley-based concentrate.
B[5]	18 24	S S	Apr. 4, 2005 Apr. 11, 2005	AA, BB, HO, LM	FR, HO	The spring-born steers grazed pasture during the grazing seasons either side of a store winter period and were finished during their second winter on barley-based concentrate diets and ad libitum grass silage.
D[6]	73	B	Jun. 27, 2006	BB, CH, FR, HO, LM, SI	AA, BB, CH, FR, HE, HO, LM, SI	Following purchase after weaning, bulls were given ad libitum access to a barley-based concentrate diet in which grass silage was offered at 1 kg of DM·animal^{-1} daily.
E	6	S	Mar. 23, 2007	CH, SI	CH, LM	The spring-born suckled calves grazed with their dam until weaning before being housed indoors for the first winter period and offered grass silage ad libitum plus 1 kg of concentrates each daily. At the end of the first winter indoor period, the animals were turned out to pasture and rotationally grazed. The animals were housed indoors on slats for the second winter and offered grass silage ad libitum and 4.5 kg of a barley-based concentrate in one single feed daily.
F	11	S	Mar. 23, 2007	CH, SI	CH, LM	Same description as in Exp. E until the second winter during which the animals were housed on slats with access to out-wintering pad (wood chips) and offered maize silage ad libitum and 4.5 kg of a high protein concentrate in one single morning feed daily.
G[6]	34 33	S S	Apr. 13, 2007 Apr. 27, 2007	BB, CH FR, LM, SI	AA, CH FR, HE, HO, LM, SI	Following purchase after weaning and housing over their first winter, steers were grazed in 2 batches under a rotational grazing, paddock-based system. Steers were finished indoors during the second winter with ad libitum access to a barley-based concentrate and 1 kg of DM grass silage per animal per day.
H[7]	42 45 44 40	S S S S	Feb. 6, 2008 Apr. 2, 2008 Apr. 30, 2008 Jun. 11, 2008	AA, BB FR, HO	FR, HO	Animals were purchased at 2 to 6 wk of age. Following weaning at approximately 10 wk of age, animals were grazed at pasture until their first housing at winter when they were offered ad libitum grass silage plus 1.5 kg of concentrates daily. All animals were grazed during the second grazing season and were finished indoors during their second winter on a total mixed ration of 70% concentrates + 30% grass silage.

[1]Number of animals.
[2]S = steer; B = bull.
[3]Date of slaughter.
[4]Main sire (dam) breeds (breed fraction ≥50% of total breed fraction); AA: Aberdeen Angus, BB: Belgian Blue, CH: Charolais, FR: Friesian, HO: Holstein, HE: Hereford, LM: Limousin, SI: Beef Simmental.
[5]Cummins et al. (2007).
[6]A. M. Clarke (Teagasc Beef Research Center, Dunsany, Co. Meath, Ireland), M. J. Drennan, M. McGee (Teagasc Beef Research Center), D. A. Kenny (Teagasc Beef Research Center), R. D. Evans (Irish Cattle Breeding Federation, Bandon, Co. Cork, Ireland), and D. P. Berry, unpublished data.
[7]Campion et al. (2008).

The retained forequarter cuts were the fore shin, brisket, ribs 1 (nearer to the head) to 5, ribs 6 to 13, shoulder, chuck, and neck. The flank was left attached to ribs 6 to 13. The 2 sets of ribs were summed as ribs. The shoulder was the sum of the clod cut and the whole outside shoulder muscles (blade steak, braising muscle, chuck tender, and leg of mutton cut). 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. Two overall variables were also investigated: forequarter meat weight, summing the primal cut, combined primal cuts, and lean trimmings weights from the forequarter; and total forequarter weight, representing the total meat, fat, and bone weight from the forequarter.

The retained hindquarter cuts were the cap of ribs, cube roll, strip-loin, rump, tail of rump, round, heel, and hind 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 LM cut between the 10th thoracic vertebrae and the rump. The sum of the rump and tail of rump cuts was labeled sirloin. The fillet, also known as the tenderloin, is the M. psoas, inside the loin area. The round is the main part of the hind leg, summing the silverside, topside, knuckle, and salmon cuts. The hind shin and heel cuts were grouped as hind shin. Two overall variables were also investigated: hindquarter meat weight, summing the primal cuts, combined primal cuts, and lean trimmings weights from the hind-

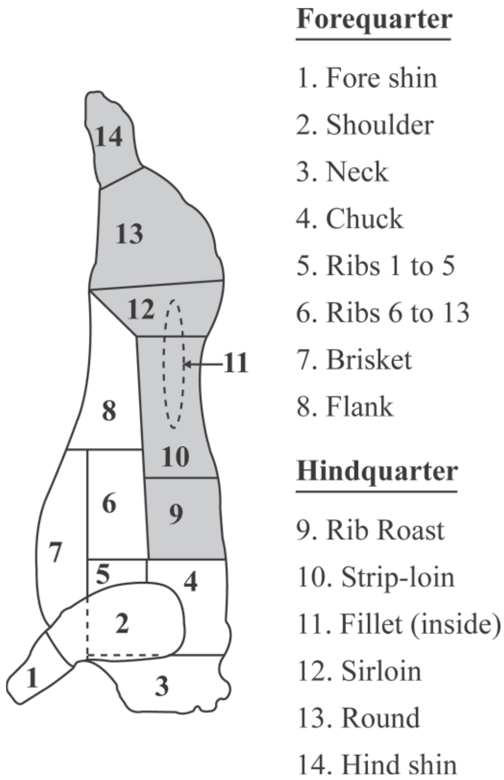

Figure 1. Location of various beef cuts (Gerrard and Mallion, 1977; Jones et al., 2004).

quarter; and total hindquarter weight, representing the total meat, fat, and bone weight from the hindquarter. Primal cut weights and combined primal cut weight in the experimental data set will be referred to in the rest of this paper as the wholesale cut weight in the experimental data set.

Commercial Data Set

A total of 3,501 carcasses cut into primal cuts from purebred and crossbred animals slaughtered between 1999 and 2005 were made available by an Irish supermarket chain. These data will be referred to as the commercial data. All of the animals were processed through the same meat processing plant. Animals with unknown sire (n = 2,502), as well as animals lacking information on herd before slaughter (n = 16), were removed. Additionally, animals slaughtered at less than 12 mo of age (n = 2) were discarded. Age of the dam was grouped into 4 categories: 2 to 3 yr old (n = 130), 4 to 7 yr old (n = 314), $\geq$8 yr old (n = 72), and missing data (n = 119). Heterosis and recombination loss were computed using the formula of Van der Werf and De Boer (1989) as described previously.

Contemporary groups of slaughter were generated using the iterative algorithm of Crump et al. (1997) parameterized by the minimum (30 d) and maximum (120 d) span of a group, and the minimum number of records (n = 4) per group. The composition of contemporary groups was based on finishing herd, date of slaughter, and intervals between consecutive slaughter dates as the variables of interest. First, consecutive animals (ranked on slaughter date) are put into groups according to their slaughter dates and the minimum span of days defined in the parameter file. This step is then repeated considering the start and end slaughter date of the groups and the minimum span defined in the parameter file. Second, contemporary groups are created by reading the groups created previously and clustering consecutive groups according to the maximum span and the minimum records required per group. This step is then repeated considering the maximum span and the minimum records required per group in the parameter file. As a result, 315 animals were discarded from the analysis because of the inability to assign them to a contemporary group of sufficient size. After further restrictions were applied on the weight of the individual cuts (see below), a total of 83 contemporary groups were created, which included 635 animals from 91 sires in 41 different herds. These animals consisted of heifers (n = 575), bulls (n = 26), or steers (n = 34) and were mostly crossbred animals (n = 621 crossbred and n = 14 purebred animals). The sires of these animals were 96% purebred, mainly represented by Belgian Blue (n = 386), Limousin (n = 110), and Charolais (n = 83). The dams were 98% crossbred, where the most prevalent breeds represented were Holstein (n = 353), Limousin (n = 133), Charolais (n = 36), and Simmental (n = 36). Because the average slaughter age of the heifers was 21.5 mo and 66% were born in early spring (January to March), the overall rearing system can be described as a 21-mo-old heifer production system from spring-born calves as outlined by Keane et al. (2008). Heifers after their first winter are fed grazed grass after which they are finished indoors over a 2-mo period on a finishing diet consisting of concentrates and ad libitum grass silage.

Cold carcass weight was recorded as described above for the experimental data set. Due to the recent storing (from 2001) of EUROP classification in the national database, conformation and fat grading, transformed to a 15-point scale as outlined by Hickey et al. (2007), were available for only a limited number of animals. The carcasses were trimmed of excessive fat, and the fat depth left averaged 5 mm when measured along the LM. Additional to the routinely recorded carcass traits, information on individual primal cuts was also made available. The primal cutting procedure used on these animals generated 14 different cuts, 7 taken in the 5-rib forequarter, 5 in the 8-rib hindquarter, and 2 from both locations. Not all of these different cuts were retained for estimation of variance components, and some were grouped together into combined primal cuts. The location of the retained cuts can be identified in Figure 1.

Primal cuts retained for the analysis from the forequarter were the chuck, a portion of the shoulder labeled the blade, flat ribs, brisket, and flank. The blade is a combined primal cut gathering the clod, the braising muscle, and the chuck tender. The flat rib cut represented only part of the rib set and was taken from ribs 1 to 5. The retained hindquarter primal cuts were rib roast, strip-loin, sirloin, fillet, and round. Due to occasional retail demand, T-bones steaks, whole strip-loin and fillet weights were only available on a reduced data set, the T-bone steak being cut through the strip-loin and the fillet. Two cuts, the lean trimmings and the diced beef, were generated from the forequarter and the hindquarter. In addition, the sum of the primal cuts, combined primals, diced beef, and lean trimmings weights defined the total retail product weight and the proportion of the total retail product weight over the cold carcass weight defined the retail product percentage. Thus, the retail product weight consisted of total meat weight (describing the meat part of the cuts) and total dressing fat weight (describing the variable fat weight left on the cuts). The sum of the primal cuts and combined primal cuts within the forequarter and hindquarter will be referred to as forequarter wholesale cut weight and hindquarter wholesale cut weight, respectively. Within carcass trait, observations greater than $\pm$4 SD from the mean estimated within sex by breed groups were set to missing. If cold carcass weight or one of the major cuts (chuck, brisket, blade, rib-roast, sirloin, and round) was missing, the animal was removed from the analysis (n = 31). Primal cut weights and combined primal cut weight in the commercial data set will be referred to as the wholesale cut weight in the commercial data set.

Analysis

Despite the similarities observed in the cutting procedures between the experimental and the commercial data sets, (co)variance components were estimated within each data set separately to account for potential differences in the traits. Model building for fixed effects was done using PROC GLM (SAS Inst. Inc., Cary, NC) for data sets and (co)variance components were estimated in ASREML (Gilmour et al., 2006). The choice of fixed effects was based on the data available. The models were generated for each data set separately based on backward elimination ($P > 0.05$) of factors that were not associated with the dependent variable; significance was based on the *F*-test. Two-way interactions were also tested for associations with the dependent variable.

For the experimental and the commercial data set, the overall mixed linear model can be written as

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{ZQg} + \mathbf{e},$$

where $\mathbf{y}$ is the matrix of records, $\mathbf{b}$ is the matrix of fixed effects, $\mathbf{u}$ is the matrix of random effects, $\mathbf{g}$ is the matrix of breed groups, $\mathbf{e}$ is the vector of residual effects, and the $\mathbf{X}$, $\mathbf{Z}$, and $\mathbf{Q}$ matrices are the respective design matrices.

The mixed linear animal model used in the experimental data set included contemporary group and dam age, included as class effects, and heterosis and age at slaughter centered within sex, both treated as continuous variables, as well as the breed group effect. Factors that did not affect ($P > 0.05$) any of the traits investigated included whether the animal was a singleton or not, and recombination loss. The effect of the sex of the animal was confounded with the contemporary group. Relationships among animals were accounted for using a relationship matrix. A total of 8,300 animals were included in the pedigree file, and unknown ancestors were included as phantom groups of the Belgian Blue, Charolais, Friesian, Holstein, Limousin, Angus, Simmental, and unknown breeds in the pedigree file.

The mixed linear animal model used in the commercial data included the class effects of contemporary group, sex of the animal, and the fixed regression of age at slaughter, which was included as a quadratic regression, as well as in a 2-way interaction with sex of the animal and breed group effect. Heterosis (continuous variable) and recombination loss of the animal (continuous variable), whether the animal was a singleton or not, and age of the dam at the birth of the animal, did not significantly affect any of the traits analyzed ($P > 0.05$). Relationships among 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 in the pedigree file.

In a separate series of analyses, carcass weight was included as a covariate in the model to investigate whether the distribution of carcass cuts was heritable. For the experimental and the commercial data sets, heritability estimates were obtained from single trait analyses. The coefficient of genetic variation ($\mathbf{CV_g}$) for each trait was calculated as the genetic SD divided by the mean (Houle, 1992). As multitrait (3×3 and more) analyses failed to converge, a series of bivariate analyses was used to calculate the correlations between carcass weight, carcass conformation, carcass fat, chuck, shoulder, brisket, rib roast, strip-loin, sirloin, round, and fillet. Fore shin, hind shin, ribs, and flank were not included in the matrix given their relatively low importance for the industry or due to convergence difficulty (ribs). The resulting genetic covariance matrix was bended using the procedure (unweighted option) of Jorjani et al. (2003) to ensure that it was positive definite.

Table 2. Overall mean, phenotypic SD (σ_p), heritability (h^2), and coefficient of genetic variation (CV_g) for carcass traits and cut weight of 413 bulls and steers in the experimental data set

Trait	Mean	σ_p	h^2 (SE)	CV_g, %
Abattoir carcass measure				
Cold carcass wt, kg	337	29.07	0.48 (0.21)	6.0
Carcass conformation (scale 1 to 15)	7	1.14	0.45 (0.21)	10.5
Carcass fat (scale 1 to 15)	7	1.21	0.33 (0.18)	10.1
Forequarter				
Fore shin, kg	5	0.66	0.39 (0.19)	8.1
Brisket, kg	10	1.74	0.25 (0.19)	8.6
Ribs,[1] kg	35	4.42	0.03 (0.15)	2.2
Chuck,[2] kg	28	4.33	0.83 (0.24)	14.2
Shoulder, kg	28	3.44	0.79 (0.23)	11.1
Forequarter meat wt,[3] kg	120	12.28	0.62 (0.23)	8.0
Total forequarter wt,[4] kg	181	16.77	0.42 (0.20)	6.0
Hindquarter				
Rib roast, kg	10	1.35	0.14 (0.16)	5.3
Strip-loin, kg	11	1.43	0.49 (0.22)	9.0
Sirloin, kg	13	1.87	0.67 (0.22)	11.6
Round, kg	48	5.43	0.86 (0.23)	10.6
Fillet, kg	6	0.64	0.29 (0.20)	6.0
Hind shin, kg	9	0.98	0.73 (0.22)	9.1
Hindquarter meat wt,[3] kg	110	10.82	0.70 (0.23)	8.2
Total hindquarter wt,[4] kg	155	12.83	0.57 (0.21)	6.3
Total carcass measure				
Kidney and pelvic fat, kg	10	3.49	0.09 (0.17)	10.9
Total meat wt,[5] kg	230	22.35	0.68 (0.23)	8.0
Meat percentage,[6] %	68	0.03	0.50 (0.21)	2.6
Total fat wt, kg	41	9.41	0.27 (0.18)	12.0
Total bone wt, kg	65	5.59	0.75 (0.22)	7.5

[1]The sum of ribs numbered 1 to 5 and 6 to 13.
[2]The sum of chuck and neck cuts.
[3]The meat weight for the fore/hindquarter; weight of wholesale cuts and lean trimmings.
[4]Total forequarter/hindquarter weight; wholesale cuts, lean trimmings, fat, and bones.
[5]The sum of the forequarter and hindquarter meat weights.
[6]The total meat weight to the cold carcass weight.

RESULTS

Experimental Data

The average cold carcass weight across all animals was 337 kg, and the average total meat weight was 230 kg, giving a meat percentage of 68% of the total cold carcass weight (Table 2). The average EUROP conformation and fat grades in the animals in the present study corresponded respectively to R− (i.e., good muscle development), and 3= (i.e., fleshy, almost everywhere covered with fat with the exception of the round and shoulder). The total forequarter weight represented on average 54% of the carcass weight, and the heaviest cut of the forequarter was the ribs (35 kg; 17% of the retail cut weight). The round cut was the largest cut in the hindquarter (48 kg; 24% of the retail cut weight), and the smallest was the tenderloin, averaging 6 kg (3% of the retail cut weight). The average weight for the total hindquarter was 155 kg (46% of the cold carcass weight).

Heritability of cold carcass weight and total meat weight was 0.48 and 0.68, respectively. In the forequarter, the shoulder and the chuck had the greatest heritability (0.79 and 0.83, respectively); the least heritability estimate was for the ribs (0.03). The heritability for the forequarter meat weight was 0.62. In the hindquarter, the round cut was most heritable (0.86), whereas the least heritability estimates were for the rib roast (0.14) and the fillet (0.29). The heritability for the hindquarter meat weight was 0.70. The CV_g of the cut weights across the carcass varied from 2.2% (ribs) to 14.2% (chuck).

Phenotypically, carcass weight and conformation were positively associated with the different wholesale cut weights, whereas the phenotypic correlations between carcass fat and the wholesale cut weight were all close to zero (Table 3). Few genetic correlations with carcass weight, conformation, and fat score were more than twice their respective SE. However, carcass weight was positively genetically correlated with the different cut weights, whereas carcass fat score was negatively genetically correlated with the different cuts. With the exception of the moderate genetic correlation between the brisket and the rib roast (0.38), the genetic correlations among the different wholesale cut weights were generally strong and positive ($\geq$0.47).

Using the model including carcass weight as a covariate, heritability for the forequarter cuts ranged from 0.04 (ribs) to 0.65 (chuck); the heritabilities for forequarter meat weight and total forequarter weight were 0.39 and 0.51, respectively. Heritability estimates for the different hindquarter cuts ranged from 0.08 (fillet) to 0.61 (round); heritability estimates for hindquarter meat weight and total hindquarter weight were 0.68 and 0.66, respectively.

Commercial Data

Average cold carcass weight was 290 kg, and the total retail product weight averaged 192 kg, which gave a retail product percentage of 66% of the total cold carcass weight (Table 4). 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 O, R, and U) were represented in the data set with 70% of the animals graded as class R. Five carcass fat classes (equivalent to class 1, 2, 3, 4, and 4L in the EUROP scale) were represented in the data set with 65% of the animals residing in class 3. Within the forequarter, the chuck and the blade each made up 16% of the forequarter primal weight, which averaged 38 kg (20% of total meat weight). The round cut made up the major proportion (56%) of the hindquarter primal weight, whereas the tenderloin averaged 5 kg (6% of hindquarter primal weight) and represented the smallest proportion of the hindquarter cuts. The average weight of the hindquarter meat was 77 kg (40% of the total meat weight). The trimmings and diced beef represented 28% of the cold carcass weight (43% of the total meat weight).

Heritability of cold carcass weight and total meat weight was 0.59 and 0.54, respectively. Heritability estimates for conformation and fat grading were also high (0.78 and 0.63 for carcass conformation and fat grade, respectively). In general, heritability estimates of the different joints in the forequarter and hindquarter were all moderate, ranging from 0.28 (flat ribs) to 0.62 (fillet). The CV_g of the cut weights across the carcass varied from 5.9% (round) to 10.0% (brisket, flank).

The phenotypic and genetic correlations between the cold carcass weight and the various wholesale cut weights were moderately to strongly positive (Table 5); the phenotypic correlations with carcass weight ranged from 0.48 (brisket) to 0.77 (round and blade), whereas the genetic correlations with carcass weight ranged from 0.45 (chuck) to 0.67 (tenderloin). The phenotypic and genetic correlations between carcass conformation and the different cuts were all positive. The phenotypic correlations between carcass fat and the different wholesale weights tended to be negative or close to zero, whereas the genetic correlations were mostly negative, but not different from zero. Among the different wholesale cut weights, all phenotypic correlations were positive and moderate, ranging from 0.44 to 0.76. The genetic correlations between the cuts were also positive,

Table 3. Genetic (above the diagonal) and phenotypic[1] (below the diagonal) correlations (SE in parentheses) between various carcass traits and cuts of bulls/steers from the Teagasc beef research center experimental data set

Item	CCW	CCON	CFAT	Chuck	Shoulder	Brisket	Rib roast	Strip-loin	Sirloin	Round	Fillet
CCW		−0.24 (0.37)	−0.14 (0.39)	0.75 (0.12)	0.88 (0.09)	0.63 (0.27)	0.70 (0.36)	0.47 (0.25)	0.87 (0.10)	0.84 (0.08)	0.83 (0.14)
CCON	0.36		0.35 (0.35)	0.30 (0.14)	−0.04 (0.30)	−0.24 (0.45)	0.09 (0.55)	−0.20 (0.41)	0.30 (0.24)	0.25 (0.26)	−0.12 (0.46)
CFAT	0.21	0.05		−0.26 (0.31)	−0.37 (0.31)	−0.59 (0.48)	−0.45 (0.67)	−0.59 (0.35)	−0.41 (0.31)	−0.45 (0.29)	−0.29 (0.43)
Chuck	0.69	0.31	−0.04		0.70 (0.13)	0.47 (0.28)	0.86 (0.23)	0.78 (0.14)	0.82 (0.09)	0.83 (0.09)	0.84 (0.16)
Shoulder	0.70	0.31	−0.04	0.57		0.68 (0.23)	0.79 (0.27)	0.68 (0.16)	0.93 (0.07)	0.83 (0.09)	0.79 (0.11)
Brisket	0.53	0.34	−0.06	0.49	0.48		0.38 (0.56)	0.52 (0.15)	0.70 (0.20)	0.78 (0.19)	0.79 (0.23)
Rib roast	0.56	0.4	−0.03	0.47	0.55	0.43		0.81 (0.11)	0.80 (0.38)	0.79 (0.27)	0.70 (0.10)
Strip-loin	0.65	0.41	−0.00	0.56	0.55	0.46	0.54		0.81 (0.11)	0.78 (0.12)	0.67 (0.24)
Sirloin	0.65	0.34	−0.11	0.60	0.63	0.52	0.50	0.60		0.93 (0.05)	0.83 (0.09)
Round	0.77	0.45	−0.07	0.65	0.70	0.59	0.57	0.66	0.72		0.93 (0.12)
Fillet	0.66	0.34	−0.06	0.52	0.60	0.50	0.59	0.56	0.68	0.69	

[1]CCW: cold carcass weight; CCON: carcass conformation; CFAT: carcass fat. All SE of the phenotypic correlations were ≤0.06.

Table 4. Number of observations (n), overall mean, phenotypic SD (σ_p), heritability (h^2), and coefficient of genetic variation (CV_g) for the carcass traits from an Irish commercial data set

Trait	n	Mean	σ_p	h^2 (SE)	CV_g, %
Abattoir carcass measure					
Cold carcass wt, kg	635	290	20.66	0.59 (0.20)	5.5
Carcass conformation (scale 1 to 15)	345	9	1.23	0.78 (0.27)	12.5
Carcass fat (scale 1 to 15)	345	6	1.14	0.63 (0.26)	14.6
Forequarter					
Blade,[1] kg	635	12	1.06	0.61 (0.20)	7.1
Chuck, kg	635	13	1.46	0.41 (0.20)	7.3
Brisket, kg	635	8	1.12	0.47 (0.18)	10.0
Flat ribs,[2] kg	628	5	0.63	0.28 (0.15)	7.1
Flank, kg	451	2	0.28	0.37 (0.26)	10.0
Forequarter wholesale cuts wt,[3] kg	635	38	6.86	0.46 (0.18)	6.4
Hindquarter					
Rib roast, kg	635	8	0.94	0.40 (0.19)	7.6
Strip-loin, kg	523	11	1.05	0.41 (0.22)	6.2
Sirloin, kg	635	10	0.95	0.55 (0.20)	7.3
Round, kg	635	43	3.88	0.42 (0.19)	5.9
Fillet, kg	520	5	0.45	0.62 (0.20)	7.9
Hindquarter wholesale cuts wt,[3] kg	635	77	6.86	0.34 (0.20)	5.2
Other weights					
Total lean trimmings,[4] kg	635	64	6.36	0.46 (0.18)	6.8
Total dice beef,[4] kg	634	18	2.17	0.74 (0.19)	10.7
Total carcass measure					
Total retail product wt,[5] kg	635	192	16.34	0.54 (0.19)	6.2
Retail product percentage,[6] %	635	66	3.47	0.86 (0.17)	4.9

[1]Part of the shoulder.
[2]Ribs numbered 1 to 5.
[3]The weight of wholesale cuts for the fore/hindquarter.
[4]Cut taken in the fore- or in the hindquarter.
[5]The sum of the forequarter, hindquarter, and other weights.
[6]Total retail product weight to cold carcass weight.

but stronger than their respective phenotypic correlations, ranging from 0.35 to 0.87.

Using the model including carcass weight as covariate, heritability for the forequarter cuts ranged from 0.34 (flat ribs) to 0.91 (blade); heritability of forequarter wholesale cut weight was 0.69. The heritability of hindquarter cuts ranged from 0.31 (rib roast) to 0.72 (round); the heritability of hindquarter wholesale cut weight was 0.55.

DISCUSSION

The objective of this study was to use commercial and experimental data to estimate genetic parameters for different beef wholesale cut weights and to determine their correlations with the currently recorded carcass weight, carcass conformation, and carcass fat.

The 2 crossbred populations used in this study gave a fair representation of the types of animals on Irish beef farms. Evans et al. (2007) showed a high interdependency between dairy and beef herds in Ireland, where, in 2005, 58% of the calves born were beef crosses or beef-dairy crosses. The proportion of animals with unknown sires in the commercial data set also reflects reality in that there is a low level of sire recording at calf registration. The Irish Legislation by Statutory Instrument S.I.276/1999 (transposed from European Regulation 1760/2000 on identification and registration of bovine) specifies the compulsory recording, on the maternal side, of the breed and identification of the dam, and on the paternal side, of only the breed of the sire.

Both data sets used in the present study were relatively small. However, across the literature reviewed for the genetic analysis of primal cuts, the populations studied were also of limited size and comparable with both of our data sets; Cantet et al. (2003) used 474 Angus animals, Cundiff et al. (1969) used 287 Hereford-, Angus-, and Shorthorn-crossed animals, and Brackelsberg et al. (1971) used 257 Hereford- and Angus-sired animals. Other studies using larger data sets focused on overall retail meat, fat, and bone yields and did not present estimates for the primal cuts; Shackelford et al. (1995) used 2,762 purebred and composite animals, Koch et al. (1982) studied 2,453 steers of various biological backgrounds, and Morris et al. (1999) used 1,962 animals from 3 large multi-breed breeding experiments.

The current beef genetic evaluation system for carcass traits in Ireland is across breed, and the breeding objective includes a positive economic weight on carcass weight and carcass conformation, but a negative

Table 5. Genetic (above the diagonal) and phenotypic[1] (below the diagonal) correlations (SE in parentheses) between various carcass traits and cuts estimated from the commercial data set

Item	CCW	CCON	CFAT	Chuck	Blade	Brisket	Rib roast	Strip-loin	Sirloin	Round	Fillet
CCW		−0.15 (0.20)	0.38 (0.27)	0.45 (0.23)	0.63 (0.14)	0.49 (0.22)	0.66 (0.17)	0.54 (0.21)	0.59 (0.15)	0.62 (0.17)	0.67 (0.14)
CCON	0.20		−0.20 (0.31)	0.06 (0.37)	0.16 (0.29)	0.41 (0.29)	0.20 (0.35)	0.62 (0.25)	0.27 (0.28)	0.20 (0.34)	0.11 (0.29)
CFAT	0.22	−0.16		−0.10 (0.41)	−0.18 (0.33)	−0.19 (0.33)	−0.59 (0.44)	−0.25 (0.45)	−0.11 (0.35)	−0.34 (0.39)	−0.31 (0.35)
Chuck	0.65	0.28	−0.06		0.77 (0.16)	0.63 (0.24)	0.75 (0.15)	0.44 (0.33)	0.51 (0.24)	0.68 (0.21)	0.74 (0.18)
Blade	0.77	0.30	−0.06	0.66		0.87 (0.11)	0.82 (0.08)	0.46 (0.26)	0.81 (0.08)	0.85 (0.10)	0.85 (0.07)
Brisket	0.48	0.26	−0.23	0.48	0.59		0.82 (0.09)	0.74 (0.19)	0.74 (0.17)	0.73 (0.17)	0.71 (0.15)
Rib roast	0.60	0.26	−0.09	0.52	0.69	0.60		0.66 (0.15)	0.66 (0.14)	0.78 (0.11)	0.77 (0.12)
Strip-loin	0.68	0.36	0.07	0.52	0.57	0.44	0.54		0.41 (0.30)	0.35 (0.32)	0.46 (0.26)
Sirloin	0.71	0.36	−0.02	0.56	0.69	0.50	0.57	0.57		0.77 (0.12)	0.45 (0.16)
Round	0.77	0.42	−0.16	0.63	0.76	0.59	0.63	0.65	0.73		0.78 (0.12)
Fillet	0.68	0.24	−0.12	0.63	0.67	0.56	0.61	0.53	0.57	0.74	

[1]CCW: cold carcass weight; CCON: carcass conformation; CFAT: carcass fat. All SE of the phenotypic correlations were ≤0.08.

economic weight on carcass fat (Evans et al., 2007). The breeding objective also includes a negative economic weight on cow mature BW (Amer et al., 2001).

Trait Means and Heritability Estimates

The 2 data sets, commercial and experimental, used in the present study were different in origin in that the majority of the experimental data set was composed of steers (82% of animals), whereas the commercial data were made up of predominantly heifers (91% of animals). This was reflected in differences in observed average carcass weight between the 2 data sets: 337 and 290 kg observed in the experimental and commercial data sets, respectively. The heritability estimates observed in the experimental and the commercial data set for cold carcass weight were similar and are in accordance with the mean estimate of 0.40 reported by Rios Utrera and Van Vleck (2004) after an extensive review of heritability estimates for carcass traits across 56 studies.

The large heritability estimates observed in the commercial data set for carcass conformation and fat, albeit with large SE, may be due to the poor distribution of the data in that data set. However, the heritabilities of EUROP carcass conformation and fat grading vary considerably between populations. Using a large data set on Irish crossbred cattle, Hickey et al. (2007) reported heritability estimates ranging from 0.04 to 0.36, and from 0.00 to 0.24 for conformation and fat, respectively, across 8 breed groups. Eriksson et al. (2003), using 2 distinct purebred populations of Swedish Charolais and Hereford, reported heritability estimates of 0.34 (Charolais) and 0.22 (Hereford) for carcass conformation, and 0.38 (Charolais) and 0.27 (Hereford) for carcass fat grading.

The meat percentage and the retail product percentage were similar across the experimental (68%) and commercial (66%) data sets, reflecting differences in cutting procedures between the experimental and the commercial data set; the commercial cutting procedure applied a more severe cutting procedure on the individual cuts with the objective of neat presentation of the cuts on the supermarket shelves. These estimates were also consistent with values reported in the literature, which vary from 66 to 68% (Koch et al., 1982; Shackelford et al., 1995; Morris et al., 1999). The heritabilities for total meat weight in the experimental data set (0.68) and for total retail product weight in the commercial data set (0.54) were similar to those found by Koch et al. (1982; 0.58), Shackelford et al. (1995; 0.67), and Morris et al. (1999; 0.48), despite some differences in the definition of the trait; sum of roast and steak meat (Koch et al., 1982), sum of the weight of the boneless, totally trimmed retail cuts and 20% fat lean trim (Shackelford et al., 1995), or carcass components weight trimmed of fat (Morris et al., 1999).

Between the 2 data sets, the individual cuts were generally heavier in the experimental data set than in the commercial data set, reflecting i) the difference in the representation of different sexes in the data sets and ii) the difference in cutting procedure (i.e., cutting and subcutaneous and seam fat trimming) as noted previously.

The average forequarter primal weight differed between the experimental and commercial data sets, at 106 kg (31% of carcass weight) and 38 kg (13% of carcass weight), respectively. The difference was mainly attributable to the different cutting procedures adopted, as well as the different carcass weights, in the 2 data sets. In the commercial data set, the carcass cutting was driven by retailer demand and so, to a certain extent, by the cooking habits. Three categories of beef cuts exist in Ireland (Board Bia, 2008), which include the roast cuts (part of the chuck, brisket), the pot roast or braising cuts (part of the chuck, flat ribs, and flank), and the casserole cuts (blade). The remaining parts of the forequarter (neck, part of the shoulder muscles, part of the rib set, and part of the flank) are categorized as lean trimmings or "dice and stew beef," to be sold as diced (stir fry) and ground beef. The total lean trimmings and total dice beef can be taken from the forequarter and the hindquarter.

The heritability of total forequarter weight in the experimental data set (0.42) is similar to the estimate of 0.49 reported by Brackelsberg et al. (1971). The moderate to high heritability estimates in the present study for the different forequarter wholesale weights also corroborates previous estimates in other studies. Cundiff et al. (1969) reported heritability estimates ranging from 0.34 to 0.49 for the chuck and from 0.38 to 0.44 for the rib; Brackelsberg et al. (1971) calculated a moderate heritability (0.42) for the composite cut called chuck and rib. However, large differences in heritability estimates were observed between the experimental and commercial data sets for the same traits (for example, brisket, chuck, round, fillet). These observed discrepancies may be due to several factors such as i) population specific genetic parameters and ii) possible differences in genetic parameters between sexes; Crews and Kemp (2001) reported large differences in additive genetic variance for the LM area between bulls and heifers, iii) possible differences in the cutting methods even for well located cuts such as the chuck or brisket, and iv) possible confounding effects between genetics and unknown environmental effects. In addition, relatively large SE were observed for the heritability estimates of most traits in this study.

Average hindquarter meat weight (sum of the wholesale cuts) was slightly greater in the experimental data set (97 kg; 29% of the cold carcass weight) than in the commercial data set (77 kg; 27% of the cold carcass weight). These small differences could be due to differences observed in the populations (breed, sex), but are more likely due to differences in cutting practices between the 2 data sets as described previously. The heritability estimate for total hindquarter weight (0.57) in the experimental data set is similar to the heritability of 0.57 reported by Brackelsberg et al. (1971) and 0.46 reported by Cantet et al. (2003) for the same trait.

The generally high heritability estimates for the wholesale cuts located in the hindquarter in the present study agree with previous estimates. Cundiff et al. (1969) reported heritability estimates ranging from 0.07 to 0.48 for the loin and from 0.42 to 0.68 for the round, whereas Brackelsberg et al. (1971) reported a high heritability (0.81) for the composite cut called round and loin.

The CV_g for carcass weight in both data sets (6.0% for the experimental data set and 5.5% for the commercial data set) was similar to the average of 4.4% calculated from the results of Hickey et al. (2007) across 8 cattle populations in Ireland. The CV_g for carcass conformation and fat in both of our studies were greater (>10.1%) than those calculated from the results presented by Hickey et al. (2007), where the average CV_g for both carcass conformation and fat was 8.0%. The CV_g for the different wholesale cut weights (2.2 to 14.2%) is consistent with the CV_g reported in other studies for other performance traits such as growth rate (Arthur et al., 2001; 4.6 to 7.2%), feed intake (Arthur et al., 2001; 6.9 to 7.2%), and weaning weight (Phocas and Laloë, 2004; 6.0 to 8.0%).

From the experimental study, the heritability estimate for total bone weight (0.75) was greater than heritability estimates reported in the literature. Shackelford et al. (1995) reported a heritability of 0.62 for carcass bones, whereas Koch et al. (1982) and Morris et al. (1999) reported heritability estimates of 0.57 and 0.51, respectively, for the same overall trait. For total fat weight, the low heritability observed in our experimental data set (0.27), although in agreement with the estimate reported by Morris et al. (1999; 0.30), is less than the heritability estimates reported by Shackelford et al. (1995; 0.65) and Koch et al. (1982; 0.47).

In the experimental and commercial data sets, little change in the heritability estimates of the cuts was observed when carcass weight was included as a covariate in the model. The decision to report the heritability estimates for carcass cut weights was made because farmers will be paid on the yield of each cut and because the cut weights will be included in an overall breeding objective that accounts for potential unfavorable correlated responses in traits such as mature size.

Relationship Among Carcass Traits

The phenotypic correlations among carcass conformation, carcass fat, and carcass weight across the 2 data sets are consistent with those cited by Hickey et al. (2007), ranging from 0.17 to 0.38. The genetic correlations observed in the experimental data set between carcass weight and EUROP conformation and fat grading were negative (−0.24 to −0.14) and different from the positive, albeit weak, genetic correlations (0.11 to 0.26) reported by Hickey et al. (2007). Nonetheless, large SE were associated with all genetic correlations estimated in the present study, reflecting the limited sample size. As a result, the genetic correlation estimates were not statistically different from zero.

The moderate to strong positive genetic correlations between carcass weight and the various wholesale cut weights in the present study were not unexpected given the part whole relationship between the different cuts and carcass weight. Therefore, selection for greater carcass weight will increase the weight of each of the cuts. Selection for increased carcass conformation will also be associated with an increase in individual wholesale cut weights with the exception of the shoulder, brisket, and strip-loin cuts as estimated from the experimental data, although the SE of the correlations were large. Carcass conformation and carcass fat tended to be more positively genetically correlated with the different wholesale cuts in the commercial data set compared with the experimental data set, thus reflecting the difference in the fat trimming procedure applied to the cuts in the 2 data sets.

The genetic correlations between the different wholesale cut weights were moderate to strongly positive, in agreement with Brackelsberg et al. (1971), who also documented moderate to strong genetic correlations between the studied cuts (round and loin cut, chuck and rib cut, and round, loin and rib cut) ranging from 0.16 to 1.00. Cundiff et al. (1969) observed strong genetic correlations between 4 beef cuts (minimum genetic correlation of 0.72), namely, the round, loin, rib, and chuck. The results from our study show that direct selection on a primal beef cut would result in indirect positive genetic gain in all of the cuts, although some of the correlations were less than unity.

The existence of moderate to large heritability estimates, albeit with large SE, and large CV_g suggests that genetic selection for individual carcass cut weight may be fruitful. Genetic correlations among all beef wholesale cut weights were moderate to strongly positive, although some were less than unity, albeit sometimes with large SE, indicating a potential benefit of placing more emphasis on some greater value cuts to increase genetic gain in carcass value. This is further substantiated by the strong positive genetic correlations between the carcass weight and the cuts, implying i) that selection for increased carcass weight will, on average, increase the weight of each cut and ii) 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 weights of individual beef carcass cuts and to subsequently investigate the feasibility of genetically selecting for these traits to improve carcass value.

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Livestock Science 137 (2011) 130–140

Contents lists available at ScienceDirect

Livestock Science

journal homepage: www.elsevier.com/locate/livsci

Use of digital images to predict carcass cut yields in cattle☆

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ARTICLE INFO

Article history:
Received 5 February 2010
Received in revised form 22 October 2010
Accepted 26 October 2010

Keywords:
Accuracy
Carcass cut
Video image analysis
Beef

ABSTRACT

The objective of this study was to assess the potential of video image analysis (VIA) in predicting various wholesale carcass cuts in cattle. Video image analysis and meat cut weights were available from two different sources: an experimental (n = 346) and a commercial dataset (n = 281). The cattle used were crossbred steers (predominant breeds were Belgian Blue, Angus, Friesian, Charolais, Holstein, Limousin, and Simmental) in the experimental dataset, and crossbred heifers (predominant breeds were Limousin, Belgian Blue, Charolais, and Simmental) in the commercial dataset. In both datasets, the meat cuts were grouped into four groups based on retail value: Low Value Cuts (LVC), Medium Value Cuts (MVC), High Value Cuts (HVC), and Very High Value Cuts (VHVC); total meat weight was calculated as the sum of the individual meat cut weights. In addition, total bone weight and total fat weight were available in the experimental dataset. In both datasets, a calibration and a validation sub-dataset were created for each of the carcass cut groups. Multiple regression analyses were applied to each calibration dataset to predict the cuts from using three different sets of models based on the predictors: 1) carcass weight only, 2) carcass weight plus EUROP carcass classification, and 3) carcass weight plus VIA parameters. The accuracy of predicting yields of cuts was superior to prediction of cut yields as a proportion of the carcass weight. Across both the experimental and the commercial datasets, the proportion of variation of wholesale cut yields in the validation dataset explained (R^2) ranged from 0.33 (total fat weight in the experimental dataset) to 0.91 (total meat weight in the experimental dataset) using carcass weight as the sole predictor. The R^2 increased to between 0.65 (LVC in the commercial dataset) and 0.97 (total meat weight in the experimental dataset) when carcass weight plus VIA variables were used as predictors. In the analyses of both the experimental and the commercial data, models that included the VIA variables had the lowest root mean square error of prediction across traits. Mean bias and correlations between the residuals and predicted values were generally not different from zero. Results from this study show that wholesale cuts in steers and heifers can be accurately predicted using multiple regression models incorporating carcass weight and VIA variables. The carcass images routinely stored provide a powerful tool for use in a beef breeding program to select for more valuable carcasses.

1. Introduction

The retail value of a beef carcass varies with the distribution of the individual meat cuts. The EUROP carcass classification system, used in the European Union, provides a superficial appraisal of the carcass value, and cannot accurately account for variation in carcass composition. The

☆ The authors gratefully acknowledge access by the Irish supermarket chain to their database on carcass cuts weight, the work input of L. Kreuchwig (EplusV, GmbH, Oranienburg, Germany), as well as the Walsh Fellowship finance granted by the Irish Ministry of Fishery and Food to this project.
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1871-1413/$ – see front matter © 2010 Elsevier B.V. All rights reserved.
doi:10.1016/j.livsci.2010.10.012

aim of EUROP conformation grading described in the European Council regulation 1208/81 of 28 April 1981 is to give an appreciation of the carcass profiles, in particular the round, back, and shoulder. The conformation classification system uses the letter E (excellent), U, R, O, and P (poor) to describe the conformation of the carcass. The carcass fat classification system uses the scale 1 (low), 2, 3, 4 and 5 (very high) to measure the amount of fat on the outside of the carcass and in the thoracic cavity.

EUROP carcass classification in Ireland was originally based on subjective assessment by trained personnel, but is now undertaken using Video Image Analysis (**VIA**) on calibrated classification machines. Boggaard et al. (1996) presented the limitations of European beef carcass grading operated by expert classifiers: bias can occur between groups of carcasses, classifiers judgment can vary over time, and differences can be observed between classifiers. Objective carcass grading as operated by grading machines overcomes these weaknesses. In Ireland, the accuracy (R^2) and fit (bias) of three classification machines (VIAscan, VBS2000, and BCC2) at predicting carcass classification in abattoir condition for conformation and fat against a reference classification established by experts was documented by Allen and Finnerty (2000). The accuracy (R^2) in predicting EUROP conformation on a 15-point scale was 0.85 for the VBS2000, 0.83 for the VIAscan, and 0.86 for the BCC2 system. The accuracy (R^2) in predicting EUROP fat on a 15-point scale was 0.85 for the VBS2000, 0.85 for the VIAscan, and 0.88 for the BCC2 system. This study (Allen and Finnerty, 2000), based on accuracy and bias (i.e., under- and over-prediction of the grading), indicated that each of the three machines had the potential to be used for classification purposes. A formal authorisation trial of the three systems was undertaken in Ireland in 2003 and each of the mechanical grading systems exceeded the performance criteria laid down in the regulation 1215/2003 for authorisation. The use of the VBS2000 carcass grading machine was since recommended by the meat processing industry for EUROP mechanical grading in Irish slaughter houses. Since 2005, a copy of the two pictures (tiff format) taken after slaughter by the VBS2000 mechanical grading machine (E + V GmbH, Germany) for each carcass to derive the EUROP conformation and fat grading have been stored in the Irish Cattle Breeding Federation database.

The yields of wholesale cuts determine the actual value of a carcass for retailers, and availability of carcass images provides a great opportunity to more accurately assess the true retail value compared to current classification systems. Several previous studies have investigated the potential of using image analysis to predict meat cuts in cattle. Brinks et al. (1964) used linear measurements obtained by stereo-photogrammetry (i.e., estimation of the three dimensional coordinates of reference points placed on the animal) to predict wholesale cuts in 38 steers. The accuracy of prediction in that study varied from 0.91 (loin weight) to 0.97 (forequarter weight). In an attempt to speed up the process of taking live measurements on animals, Clark et al. (1976) used electrogrammetry technology on 40 steers to quantify several beef wholesale weights. As animals walked through an illuminated chute, photocells recorded both a side and a top view from which 25 parameters were derived. The experiment required 10 runs per animal and the accuracy of prediction ranged from 0.60 (rib weight) to 0.77 (chuck weight). Using the analysis of 12^{th} rib sections on two Chinese cattle crossbred populations, Chen et al. (2007) created groups of top grade retail cuts and found a maximum accuracy of prediction of 0.83. Using carcass images of 443 sheep under abattoir conditions, Ruis-Vilarrasa et al. (2009) derived five primal meat yields (leg, chump, loin, breast, and shoulder); the accuracy of prediction obtained using video analysis technology was up to 0.97.

Other countries have developed carcass grading systems based on the carcass composition using VIA and meat quality. The United Stated have developed a dual grading (U.S. Standards for Grades of Carcass Beef) on yield (i.e., yield of closely trimmed boneless retail cuts expected to be derived from the major wholesale cuts), and quality (i.e., characteristics of the meat which predict the palatability of the lean, based on marbling and maturity) (http://www.ams.usda.gov). Canada, through the Canadian Beef Grading Agency (http://www.beefgradingagency.ca), has adopted a similar beef grading (Livestock and Poultry Carcass Grading Regulations (SOR/92-541)) also based on carcass yields and carcass quality. Beef carcass grading in Australia (Meat Standard Australia Eating Quality Prediction Model SP2000), through the Meat Standard Australia, is based on specific carcass measurements using VIA (meat colour, fat depth, marbling) and is entirely orientated towards meat tenderness and includes cooking recommendation (http://www.mla.com.au).

As VIA technology was installed in Ireland for generating EUROP grading for conformation and fat, it became apparent that that this new grading instrument could have potential beyond EUROP classification. The objective of this study was therefore to investigate the accuracy of VIA in predicting carcass cut yields using carcass images taken at slaughter.

2. Material and methods

Data used in the present study were obtained from existing databases. Hence animal care and use committee approval was not necessary for this study. The carcass cut data used in the present study are described in detail by Pabiou et al. (2009), but are also briefly discussed below.

The digital images taken by the VBS2000 carcass grading machine (E + V GmbH, Germany) at slaughter and used to derive the EUROP conformation and fat grading across 26 abattoirs in Ireland, were stored at the Irish Cattle Breeding Federation. Using a one-color angled camera, the VBS2000 takes a two-dimensional picture and, after superposition of a dark filter, a three dimensional picture. Raw output data of the images comprised of 428 VIA variables describing linear measurements of carcass dimensions, carcass contour and carcass color measurements.

2.1. Experimental dataset

A total of 419 carcasses (346 steers and 73 bulls) slaughtered between 2005 and 2008 with VBS2000 digital images were included in this dataset (hereafter referred to as the "experimental dataset"). The animals were a sub-sample of a larger experimental dataset included in the study of Pabiou et al. (2009). In this dataset, each carcass was dissected into 23 different cuts: fore-shin, ribs 1 to 6, ribs 7 to 13, flank, brisket, chuck, neck, clod, blade steak, braising muscle, chuck tender, leg of mutton cut, cap of ribs, cube roll, strip-loin, rump, tail of rump, silverside, topside, knuckle, salmon cut, fillet, and hind-shin (Pabiou et al., 2009). Additionally, total lean trimmings, total fat and total bone weights were available from this experiment. Total meat weight was calculated as the sum of the primal cuts and the lean trimmings weights.

Only data on the steers were retained for estimation of prediction equations. Of the 346 steers available, 92% were crossbred and sires (n = 239) were purebred males (Belgian Blue 26%, Angus 22%, Friesian 15%, Charolais 15%, Holstein 12%, Limousin 5% , and Simmental 5%). A total of 16% (n = 54) of the dams were purebred and the dominant breed was Holstein. The remaining dams were crossbred females, and the most prevalent breeds were Holstein (39%), Limousin (12%), Friesian (12%), Charolais (11%), and Simmental (9%). The average of the steers at slaughter was 750 days.

Cold carcass weight as well as carcass conformation and carcass fat grade, scored using the EUROP classification mechanical grading system, is recorded for all cattle slaughtered in Ireland. In the present study the EUROP classification grades were transformed to a 15-point linear scale as outlined by Hickey et al. (2007). The kidney and channel fat and the kidney knobs were removed prior to carcass weighing.

Four groups of wholesale cut weights, hereon in referred to as wholesale cuts, were created according to their retail values: Lower Value Cut group (**LVC**) including fore- and hind-shins, ribs 1 to 6, ribs 7 to 13, flank, brisket, neck, and lean trimmings; Medium Value Cut group (**MVC**) comprising of the weight of the shoulder (i.e., clod, blade steak, braising muscle, chuck tender, leg of mutton cut) and the chuck cuts; High Value Cut group (**HVC**) including the sirloin (i.e., rump and tail of rump) and the round (i.e., silverside, topside, knuckle, salmon cut) cut weights; Very High Value Cut group (**VHVC**) comprising of the weights of the rib-roast (i.e., cap of ribs, cube roll), strip-loin, and fillet cuts. LVC, MVC, HVC, and VHVC will be referred to as ‘wholesale cuts’. Total carcass meat weight, total carcass fat weight and total bone weight were calculated by respectively summing the meat, fat and bone weight of the carcass. Total meat, fat, and bone weights will be referred to as ‘overall weights’. The proportions of the four wholesale cut weights and the three overall weights relative to carcass weight were also calculated.

2.2. Commercial dataset

A total of 281 heifer carcasses slaughtered between 2005 and 2008 with VBS2000 digital images were included in this dataset (hereafter referred to as the “commercial dataset”). The animals were a sub-sample of a larger commercial dataset included in the study of Pabiou et al. (2009). All the animals were processed through the same meat processing plant. Each carcass was dissected into 12 primal cuts: chuck, clod, braising muscle, chuck tender, ribs 1 to 5, brisket, flank, rib-roast (i.e., cap of ribs and cube roll), strip-loin, sirloin (i.e., rump and tail of rump), round (i.e., silverside, topside, knuckle, and salmon cut), fillet (Pabiou et al., 2009). In addition, lean trimmings and diced beef weights were also available. The sum of the primal cuts, the lean trimmings, and the diced beef composed the total meat weight. No measurements on fat or bone were available in the heifer dataset.

Of the 281 heifers, 96% were crossbred and all known sires (n = 88) were purebred males (Limousin 50%, Belgian Blue 22%, Charolais 16%, Simmental 9%, and other breeds 3%). All dams were known and 97% of them were crossbred females (n = 269) where the most prevalent breeds consisted of Limousin (38%), Charolais (19%), Simmental (18%), and Holstein (12%). The average slaughter age of the heifers was 574 days.

Cold carcass weight, carcass conformation and carcass fat grade were also recorded for each animal slaughtered as described previously, the VIA-based VBS2000 EUROP classification grades also being transformed to a 15-point linear scale.

Four groups of wholesale cuts were created which differed somewhat from definitions in the experimental dataset due to different cutting procedures: Lower Value Cut group (**LVC**) include lean trimmings, ribs, flank, and brisket; Medium Value Cut group (**MVC**) include the weights of the blade (i.e., clod, braising muscle, chuck tender) and the chuck cuts; High Value Cut group (**HVC**) include the sirloin and the round cut weights; and Very High Value Cut group (**VHVC**) include the weights of the rib-roast, strip-loin, and fillet cuts. Details of the carcass dissection describing 14 different cuts, seven in the forequarter, five in the hindquarter, and two cuts across both locations were described previously (Pabiou et al., 2009). LVC, MVC, HVC, and VHVC will be referred to as ‘wholesale cuts’. Additionally, total meat weight was calculated as the sum of all four wholesale cut group weights; total carcass fat weight and total bone weight were not available in this dataset. Total meat weight will be referred to as an ‘overall weight’. The proportion of the four wholesale cut weights and total meat weight relative to carcass weight were also calculated.

2.3. Models and statistical analysis

For each of the wholesale weights, the overall weights, and proportions relative to carcass weight, three alternative prediction models were evaluated within the experimental and commercial dataset separately: 1) a baseline model for comparisons including carcass weight only; 2) model including carcass weight plus EUROP classification for conformation and fat; and 3) model including carcass weight plus VIA parameters (hereafter referred to as Model 1, Model 2, and Model 3, respectively). EUROP gradings for both conformation and fat score, as well as carcass weight, were forced into all predictions for Model 2. Note that the EUROP classification for conformation and fat were from mechanical grading, previously developed also using VIA parameters (Allen and Finnerty, 2000).

Several statistical approaches were preliminary tested on the experimental dataset to relate the 428 parameters from the VIA images to wholesale cut weights (i.e., model 3 above). These included stepwise regression, partial least square regression (**PLS**), least absolute shrinkage and selection operator (**LASSO**; Tibshirani, 1996), principal component analysis (**PCA**), and canonical correlation analysis (**CCA**). Stepwise regression is a widely used standard procedure for variable selection which sequentially introduces and discards predictors in the model one at a time based on a certain significance level. Selection of variables for the model in the present study, also described by Ruis-Vilarrasa et al. (2009), was based on minimising the root mean square error of prediction within the calibration dataset. In our study, the regressions adjusted for cold carcass weight were applied to a maximum of eight times to regress, one at a time the dependent variables. PLS regression maximises the covariance between scores of predictors and scores of response variables; the maximum number of scores of predictors considered to validate the regression was set to 15, and the statistical test for model assessment was the predicted residual sum of squares. The LASSO regression method is a constrained form of least square regression and minimizes the usual sum of squared errors, with a bound on the sum of the absolute values of the coefficients. The PCA was not directly applied to the wholesale cut weights, but to the dissection cut weights ($n = 23$), and all 23 dimensions were kept; a stepwise regression (significance level for inclusion and exclusion of predictors were set to 0.30 and 0.05, respectively) was then applied to get the best combination of VIA variables that predict the PCA primal meat yield dimensions. The predicted PCA primal meat yield dimensions were then back transformed into primal yields, and then into wholesale cuts weight. The CCA applied data reduction on both the dissection cut weights ($n = 23$) and the VIA variables ($n = 428$) in order to maximise the correlation between their canonical scores. Because of the large number of VIA variables compared to the number of observations in the dataset ($n = 346$ in the experimental dataset), a PCA was applied beforehand to the VIA variables, and 23 PCA VIA dimensions were kept for the CCA. The predicted dissection canonical scores were then back transformed into dissection cut weights, and then into wholesale cuts weight.

2.4. Validation

For each of the dependent variables, the experimental and commercial datasets were individually stratified based on mean, and then randomly split into a calibration dataset (to derive the regressions coefficients) and a validation dataset (to assess the accuracy and the fit of the regression developed in the calibration dataset) for the trait under investigation. In the experimental dataset, 232 steers (67% of the steer population) were included in the calibration dataset and 114 steers were included in the validation dataset; in the commercial dataset, the respective numbers were 189 (67% of the heifer population) and 92 heifers.

Regression models were developed in each calibration dataset and were subsequently applied to their respective validation dataset and the accuracy of prediction assessed. Statistics used to quantify the quality of predictions included the mean bias (a t-test was performed to test for significance from zero), the Root Mean Square Error (**RMSE**), the accuracy of prediction ($\mathbf{R^2}$), and the correlation between the predicted values and the residuals ($\mathbf{r_e}$) to investigate the presence of systematic bias.

The correlations between the four wholesale cut weights predicted for the different models were calculated to investigate how well the predictions captured variation in carcass composition. The eigenvalues of these correlation matrices were then computed to summarise their correlation structure. Eigenvalues were also calculated for the correlations between the (true) wholesale weights in order to illustrate how close the predicted correlation structure among the cuts reflected the true correlation structure. Within each model, the largest eigenvalue expressed as a percentage of the matrix trace can be used as a summary indicator for each of the correlation tables and will be referred to as 'largest percentage eigenvalue'. An eigenvalue close to one means that there are strong correlations between predicted wholesale cuts, and therefore little possibility of individually selecting on wholesale cuts. A correlation structure between the predicted wholesale cuts close to the correlation between the actual cuts is ideal.

Prediction equations for proportions of wholesale cut weights and overall weights were generated separately hereon referred to as 'predicted proportion', but prediction proportions were also calculated using the ratios of the relevant predicted cut weights to actual carcass weight (hereon referred to as 'calculated proportion').

Additionally, the prediction equations developed from the steer data were applied separately to the 74 bulls also present in the experimental dataset, and the fit assessed.

2.5. Breed effects

The possible existence of systematic bias in the estimation of different cuts was quantified across different breed types in the experimental dataset. A fixed effect linear model (PROC GLM; SAS, 2003) was used to regress the residuals from the validation dataset on breed composition of each animal. Animals were grouped by their primary and secondary breed fractions and are described as such. The primary breed fraction of the experimental animals was categorised as: Charolais, Angus, Belgian Blue, "Other beef" (including Simmental and Hereford breeds), and "Dairy breeds". The secondary breed fraction for both datasets was categorised as being either Beef or Dairy breed.

3. Results

The RMSE for prediction of wholesale cut yield was, on average, lowest for stepwise regression, followed by PLS, PCA, LASSO and finally CCA gave the poorest predictions (Table 1). The ranking of methods on the accuracy of prediction (R^2) was similar. The methods did not differ notably in bias and r_e, except for the significant systematic bias observed for LASSO. The stepwise regression gave the best results (in terms of RMSE and R^2) and is the only method described from hereon in.

In the experimental dataset, the average cold carcass weight of the steers was 332 kg consisting of 227 kg meat, 41 kg fat, and 64 kg bones (Table 2). Average weight of the four groups of wholesale cut weights was 98 kg, 43 kg, 60 kg, and 26 kg for the LVC, MVC, HVC, and VHVC, respectively. Carcass weight comprised of 29% LVC, 13% MVC, 18% HVC, and 8% VHVC. The average carcass weight of the bulls was 321 kg; the total meat weight, fat weight, and bone weight were 230, 30, and 61 kg, respectively. LVC, MVC, HVC, and VHVC averaged 93 kg (29% of the carcass weight), 49 kg (15% of the carcass weight), 62 kg (19% of the carcass weight), and

Table 1
Mean bias (kg), residual root mean square error (RMSE; kg), coefficient of determination (R^2), and correlation between residuals and predicted weights (r_e) for the four groups of wholesale cuts using stepwise regression, partial least square analysis (PLS), principal component analysis (PCA), canonical correlation analysis (CCA), and least absolute shrinkage and selection operator (LASSO) in the validation dataset of 114 steers from the experimental dataset.

Method/Wholesale cut	Bias	RMSE	R^2	r_e
Stepwise regression				
Lower value cuts	0.15	5.6	0.92	−0.08
Medium value cuts	0.13	2.73	0.86	−0.1
High value cuts	1.18**	3.27	0.93	0.05
Very high value cuts	−0.11	1.75	0.84	−0.01
PLS				
Lower value cuts	0.53	6.06	0.90	−0.06
Medium value cuts	−0.07	3.74	0.74	−0.18
High value cuts	0.64	3.56	0.91	0.05
Very high value cuts	−0.17	2.13	0.77	−0.03
PCA				
Lower value cuts	−0.90	5.87	0.87	−0.27*
Medium value cuts	−0.22	6.00	0.81	−0.01
High value cuts	0.50	3.47	0.92	−0.01
Very high value cuts	0.20	1.80	0.85	−0.12
CCA				
Lower value cuts	1.26	7.63	0.80	0.41***
Medium value cuts	−0.37	9.67	0.51	−0.07
High value cuts	0.86	6.54	0.72	−0.15
Very high value cuts	0.40	2.61	0.68	−0.04
LASSO				
Lower value cuts	−0.51	7.38	0.87	0.36***
Medium value cuts	0.18	3.80	0.76	0.33***
High value cuts	0.66	5.12	0.89	0.63***
Very high value cuts	−0.02	2.55	0.77	0.55***

*, ** , ***: Bias/Correlation different from zero at $P<0.05$, $P<0.01$, $P<0.001$, respectively.

26 kg (8% of the carcass weight), respectively. In the commercial dataset, the average cold carcass weight was 283 kg; the average meat yield was 183 kg. The average weights for LVC, MVC, HVC, and VHVC were 94 kg (34% of the carcass weight), 20 kg (7% of the carcass weight), 47 kg (17% of the carcass weight), and 22 kg (7% of the carcass weight), respectively.

3.1. Predictions using carcass weight

The accuracy of prediction (R^2) for the overall weights of the steers in the experimental dataset (Table 3) was greater than 0.33 (total fat weight); R^2 of the wholesale cut weights were 0.74 (MVC, VHVC), 0.75 (HVC), and 0.87 (LVC). The correlations between residuals and predicted weight traits were not different from zero across all traits in the experimental dataset. For the heifers in the commercial dataset (Table 4), accuracies of prediction for wholesale cut weights was 0.46 (LVC), 0.62 (MVC), and 0.68 (HVC and VHVC).

Since carcass weight was the only predictor in the model, all correlations between predicted wholesale cut weights were equal to 1 in both the experimental and the commercial study.

The accuracy of predictions was similar between predicted proportions and calculated proportions of yields in the experimental dataset (Table 5) and the commercial dataset (Table 6). The maximum R^2 were 0.29 (calculated proportion for total bone) and 0.16 (calculated proportion for VHVC) in the experimental and the commercial dataset, respectively.

Table 2
Mean, phenotypic standard deviation (s), minimum (Min), maximum (Max), and coefficient of variation (CV) for carcass traits of the steers and bulls in the experimental dataset, and of the heifers in the commercial dataset.

	Steers (n = 346)				Bulls (n = 74)				Heifers (n = 281)			
	Mean (s)	Min	Max	CV	Mean (s)	Min	Max	CV	Mean (s)	Min	Max	CV
Carcass weight (kg)	332 (50.8)	233	501	15%	321 (57.6)	207	475	18%	283 (27.7)	194	412	10%
Carcass conformation [a]	7.0 (2.1)	2	12	29%	9.5 (2.5)	4	14	26%	8.5 (1.3)	5	14	15%
Carcass fat [a]	7.0 (1.5)	3	10	23%	6.2 (1.1)	4	10	18%	6.0 (1.4)	3	14	23%
Overall weight (kg)												
Total meat	227 (39.4)	148	359	17%	230 (49.0)	135	340	21%	183 (21.6)	123	288	12%
Total fat	41 (13.0)	12	83	31%	30 (8.7)	12	50	29%	†	†	†	†
Total bone	64 (7.4)	47	86	12%	61 (7.3)	47	86	12%	†	†	†	†
Overall percentages (% of carcass weight)												
Total meat %	68 (3.3)	60	76	5%	71 (4.0)	63	83	6%	65 (3.3)	56	77	5%
Total fat %	13 (2.9)	5	19	23%	10 (2.5)	3	16	26%	†	†	†	†
Total bone %	19 (1.5)	15	25	8%	19 (2.3)	13	25	12%	†	†	†	†
Wholesale weight groups (kg)												
Lower value cuts	98 (18.6)	64	161	19%	93 (19.9)	53	150	21%	94 (12.0)	61	154	13%
Medium value cuts	43 (7.2)	28	64	17%	49 (10.5)	30	75	22%	20 (2.6)	12	29	13%
High value cuts	60 (11.8)	37	103	20%	62 (14.6)	37	95	24%	47 (6.0)	32	73	13%
Very high value cuts	26 (4.4)	17	40	17%	26 (5.7)	16	36	22%	22 (2.3)	14	32	11%
Wholesale percentages (% of carcass weight)												
Lower value cuts %	29 (1.5)	26	33	5%	29 (1.8)	25	34	6%	34 (2.0)	29	41	6%
Medium value cuts %	13 (0.9)	11	15	7%	15 (1.2)	13	19	8%	7 (0.3)	5	8	5%
High value cuts %	18 (1.6)	14	22	9%	19 (1.8)	15	24	9%	17 (0.9)	14	21	5%
Very high value cuts %	8 (0.5)	7	9	7%	8 (0.7)	6	10	9%	7 (0.3)	7	8	4%

†Data not available.
[a] Linear scale 1 to 15.

Table 3
Mean bias (kg), residual root mean square error (RMSE; kg), coefficient of determination (R^2), and correlation between residuals and predicted weights (r_e) in the validation dataset of wholesale cut weights and overall weights from 114 steers in the experimental dataset using models containing carcass weight (CCW), carcass weight and EUROP grading for conformation and fat (CCW plus EUROP), and carcass weight and VIA variables (CCW plus VIA) developed in the calibration dataset of 232 steers.

	CCW				CCW plus EUROP				CCW plus VIA			
	Bias (s.e)	RMSE	R^2	r_e	Bias (s.e)	RMSE	R^2	r_e	Bias (s.e)	RMSE	R^2	r_e
Overall weights (kg)												
Total meat	−1.02 (1.104)	11.78	0.91	0.07	−1.06 (0.70)	7.43	0.97	−0.16*	−0.74 (0.63)	6.77	0.97	−0.02
Total fat	−0.36 (1.003)	10.71	0.33	−0.03	−0.76 (0.62)	6.67	0.74	−0.01	−0.58 (0.60)	6.38	0.77	−0.13
Total bone	0.00 (0.404)	4.31	0.66	−0.03	0.18 (0.32)	3.38	0.79	−0.09	0.32 (0.30)	3.22	0.81	−0.12
Wholesale weights (kg)												
Lower value cuts	−0.59 (0.647)	6.92	0.87	−0.10	−0.34 (0.61)	6.54	0.89	−0.07	0.15 (0.52)	5.60	0.92	−0.08
Medium value cuts	0.03 (0.348)	3.73	0.74	−0.02	−0.01 (0.31)	3.36	0.79	−0.00	0.13 (0.26)	2.73	0.86	−0.10
High value cuts	0.76 (0.564)	6.03	0.75	−0.04	1.10 (0.37)**	3.91	0.89	−0.01	1.18 (0.31)**	3.27	0.93	0.05
Very high value cuts	−0.01 (0.214)	2.28	0.74	−0.11	−0.09 (0.16)	1.74	0.85	0.01	−0.11 (0.16)	1.75	0.84	−0.01

Bias/Correlation different from zero at P<0.01 (**) or P<0.05 (*).

3.2. Predictions using carcass weight plus EUROP gradings

In the experimental dataset, bias of prediction in the steers across the different carcass cut traits were generally not different from zero with the exception of the prediction of HVC (Table 3), indicating an average underestimation of 1.10 kg of predicted HVC (2% of HVC weight). RMSE across the wholesale and overall weights ranged from 1.74 kg (VHVC) to 7.43 kg (total meat weight). The accuracy of prediction was 0.97, 0.74, and 0.79 for total meat weight, total fat weight, and total bone weight, respectively, and ranged from 0.79 (MVC weight) to 0.89 (LVC weight and HVC weight). The correlation between residuals and predicted weights was different from zero ($P<0.05$) for total meat weight ($r_e=-0.16$) implying an overestimation of predicted total meat weight for steers with large meat yield, and vice versa for steers with low meat yield.

In the commercial dataset, there was no significant bias of prediction (Table 4). RMSE for wholesale cut weights ranged from 1.20 kg (VHVC) to 7.35 kg (LVC). R^2 was 0.80 for total meat weight, and ranged from 0.57 (LVC) to 0.81 (HVC) across the four groups of wholesale cut weights. The correlation between residuals and predicted weights differed ($P<0.001$) from zero for VHVC ($r_e=-0.37$), indicating overestimation of the predicted weight for the heifers with heavy VHVC weight.

In the experimental dataset, accuracies (R^2) of overall predicted proportions and overall calculated proportions were greater than 0.75 and 0.63, respectively in the steers (Table 5). The accuracy of predicted proportions and calculated proportions for the wholesale cuts ranged from 0.31 (MVC) to 0.81 (HVC) and from 0.14 (LVC) to 0.63 (HVC), respectively. In the commercial dataset, R^2 of predicted proportion and calculated proportion of total meat were 0.50 and 0.18, respectively (Table 6). The R^2 ranged from 0.31 (VHVC) to 0.49 (LVC) and from 0.05 (VHVC) to 0.30 (HVC) for the predicted proportions and calculated proportions of wholesale yields, respectively.

The largest percentage eigenvalue of the correlation matrix between the four wholesale cut weights was 98% and 99% in the experimental and the commercial study, respectively. The largest percentage eigenvalue of the correlation matrix between the four true wholesale cut weights was 88% and 86% in the experimental and the commercial datasets, respectively.

3.3. Predictions using carcass weight and VIA variables

In the experimental dataset, HVC were, on average, underestimated ($P<0.01$) in the steers by 1.18 kg (Table 3). The RMSE was 6.77, 6.38, and 3.22 kg for total meat weight, total fat weight, and total bone weight, respectively. The

Table 4
Mean bias (kg), residual root mean square error (RMSE; kg), coefficient of determination (R^2), and correlation between residuals and predicted weights (r_e) in the validation dataset of wholesale cut weights and overall weights from 92 heifers in the commercial dataset using models containing carcass weight (CCW), carcass weight and EUROP grading for conformation and fat (CCW plus EUROP), and carcass weight and VIA variables (CCW plus VIA) developed in the calibration dataset of 189 heifers.

	CCW				CCW plus EUROP				CCW plus VIA			
	Bias (s.e)	RMSE	R^2	r_e	Bias (s.e)	RMSE	R^2	r_e	Bias (s.e)	RMSE	R^2	r_e
Overall weight (kg)												
Total meat	−1.25 (1.18)	11.31	0.68	−0.07	−0.36 (0.95)	9.07	0.80	0.15	−0.24 (0.83)	8.00	0.84	0.06
Wholesale weights (kg)												
Lower value cuts	−0.87 (0.87)	8.32	0.46	−0.15	−1.08 (0.77)	7.35	0.57	−0.04	−0.01 (0.69)	6.62	0.65	0.07
Medium value cuts	−0.11 (0.16)	1.53	0.62	−0.05	−0.10 (0.15)	1.43	0.67	0.01	−0.12 (0.14)	1.37	0.70	−0.03
High value cuts	−0.31 (0.33)	3.16	0.68	−0.04	−0.19 (0.26)	2.47	0.81	0.07	0.01 (0.23)	2.16	0.85	−0.01
Very high value cuts	0.09 (0.13)	1.28	0.68	−0.40**	0.14 (0.13)	1.20	0.71	−0.37**	0.04 (0.13)	1.24	0.72	−0.44**

** Correlation different from zero at P<0.01.

Table 5
Mean bias (kg), residual root mean square error (RMSE; kg), coefficient of determination (R^2), and correlation between residuals and predicted weights (r_e) in the validation dataset of predicted proportions and calculated proportions from 114 steers in the experimental dataset using models containing carcass weight (CCW), carcass weight and EUROP grading for conformation and fat (CCW plus EUROP), and carcass weight and VIA variables (CCW plus VIA) developed in the calibration dataset of 232 steers.

	CCW				CCW plus EUROP				CCW plus VIA			
	Bias (s.e)	RMSE	R^2	r_e	Bias (s.e)	RMSE	R^2	r_e	Bias (s.e)	RMSE	R^2	r_e
Overall predicted proportions (%)												
Total meat	−0.40 (0.30)	3.23	0.04	−0.09	−0.52 (0.13)*	1.41	0.82	0.02	−0.10 (0.17)	1.77	0.75	−0.38***
Total fat	0.53 (0.27)*	2.85	0.01	−0.04	0.27 (0.13)*	1.43	0.75	−0.03	0.39 (0.17)*	1.80	0.69	−0.45***
Total bone	−0.04 (0.10)	1.04	0.47	−0.20	0.05 (0.06)	0.70	0.77	−0.29**	0.07 (0.09)	0.92	0.74	−0.64***
Overall calculated proportions (%)												
Total meat	−0.25 (0.32)	3.45	0.04	−0.09	−0.36 (0.17)*	1.79	0.74	−0.02	−0.03 (0.18)	1.90	0.71	−0.11
Total fat	0.18 (0.30)	3.15	0.01	−0.01	−0.09 (0.18)	1.93	0.63	−0.05	−0.24 (0.16)	1.70	0.72	−0.13
Total bone	−0.14 (0.14)	1.52	0.29	−0.13	−0.04 (0.10)	1.09	0.63	−0.03	0.07 (0.08)	0.90	0.75	0.03
Wholesale predicted proportions (%)												
Lower value cuts	−0.06 (0.12)	1.34	0.20	0.03	−0.08 (0.11)	1.14	0.42	0.07	−0.11 (0.14)	1.49	0.43	−0.66***
Medium value cuts	−0.01 (0.09)	0.98	0.05	0.19	0.00 (0.08)	0.82	0.31	0.05	−0.03 (0.08)	0.83	0.50	−0.55***
High value cuts	0.13 (0.15)	1.57	0.04	−0.04	0.01 (0.07)	0.71	0.81	0.09	0.17 (0.09)	1.02	0.69	−0.50***
Very high value cuts	0.05 (0.05)	0.52	0.00	−0.15	−0.02 (0.03)	0.30	0.66	0.30*	0.03 (0.05)	0.50	0.49	−0.67***
Wholesale calculated proportions (%)												
Lower value cuts	0.10 (0.17)	1.84	0.12	0.05	0.07 (0.17)	1.83	0.14	−0.09	0.06 (0.13)	1.42	0.47	−0.08
Medium value cuts	0.00 (0.11)	1.16	0.02	0.15	0.01 (0.09)	1.00	0.25	0.05	−0.01 (0.07)	0.76	0.57	−0.04
High value cuts	−0.04 (0.17)	1.87	0.00	−0.16	−0.18 (0.10)	1.12	0.63	0.05	−0.01 (0.09)	0.97	0.73	−0.02
Very high value cuts	0.05 (0.07)	0.70	0.00	−0.16	−0.02 (0.05)	0.52	0.45	0.08	0.01 (0.04)	0.48	0.52	0.02

Bias/Correlation different from zero at $P<0.01$ (**) or $P<0.05$ (*).

RMSE ranged from 1.75 kg (VHVC) to 5.60 kg (LVC) for the wholesale cut weights. Accuracy (R^2) for total meat weight, total fat weight, and total bone weight were 0.97, 0.77, and 0.81, respectively, and 0.92, 0.86, 0.93, and 0.84 for LVC, MVC, HVC, and VHVC weights, respectively. The correlation between residuals and predicted weights were not different from zero.

In the commercial dataset (Table 4), there was no significant bias of prediction and the RMSE was 8.00 kg for total meat weight, and ranged from 1.24 kg (VHVC) to 6.62 kg (LVC) across the four wholesale cut weights. The accuracy (R^2) of the regression model was 0.84 for total meat weight, and 0.65, 0.70, 0.85, and 0.72 for LVC, MVC, HVC, and VHVC weights, respectively. The correlation between residuals and predicted weights differed ($P<0.01$) from zero only for VHVC ($r_e = -0.44$).

In the experimental dataset, the maximum accuracy (R^2) of overall predicted proportions observed in the steers was 0.75 (total meat) (Table 5). Accuracies of predicted wholesale cut proportions were 0.43, 0.50, 0.69, and 0.49 for LVC, MVC, HVC, and VHVC, respectively. Residual correlations for predicted proportions were different from zero ($P<0.001$) for the overall and wholesale yields. Accuracy for calculated proportions were greater than 0.71 for the overall yields and ranged from 0.47 (LVC) to 0.73 (HVC) in the wholesale calculated proportions. For the overall and the wholesale

Table 6
Mean bias (kg), residual root mean square error (RMSE; kg), coefficient of determination (R^2), and correlation between residuals and predicted weights (r_e) in the validation dataset of predicted proportions and calculated proportions from 92 heifers in the commercial dataset using models containing carcass weight (CCW), carcass weight and EUROP grading for conformation and fat (CCW plus EUROP), and carcass weight and VIA variables (CCW plus VIA) developed in the calibration dataset of 189 heifers.

	CCW				CCW plus EUROP				CCW plus VIA			
	Bias (s.e)	RMSE	R^2	r_e	Bias (s.e)	RMSE	R^2	r_e	Bias (s.e)	RMSE	R^2	r_e
Overall predicted proportion (%)												
Total meat	−0.43 (0.37)	3.51	0.01	0.03	−0.11 (0.26)	2.52	0.50	−0.09	−0.29 (0.34)	3.26	0.36	−0.50***
Overall calculated proportions (%)												
Total meat	−0.11 (0.39)	3.75	0.01	0.07	0.17 (0.38)	3.63	0.18	−0.34***	0.14 (0.29)	2.81	0.47	−0.22*
Wholesale predicted proportions (%)												
Lower value cuts	0.08 (0.19)	1.86	0.00	−0.12	−0.07 (0.14)	1.32	0.49	0.08	0.08 (0.22)	2.11	0.41	−0.74***
Medium value cuts	−0.03 (0.03)	0.29	0.00	−0.28**	0.01 (0.02)	0.21	0.44	−0.11	−0.01 (0.05)	0.44	0.22	−0.82***
High value cuts	−0.08 (0.08)	0.77	0.07	0.03	0.05 (0.07)	0.62	0.40	−0.06	−0.09 (0.08)	0.78	0.41	−0.62***
Very high value cuts	0.01 (0.03)	0.27	0.16	0.15	0.00 (0.03)	0.24	0.31	−0.15	−0.01 (0.05)	0.45	0.11	−0.80***
Wholesale calculated proportions (%)												
Lower value cuts	0.03 (0.29)	2.74	0.01	−0.09	−0.23 (0.26)	2.48	0.18	−0.06	−0.09 (0.22)	2.10	0.42	−0.01
Medium value cuts	−0.03 (0.05)	0.49	0.01	−0.10	0.01 (0.05)	0.47	0.09	−0.08	−0.01 (0.05)	0.45	0.18	−0.15
High value cuts	−0.01 (0.10)	0.97	0.07	0.09	0.13 (0.09)	0.84	0.30	−0.03	0.05 (0.08)	0.74	0.46	−0.19
Very high value cuts	0.01 (0.05)	0.45	0.02	−0.01	−0.01 (0.05)	0.45	0.05	−0.23*	0.00 (0.04)	0.40	0.22	−0.12

**Correlation different from zero at $P<0.01$.

calculated proportions, all residual correlations were not significantly different from zero.

In the commercial dataset, accuracies of predicted wholesale cut proportions were 0.41, 0.22, 0.41, and 0.11 for LVC, MVC, HVC, and VHVC proportions, respectively (Table 6). Residual correlations for both overall cut proportions and wholesale proportions were significantly different from zero. The accuracy of prediction (R^2) for calculated proportions (Table 6) was 0.47 for total meat, and ranged from 0.18 (MVC) to 0.46 (HVC). Residual correlations were not different from zero.

The largest percentage eigenvalue of the correlation matrix between the four wholesale cut weights was 92% and 94% in the experimental and the commercial study, respectively.

3.4. Regression model applied to the bull dataset

In Model 1, the accuracy of predicting the wholesale cut weights in the bulls using the prediction equations developed in the steers ranged from 0.37 (total fat weight) to 0.97 (total meat weight), while the accuracy of predicting the wholesale cut weights was greater than 0.90 (HVC) (Table 7). The mean bias was significant ($P<0.05$) across all traits, and the systematic bias was not different from zero for only total meat weight and total bone weight.

The accuracy of predicting overall weights in the bulls using prediction equations developed in the steers for Model 2 was 0.69, 0.88, and 0.98 for total fat weight, total bone weight, and total meat weight, respectively (Table 7); the accuracy of prediction for predicted wholesale weights was 0.99, 0.97, 0.94, and 0.96 for LVC, MVC, HVC, and VHVC, respectively. The mean bias was not different from zero only for VHVC, while the systematic bias was not different from zero only for HVC and VHVC.

The accuracy of prediction of the different wholesale cut weights in the bulls using the prediction equations developed in steers for Model 3 was greater than 0.87. No bias was evident for this model for the prediction of total meat weight and total fat weight. Total bone weight was, on average, underestimated by 7.75 kg (Table 7). Furthermore, the weight of LVC and MVC was underestimated while HVC and VHVC weights were overestimated. Only the correlation between predicted total meat weight and total meat weight residuals was different ($P<0.001$) from zero ($r_e=0.59$).

3.5. Prediction bias across breeds

In the experimental dataset, using only carcass weight in the prediction model resulted in biased estimates for most carcass traits across breeds, especially in dairy animals (Table 8). The quantity of biased estimates was reduced considerably when EUROP classification was included in the prediction model and were reduced even further when the EUROP classifications were replaced by the VIA predictors. Only one wholesale cut (LVC in dairy animals) was overestimated when predicted using VIA. For the commercial dataset bias was zero for all breeds, regardless of which model was used to predict wholesale cut weights (result not shown).

4. Discussion

The ability to accurately predict yields of different value carcass cuts has multiple applications. Firstly, it provides an opportunity for abattoirs to more accurately quantify the value of a carcass based on the prevailing prices of the different cuts, which may subsequently be used to pay the producer. Secondly, genetic variation exists in the distribution of individual carcass cuts, and the routine availability of such data facilitates the routine estimation of breeding values for individual carcass cuts; Pabiou et al. (2009) documented significant genetic variance in carcass cuts and carcass composition using data which included those used in the present study. Finally, accurate predictions of individual cut yields as well as carcass meat, fat, and bone proportions aid in the evaluation of alternative production systems or diets in research programs without the associated expense of carcass dissections.

4.1. Representativeness of the data

The experimental and the commercial datasets comprised of crossbred steers and heifers, mostly from large continental beef breeds (Limousin, Charolais, Belgian Blue), and Holstein. This sample is representative of the breed composition of calves produced in Ireland; Evans et al. (2007) showed that

Table 7
Results for mean bias (kg), residual root mean square error (RMSE; kg), coefficient of determination (R^2), and correlation between residuals and predicted weights (r_e) from a dataset of 74 bulls based on the regression equations developed in the experimental dataset using 232 steers, and using models containing carcass weight (CCW), carcass weight and EUROP grading for conformation and fat (CCW plus EUROP), and carcass weight and VIA variables (CCW plus VIA).

	CCW				CCW plus EUROP				CCW plus VIA			
	Bias (s.e)	RMSE	R^2	r_e	Bias (s.e)	RMSE	R^2	r	Bias (s.e)	RMSE	R^2	r_e
Overall weights (kg)												
Total meat	−11.97 (0.95)*	8.18	0.97	−0.17	1.96 (0.91)*	7.84	0.98	0.54***	−0.38 (0.84)	7.22	0.99	0.59***
Total fat	9.34 (0.84)*	7.23	0.37	0.56***	2.28 (0.53)*	4.60	0.69	0.39***	0.11 (0.69)	5.89	0.56	−0.18
Total bone	9.86 (0.37)*	3.19	0.78	0.22	4.62 (0.28)*	2.38	0.88	0.28*	7.75 (0.36)*	3.12	0.82	−0.00
Wholesale weights (kg)												
Lower value cuts	22.72 (0.64)*	5.51	0.98	0.92***	24.82 (0.69)*	5.90	0.99	0.96***	3.53 (0.68)*	5.87	0.91	0.02
Medium value cuts	−3.24 (0.34)*	2.91	0.96	−0.78***	−1.63 (0.25)*	2.18	0.97	−0.71***	4.57 (0.44)*	3.82	0.87	0.09
High value cuts	−8.13 (0.54)*	4.66	0.90	−0.35**	−1.57 (0.39)*	3.40	0.94	0.22	−4.03 (0.35)*	3.03	0.96	0.11
Very high value cuts	−1.92 (0.18)*	1.52	0.95	−0.58***	0.23 (0.12)	1.06	0.96	−0.18	−1.26 (0.24)*	2.09	0.87	−0.01

*, ** , ***: Bias/Correlation different from zero at $P<0.05$, $P<0.01$, $P<0.001$, respectively.

Table 8
Mean bias (kg) overall and wholesale cuts using models with carcass weight only, carcass weight plus EUROP classification, or carcass weight plus VIA measurements for the different breed types of steers in the experimental validation dataset.

	Breed composition groups (*Primary breed fraction × secondary highest breed fraction*)						*S.E.* [(a)]
	Charolais × Beef	Other beef × Beef	Angus × Dairy	Belgian Blue × Dairy	Other beef × Dairy	Dairy × Dairy	
Average number of steers	*15*	*18*	*13*	*13*	*36*	*17*	
Model 1: Carcass weight							
Total meat weight	6.3***	−2.9	−7.6**	7.2***	−0.6	−9.3***	*2.14*
Total fat weight	−1.1	−5.0*	9.2***	−8.7***	−1.4	6.5**	*1.97*
Total bone weight	−0.1	−1.9	−1.6	−0.7	0.9	3.6***	*0.89*
Lower value cuts	−2.0	0.9	3.0	5.4**	−0.5	−2.9	*1.45*
Medium value cuts	1.4**	0.7	−2.1*	0.1	0.9	−2.8***	*0.75*
High value cuts	1.5	4.7***	−5.1***	2.7*	0.0	−4.1**	*1.11*
Very high value cuts	0.4	0.1	−0.1	1.2*	−0.7	−1.6**	*0.48*
Model 2: Carcass weight + EUROP gradings							
Total meat weight	−1.8	−5.3*	0.9	0.6	3.3	1.7	*1.61*
Total fat weight	1.3	−2.8	1.5	−2.0	−1.4	1.3	*1.48*
Total bone weight	0.6	−2.0*	−1.1	0.5	0.0	0.5	*0.74*
Lower value cuts	−2.8**	0.4	4.3*	4.4**	0.1	−1.5	*1.36*
Medium value cuts	0.8	0.5	−1.5	−0.8	1.4	−1.6*	*0.72*
High value cuts	−0.3	1.1	−1.1	−0.3	1.0	0.4	*0.89*
Very high value cuts	0.0	0.0	0.6	0.1	−0.2	−0.3	*0.39*
Model 3: Carcass weight + VIA measurements							
Total meat weight	0.8	−2.2	1.0	−1.4	0.2	0.1	*1.54*
Total fat weight	0.9	−0.1	−0.8	−3.0*	1.2	1.3	*1.43*
Total bone weight	0.8	−0.7	−0.7	0.1	−0.3	−0.8	*0.72*
Lower value cuts	−0.2	1.8	1.8	1.4	1.6	−5.4***	*1.13*
Medium value cuts	−0.2	0.4	0.3	−0.2	0.8	−0.6	*0.62*
High value cuts	−0.4	0.2	−0.4	0.9	0.1	−0.1	*0.75*
Very high value cuts	−0.2	−0.2	0.8	−0.1	−0.1	0.3	*0.39*

*, ** , ***: Estimates different from zero at $P<0.05$, $P<0.01$, $P<0.001$, respectively.
[(a)] S.E.: Pooled standard error.

the majority of calves born in 2005 were crossbred animals, and that Charolais and Limousin were the predominant sire breeds used in the Irish beef herd. Moreover, the two sample populations used in the present study represent the two dominant genders of the national kill (Department of Agriculture, Fisheries, and Food, 2009): steers (43%) and heifers (27%). Cows and bulls represent 22% and 8% of the national kill respectively (Department of Agriculture, Fisheries, and Food, 2009).

The difference in average carcass weight between the experimental and the commercial dataset in the present study is most likely due to gender differences between the two datasets. The experimental dataset used to derive the prediction equations comprised of steers, while the commercial dataset was entirely heifers. The average carcass weight in the present sample datasets of steers (average carcass weight = 332 kg) and heifers (average carcass weight = 283 kg) is similar to those reported in the national kill statistics in 2009 (steers: 351 kg, n = 635,654; heifers: 287 kg, n = 405,484) (Department of Agriculture, Fisheries, and Food, 2009).

The EUROP classes for conformation (U 15%, R 45%, O 36%, P 4%) represented in the experimental dataset were similar to those of the national kill in 2009 (U 7%, R 44%, O 42%, P 7%; Department of Agriculture, Fisheries, and Food, 2009). In the commercial dataset, the vast majority (80%) of the heifers were graded “R”, and thus showed an over-representation of well-conformed heifers as the national kill for 2009 reported the following grades for heifers: 0% “E”, 6% “U”, 55% “R”, 36% “O”, and 3% “P” (Department of Agriculture, Fisheries, and Food, 2009). This discrepancy in EUROP classes of carcass conformation was reflected in a smaller coefficient of variation in the commercial dataset (15%) compared to the experimental dataset (29%) where EUROP conformation class distribution was more balanced.

The distribution of EUROP fat grades in experimental dataset (1% grade 1, 16% grade 2, 53% grade 3, 29% grade 4, 0% grade 5) was also similar to those observed in the 2009 national kill (2% grade 1, 16% grade 2, 54% grade 3, 26% grade 4, 1% grade 5). In the commercial dataset, there was an under-representation of over-fat carcasses (grades 4 and 5: 16%) compared to the national kill average in 2009 (grades 4 and 5: 37%). The coefficient of variation for EUROP carcass fat was 23% in both the experimental and the commercial dataset. Hickey et al. (2007) reported an average coefficient of variation of 23% for carcass conformation and 21% for carcass fat after studying a large beef and dairy male and female population (n = 64,443; average carcass weight: 306 kg) in Ireland.

The total meat percentage was similar across genders: 68%, 71%, and 65% for the steers, bulls, and heifers, respectively. Other studies of various crossbred populations of steers observed similar results for the meat percentage (Koch et al., 1982; Morris et al., 1999). The total fat percentage of the steers in the present study (12% of the carcass weight) is a reflection of the predominantly continental breeds (i.e., ‘leaner’ breeds) used in Ireland. Commercial practice in Ireland for fat trimming results in, on average, five millimetres of fat on the primal cuts, whereas in the experimental dataset, the procedure aimed to remove all possible fat from the cuts. Gender differences and cutting procedures can also explain some of the phenotypic differences observed between steers, heifers, and bulls, as previously outlined by Pabiou et al. (2009).

Gender differences also existed in the distribution of the wholesale cut weights in the carcass weight (Table 2). The percentage of MVC in the carcass was markedly lower in the heifers (20%) compared to the steers (43%) and bulls (49%) and can also be explained by differences in cutting procedure between commercial and experimental datasets. The cutting-up of the forequarter in the commercial plant was dictated by the retailer demand, only keeping the main primals (chuck, shoulder, and brisket) to be sold as roast and the remaining to be diced or grounded to be sold as diced, stewed, stir-fry, or ground beef.

4.2. Prediction of total meat, total fat, and total bone weights

Inclusion of VIA variables in the prediction model improved the fit to the data, as evidenced by the lower RMSE and greater coefficients of determination, compared to just fitting carcass weight or carcass plus EUROP classification. With the exception of VHVC in the commercial dataset (Table 4) the lack of a residual correlation when predictions were undertaken using a model containing VIA variables implies no systematic bias in predictive ability. Furthermore, with the exception of total fat yield in the experimental dataset, the lack of any bias in prediction across different breed types suggests that the model developed including the VIA variables is robust.

Using RMSE as an indication of the prediction accuracy of the models, the developed models predicted total meat weight better than total fat or total bone weights. However, due to larger variation in conformation grading (i.e., CV; Table 2) and probably, but to a lesser extend a larger dataset size, the prediction of meat yield in the experimental dataset was superior to that in the commercial dataset. Williams et al. (1997) observed an R^2 of approximately 0.85 when using live ultrasonic measurements as predictors of total retail meat weight, and an R^2 of 0.84 when using carcass measurements (hot carcass weight, *longissimus dorsi* area, carcass fat thickness, and estimated percentage of kidney, pelvic and heart fat) as predictors of the same trait. Greiner et al. (2003) found comparable accuracy for predicting total meat weight; R^2 ranged from 0.78 to 0.84 when using live ultrasonic measurements, and from 0.83 to 0.87 when fitting hot carcass weight and three other carcass measurements in the models. Using image analysis of the 12th rib section on 703 carcasses, Chen et al. (2007) achieved a high accuracy of prediction for total retail cut, observing an overall R^2 equal to 0.97.

The large bias observed when the regression calculated using the steer population in the experimental dataset was applied to the 74 bulls is probably due to biological differences between the bulls and the steers. More bull carcass dissections are needed to provide accurate meat yield predictions specific to the bull population in Ireland.

4.3. Prediction of wholesale cut weights

Across both the experimental and the commercial datasets, the best predictions as measured by a high accuracy and low RMSE were obtained with Model 3. The baseline model using only carcass weight (Model 1) performed poorest. Model 2, however, is using predictor variable that themselves are a result of prediction from digital images from the VBS2000 classification machine. Although Model 2 performed relatively closely to Model 3, it was, on average, less accurate. Also, as suggested by the largest percentage eigenvalue observed in the correlation matrix between predicted cuts, Model 3 was better able to recover the variation in carcass composition (correlation structure between predicted wholesale cuts was closer to the correlation structure between the true cuts).

In both the experimental and the commercial dataset, the inclusion of EUROP classification in the model, over and above carcass weight, only slightly improved the fit to the data for the MVC and LVC groups. However, there was a considerable improvement in the prediction of HVC when EUROP classification scores were included in the model. This is consistent with the objective of the EUROP grading system for carcass conformation; the European council regulation 1208/81 of 28 April 1981 defined carcass conformation as 'the development of carcass profiles, in particular the essential parts (round, back, and shoulder)'. The main component of the HVC group is the hind thigh, which represents a volume easily appreciated on the two and three dimensional pictures taken after slaughter. In both the experimental and the commercial dataset, the accuracy of prediction was greatest for the HVC cuts ($R^2 = 0.93$ and 0.85 in the experimental commercial datasets, respectively).

The limited phenotypic variation in carcass conformation in the commercial dataset was reflected in the lower accuracy (R^2) observed for the wholesale cut weights in the commercial dataset (Table 4) compared to the experimental dataset (Table 3). Of the four groups of meat cuts defined in the experimental dataset, the lowest accuracy ($R^2 = 0.84$) was observed for the VHVC group. This is consistent with the fact that in the VHVC group of meat cuts, the fillet is included but is hidden from the camera pictures due to its positioning inside the carcass. In addition, due to its shape, the volume of the full loin (i.e., rib-roast plus strip-loin) can also be difficult to appreciate from a side view image. Using VIA technology to predict sheep meat yields, Ruis-Vilarrasa et al. (2009) also demonstrated a better accuracy of predictions for the cuts that stands out the most in the images, such as the shoulder ($R^2 = 0.96$) and the legs ($R^2 = 0.97$). The negative residual correlation observed for VHVC in the commercial dataset was largely influenced by specific carcass results ($n = 8$); when removed from the analysis, the residual correlation improved ($r_e = -0.23$; $P = 0.03$).

Across the models developed, the accuracy (R^2) observed when applying the steer regressions to the bull dataset (Table 7) were as high as the accuracy calculated for the steers (Table 3) despite some bias significantly different from zero (total bone weight and wholesale cut weights). It is therefore necessary to establish specific regressions to provide accurate meat yields predictions specific to the bull population in Ireland for Model 3. Model 2 however was more robust across genders.

4.4. Prediction of proportions

Across both the experimental and the commercial datasets, the accuracy (R^2) of predicted proportions and calculated proportions were lower than the corresponding accuracies observed for weights. Chen et al. (2007) also observed a lower accuracy of prediction in predicted proportions (e.g., total retail percentage, all breeds, $R^2=0.62$) compared to predicted weights (e.g., total retail weight, all breeds, $R^2=0.97$). Calculated proportions gave on overall better R^2 than predicted proportions.

The accuracy of prediction for predicted proportions was higher in the model using carcass weight plus the EUROP gradings compared to the model using carcass weight and VIA variable. This is consistent with the fact that the objective of EUROP grading system for conformation was to assess the volumes of the hind-leg, the back, and the shoulder relatively to the whole carcass. Thus, the predictors used in the EUROP gradings plus carcass weight model were already tailored towards predicting proportions. Conroy et al. (2010) solely used the EUROP gradings for conformation and fat to predict the calculated proportions of meat, fat and bones and observed accuracies (R^2) of 0.78 (meat proportion), 0.74 (fat proportion), and 0.76 (bone proportion).

5. Conclusion

The objective of this study was to quantify the accuracy of VIA technology to predict groups of selected beef meat cuts using two separate datasets of steers and heifers. Stepwise regression was the most accurate statistical method for predicting carcass cuts. In our study, inclusion of VIA variables in prediction models improved the fit to the data compared to including only carcass weight or carcass weight and EUROP classification. Moreover, the eigenvalues of the correlation matrix between predicted cuts was closer to the eigenvalues of the correlation matrix between actual cuts when predictions were based on a model that included the VIA variables. This indicated a greater ability of the model with VIA variables to better differentiate between the different cuts compared to the other prediction models. Predictions of carcass cut weights gave better results than prediction of carcass cut proportions, and would be preferred in the context of the beef industry where cut weight and cut quality are the components of the payment. Additional carcass dissection data from poorer conformation heifers and more bulls would be valuable to develop and test the prediction equations further.

VIA technology is fast and non invasive technique implemented in the majority of Irish cattle abattoirs. The images routinely stored provide a powerful tool for use in a beef breeding program to select for more valuable carcasses.

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III

Animal (2011), **5:11**, pp 1720–1727 © The Animal Consortium 2011
doi:10.1017/S1751731111000917

Genetic variation in wholesale carcass cuts predicted from digital images in cattle

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(Received 29 October 2010; Accepted 31 March 2011; First published online 3 June 2011)

The objective of this study was to quantify the genetic variation in carcass cuts predicted using digital image analysis in commercial cross-bred cattle. The data set comprised 38 404 steers and 14 318 heifers from commercial Irish herds. The traits investigated included the weights of lower value cuts (LVC), medium value cuts (MVC), high value cuts (HVC), very high value cuts (VHVC) and total meat weight. In addition, the weights of total fat and total bones were available on the steers. Heritability of carcass cut weights, within gender, was estimated using an animal linear model, whereas genetic and phenotypic correlations among cuts were estimated using a sire linear model. Carcass weight was included as a covariate in all models. In the steers, heritability ranged from 0.13 (s.e. = 0.02) for VHVC to 0.49 (s.e. = 0.03) for total bone weight, and in the heifers heritability ranged from 0.15 (s.e. = 0.04) for MVC to 0.72 (s.e. = 0.06) for total meat weight. The coefficient of genetic variation for the different cuts varied from 1.4% to 3.6%. Genetic correlations between the different cut weights were all positive and ranged from 0.45 (s.e. = 0.08) to 0.89 (s.e. = 0.03) in the steers, and from 0.47 (s.e. = 0.14) to 0.82 (s.e. = 0.06) in the heifers. Genetic correlations between the wholesale cut weights and carcass conformation ranged from 0.32 (s.e. = 0.06) to 0.45 (s.e. = 0.07) in the steers, and from 0.10 (s.e. = 0.12) to 0.38 (s.e. = 0.09) in the heifers. Genetic correlations between the same wholesale cut traits in steers and heifers ranged from 0.54 (s.e. = 0.14) for MVC to 0.79 (s.e. = 0.06) for total meat weight; genetic correlations between carcass weight and carcass classification for conformation and fat score in both genders varied from 0.80 to 0.87. The existence of genetic variation in carcass cut traits, coupled with the routine availability of predicted cut weights from digital image analysis, clearly shows the potential to genetically improve carcass value.

Keywords: genetic parameters, prediction, carcass, beef, digital images

Implications

The present study shows the existence of genetic variation in carcass cuts predicted using digital image analysis in commercial cross-bred cattle. These results will greatly improve the prediction of carcass quality with subsequent benefits for payment on carcass quality, as well as providing phenotypes to aid in breeding for improved carcass quality.

Introduction

Most breeding objectives attempt to identify the most profitable animals by appropriately weighting well-defined and accurately measured phenotypes into an overall breeding goal. Inclusion of all pertinent traits in the breeding objective is fundamental to its uptake and success in increasing genetic gain for profitability. The main source of revenue for beef farmers, either directly or indirectly, is carcass value. Traits included in European breeding objectives are, however, generally limited to carcass weight, carcass conformation score and carcass fat score. As implemented by the European Council regulations 1208/81 and 2930/81, carcass conformation grading uses the letters excellent (E), very good (U), good (R), fair (O) and poor (P) to describe the conformation of the carcass with particular emphasis on the round, back and shoulder of the carcass. Under the same European regulations, carcass fat grading uses the scale 1 (low), 2 (slight), 3 (average), 4 (high) and 5 (very high) to measure the amount of fat on the outside of the carcass and in the thoracic cavity.

Carcass conformation and carcass fat score are currently predicted in Ireland using mechanical grading. Using a one-color angled camera, the classification machine takes

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a two-dimensional picture and, after superposition of a dark filter, a three-dimensional picture. Since July 2005, the Irish Cattle Breeding Federation has stored both digital images generated by the grading machines.

The 428 parameters from the classification machine describing linear measurements, surfaces and volumes, as well as carcass weight have previously been shown to be able to accurately predict four wholesale carcass cut weights grouped together by retail value: lower value cuts (LVC), medium value cuts (MVC), high value cuts (HVC) and very high value cuts (VHVC; Pabiou *et al.*, 2010). Accuracy of prediction for LVC, MVC, HVC and VHVC in steers was 0.92, 0.86, 0.93 and 0.84, respectively (Pabiou *et al.*, 2010). The comparative accuracy using EUROP grade for conformation and fat and carcass weight were lower at 0.89, 0.79, 0.89 and 0.85, for LVC, MVC, HVC and VHVC, respectively, in the same data set (Pabiou *et al.*, 2010).

Using two relatively small data sets, of which a subset was used to develop the prediction equations, Pabiou *et al.* (2009) reported large genetic variation in carcass cut weights. However, the standard errors of these estimates were large, mainly attributable to the relatively small size of the data sets in that study; one data set consisted of 413 carcass records and the other data set consisted of 635 carcass records. Therefore, the objective of this study was to use a larger data set from the national database to estimate genetic parameters for wholesale carcass cut weights predicted from digital images using the prediction equations described by Pabiou *et al.* (2010).

Material and methods

Carcass images and predicted wholesale carcass cuts

A total of 515 494 carcass images from the VBS2000 grading machine (EplusV GmbH, Oranienburg, Germany) from animals slaughtered in 15 different Irish abattoirs between November 2006 and May 2009 were available for inclusion in the analysis. A daily calibration file was also available from all abattoirs. Each calibration file consists of two images (template boards without carcass), and is necessary to recover the abattoir conditions at each slaughtering day. If the calibration file was not available (i.e. lost or damaged), the previous day's file from that abattoir was used.

Equations developed by Pabiou *et al.* (2010) to predict wholesale carcass cuts from the digital images were used in the present study to predict wholesale carcass cut weights for all carcasses. Developed steer prediction equations ($0.81 \leqslant R^2 \leqslant 0.97$) were applied to carcass images on steers, whereas the developed heifer prediction equations ($0.65 \leqslant R^2 \leqslant 0.85$) were applied to heifers. The wholesale cut weights included the following groups: LVC included the weights of the fore- and hind-shins, flank, ribs, brisket, neck and lean trimmings; MVC comprised the weights of the shoulder and the chuck cuts; HVC included the weights of the sirloin and the round; VHVC comprised the weights of the rib roast, strip loin and fillet cuts. The total saleable meat of the carcass (total meat weight) was also predicted in both the steers and the heifers. Equations were also developed in the steers to predict weight of total fat (total fat weight) and total bone (total bone weight). Total meat weight, total fat weight and total bone weight are hereon referred to as 'Overall weights'. The grouping of primal carcass cuts into wholesale cuts was based on their respective retail value, and the prediction equations were derived for the groups of wholesale carcass cuts (Pabiou *et al.*, 2010). The primal cuts components HVC and VHVC were similarly defined in steers and heifers. However, the cutting and recording procedure differed between steers and heifers for MVC; part of the shoulder weight in heifers was recorded as lean trimmings and therefore was included in LVC (Pabiou *et al.*, 2009 and 2010). Also recorded on every carcass was the cold carcass weight (hereon referred to as carcass weight), the EUROP carcass conformation and the EUROP carcass fat grade; the EUROP classification grades were transformed into a 15-point scale as outlined by Hickey *et al.* (2007).

Records were discarded if two images of the carcass were not available or if a validation calibration file was not available (i.e. lost or damaged) on the day of slaughter or the day immediately before slaughter from the same abattoir ($n = 30\,760$). Animals slaughtered younger than 10 months of age ($n = 474$), steers older than 60 months of age ($n = 289$), heifers older than 36 months of age ($n = 10\,189$), as well as animals with no known sire ($n = 355\,704$) were also discarded. Furthermore, wholesale cuts greater than three standard deviations from their respective mean, within steers and heifers separately, were discarded ($n = 2267$). Two types of contemporary groups were defined: (i) to account for both abattoir and calibration file and how these effects change over time and (ii) to account for herd-specific management factors. In Ireland, farmers tend to manage heifers and steers separately and therefore herd-specific contemporary groups were defined within sex using the iterative algorithm of Crump *et al.* (1997), parameterised by the minimum (60 days) and maximum (120 days) span of a group for date of slaughter, and the minimum number of records ($n = 5$) per group. Herd-specific contemporary groups were based on finishing herd, date of slaughter and intervals between consecutive slaughter dates as the variables of interest. First, consecutive animals (ranked on slaughter date) were assigned to groups based on their slaughter date and the minimum span of days defined in the parameter file. This step was then repeated considering the start and end slaughter date of the groups and the minimum span defined in the parameter file. Second, contemporary groups were optimised by reading the groups created previously and clustering consecutive groups according to the maximum span and the minimum records required per group. This step was then repeated considering the maximum span and the minimum records required per group in the parameter file. The edited data set consisted of 52 722 animals, of which 38 404 (73% of the data) were steers and 14 318 (27% of the data) were heifers. Steers and heifers were from 3947 and 1671 different herd-specific contemporary groups, respectively.

Statistical analyses
Genetic and residual variances, as well as heritability estimates for all traits, were estimated using a single trait animal model (ASReml; Gilmour *et al.*, 2009). These parameters were first estimated for steers and heifers separately, and subsequently by appending both data sets into a combined data set (i.e. traits in the steer and heifer data sets were considered as the same trait). The coefficient of genetic variation (CV_g) for each trait was calculated as the genetic standard deviation divided by the phenotypic mean (Houle, 1992).

Phenotypic and genetic correlations between traits, within gender, were estimated using bivariate sire linear mixed models in ASReml (Gilmour *et al.*, 2009), accounting for the relationships among sires. Genetic correlations between the same traits in steers and heifers were also estimated in ASReml (Gilmour *et al.*, 2009) using a series of bivariate sire linear mixed models where the residual covariances were set to zero. The common sires ($n = 1099$) between the steer and the heifer data sets had a total of 24 183 and 9049 progeny in the steer and heifer data sets, respectively. Covariance matrices calculated in the steers and heifers were bent using the weighted procedure of Jorjani *et al.* (2003) to ensure positive definiteness.

Relationships among animals were accounted for using a relationship matrix where unknown ancestors were included as phantom groups of the breeds: Charolais, Friesian, Holstein, Limousin, Angus, Simmental, Hereford, Belgian Blue, French hardy breeds (Salers and Aubrac), other beef breeds (Piemontese, Parthenaise, Blonde d'Aquitaine and Shorthorn) and unknown breed in both the steer and heifer pedigree files. Across all models, the relationships among all animals were traced back to at least five generations. The pedigree comprised 164 279 and 73 978 animals in the steers and heifers, respectively.

The overall mixed linear model was

$$\mathbf{y} = \mathbf{Xb} + \mathbf{ZQg} + \mathbf{Zu} + \mathbf{e}$$

where $\mathbf{y}$ is the vector of records, $\mathbf{b}$ is the vector of fixed effects, $\mathbf{u}$ is the vector of random effects, $\mathbf{g}$ is the vector of breed genetic groups, $\mathbf{e}$ is the vector of residual effects and the $\mathbf{X}$, $\mathbf{Z}$ and $\mathbf{Q}$ matrices are the respective design matrices.

Model building for fixed effects was undertaken using PROC GLM (SAS Institute, 2007). Fixed classification effects considered for inclusion in the models were damaged when the animal was born (< 3 years, 3 to 5 years, 6 to 8 years and > 8 years), whether the animal was a singleton or a multiple birth, contemporary group of herd by (gender by) slaughter date and contemporary group of abattoir by slaughter date. Covariates tested for inclusion in the model were heterosis, recombination loss and age at slaughter centred within sex. Breed effects were accounted for through the use of breed genetic groups as defined earlier. Non-linear associations were also tested for significance and a quadratic effect on age at slaughter, centred within sex, was also included in the model. Coefficients of heterosis and recombination loss were calculated for all animals as $1 - \Sigma_{i=1}^{n} \text{sire}_i \cdot \text{dam}_i$ and $1 - \Sigma_{i=1}^{n} \text{sire}_i^2 + \text{dam}_i^2/2$, respectively, where sire_i and dam_i are the proportion of breed *i* in the sire and dam, respectively.

Carcass weight was also included as a covariate in all models, with the exception of when the dependent variable was carcass weight. Wholesale carcass cut weight as a proportion of carcass weight was also considered as the dependent variable; carcass weight was not included as a covariate in these models.

Results

Phenotypic data
Average carcass weight of the steers and heifers was 344 and 290 kg, respectively (Table 1), and the average slaughter age was 833 days (i.e. 28 months) and 718 days (i.e. 24 months), respectively. The average carcass conformation of the steers (5.4, corresponding to 'O = ' in the EUROP conformation scale) was lower than the average carcass conformation of the heifers (6.8, corresponding to '*R*-' in the EUROP conformation scale). For carcass conformation, 19% and 62% of the steers (49% and 42% of the heifers) scored 'R' and 'O', respectively. For carcass fat, 54% and 26% of the steers (45% and 43% of the heifers) scored '3' and '4', respectively. Lower average carcass fat score was observed in the steers (6.5, corresponding to '3 = ' in the EUROP fat scale) compared with the heifers (7.3, corresponding to '3 + ' in the EUROP fat scale). The predicted wholesale total meat weight averaged 67% of carcass weight in the steers and 60% of the carcass weight in the heifers. The sum of the individual predicted wholesale cuts LVC, MVC, HVC and VHVC was on average 222 kg or 96% of the predicted total meat weight in the steers, and 178 kg (101% of the predicted total meat weight) in the heifers.

Heritability estimates
Heritability of carcass weight was 0.48 in the steers and 0.58 in the heifers (Table 1); the heritability for carcass weight across all data was 0.48. Heritability estimates for the EUROP classification score for conformation and fat in the steers and heifers ranged from 0.27 (fat score in steers) to 0.46 (conformation score in steers). Predicted total meat weight heritability was 0.38 and 0.72 in the steers and heifers, respectively (Table 1). Heritability for predicted wholesale cut weights ranged from 0.13 (VHVC in steers) to 0.47 (HVC in heifers) and was similar to those of carcass cuts as a proportion of carcass weight (results not shown). The coefficient of genetic variation for the wholesale cuts varied from 1.4% (LVC) to 3.6% (HVC) in the steers, and from 2.0% (MVC) to 3.1% (LVC and HVC) in the heifers.

Phenotypic and genetic correlations
Without any carcass weight adjustments in the models, the phenotypic correlations between carcass weight and LVC, MVC, HVC and VHVC were 0.95, 0.92, 0.80 and 0.78, respectively, in the steers, and 0.80, 0.84, 0.89 and 0.88, respectively, in the heifers.

Table 1 *Overall mean, phenotypic standard deviation (σ_p), coefficient of genetic variation (CV_g) and heritability estimates (h^2; standard error in parentheses) for carcass traits, predicted overall weights and predicted wholesale cut weights estimated in steers, heifers and steers and heifers combined*

	Steers ($n = 38\,404$)				Heifers ($n = 14\,318$)				Steers and heifers ($n = 52\,722$)			
	Mean	σ_p	CV_g (%)	h^2 (s.e.)	Mean	σ_p	CV_g (%)	h^2 (s.e.)	Mean	σ_p	CV_g (%)	h^2 (s.e.)
Carcass weight (kg)	344	28.3	5.7	0.48 (0.029)	290	24.0	6.3	0.58 (0.055)	329	27.5	5.8	0.48 (0.025)
Carcass conformation[1]	5.4	0.8	10.5	0.46 (0.029)	6.8	1.2	9.2	0.28 (0.042)	5.8	1.1	12.5	0.40 (0.024)
Carcass fat[2]	6.5	1.2	9.3	0.27 (0.024)	7.3	1.5	13.0	0.40 (0.049)	6.7	1.3	10.4	0.30 (0.022)
Overall weights												
Total meat (kg)	231	7.5	2.0	0.38 (0.028)	175	7.2	3.5	0.72 (0.055)	216	7.5	2.3	0.44 (0.025)
Total fat (kg)[3]	44	9.9	8.4	0.14 (0.028)								
Total bone (kg)[3]	76	2.9	2.7	0.49 (0.029)								
Wholesale cut weights												
Lower value cuts (kg)	88	3.1	1.4	0.16 (0.021)	91	5.2	3.1	0.30 (0.046)	89	3.8	1.8	0.18 (0.019)
Medium value cuts (kg)	49	1.6	1.6	0.24 (0.024)	20	1.0	2.0	0.15 (0.038)	41	1.7	2.1	0.27 (0.022)
High value cuts (kg)	60	3.6	3.6	0.37 (0.028)	46	2.1	3.1	0.47 (0.051)	56	3.3	3.7	0.40 (0.024)
Very high value cuts (kg)	25	1.5	2.2	0.13 (0.018)	21	0.9	2.2	0.26 (0.044)	24	1.4	2.4	0.17 (0.018)

[1]Scored on a 15-point scale 1 (poor) to 15 (good).
[2]Scored on a 15-point scale 1 (lean) to 15 (fat).
[3]Data not available in the heifers; see Pabiou *et al.* (2010) for the cuts available within genders.

The genetic correlations between the individual predicted wholesale cut weights were all positive (>0.45) in both the steers and heifers. The genetic correlations between the individual wholesale cuts and carcass weight were all positive and stronger than the respective phenotypic correlations, ranging from 0.32 to 0.45 in the steers (Table 2), and from 0.10 to 0.38 in the heifers (Table 3). Carcass conformation, as defined by the EUROP classification, was also positively correlated with the individual wholesale cuts in both genders; all genetic correlations were $\geqslant 0.44$. Genetic correlation between EUROP classification for conformation and total meat weight was 0.55 and 0.80 in the steers and heifers, respectively. Carcass fat EUROP classification score was negatively correlated with all wholesale cut weights in both genders (all genetic correlations $\leqslant -0.26$) and was positively correlated with total fat weight in the steers (0.36).

The genetic correlations between carcass weight and the individual wholesale cut proportions ranged from 0.00 to 0.78 in the steers, and from 0.04 to 0.30 in the heifers (results not shown). The genetic correlations between wholesale cut proportions ranged from 0.11 to 0.66 in the steers, and from 0.13 to 0.97 in the heifers (results not shown).

The genetic correlation between carcass weight measured in steers and heifers was 0.81 and a similar value (0.79) was estimated for predicted total meat weight; the respective correlation for carcass conformation score and carcass fat score was 0.80 and 0.87. The genetic correlations between the same wholesale cut weights in the steers and heifers ranged from 0.54 (MVC) to 0.76 (HVC; Table 4).

Discussion

Traits included in a breeding goal for profitability must exhibit genetic variation and ideally should be routinely measured. Carcass value makes a considerable contribution to the profitability of beef production systems and is therefore a key component of a breeding goal for profitability. Pabiou *et al.* (2010) clearly showed the ability of video image analysis (VIA), available on all animals slaughtered in Ireland, to accurately predict carcass cuts yields. To the best of our knowledge, this study is the first to present (co)variance components of wholesale carcass cut weights in cattle predicted from VIA, and clearly shows the existence of genetic variation in these traits supporting their usefulness in breeding goals.

Carcass measurements

The data used in the present study are representative of the slaughtered Irish cattle population; average carcass weight in the steers (344 kg) and heifers (290 kg) was similar to those observed in the national kill statistics in 2009, where the average carcass weight was 351 kg in steers ($n = 635\,654$) and 287 kg in heifers ($n = 405\,484$; Department of Agriculture, Fisheries, and Food, 2009). Nationally, 45% of heifer carcasses scored '3' and 37% of heifer carcasses scored '4' for carcass fat; 54% of steer carcasses scored '3' and 26% of steer carcasses scored '4' for carcass fat (Department of Agriculture, Fisheries, and Food, 2009), indicating that the sample used in this study was representative of the national kill. In comparison to the data used in the present study, 44% of the steers killed nationally scored 'R' and 42% scored 'O' for carcass conformation, whereas 55% of the heifers killed nationally scored 'R' and 37% scored 'O' for carcass conformation, thereby also signifying that the data used in the current study were representative of the national kill.

The differences between steers and heifers in mean weight LVC and MVC as a proportion of the total carcass weight could be because of gender effects, but may also be because of differences in cutting procedures in the forequarter of the animals used to develop the prediction equations as previously described by Pabiou *et al.* (2009 and 2010). LVC and MVC in the heifers were based on commercial

Table 2 *Phenotypic[1] (below diagonal) and genetic (above diagonal; standard error between parentheses) correlations between carcass weight, EUROP score for conformation and fat, and predicted wholesale cut weights in steers (n = 38 404)*

	Carcass weight	EUROP carcass conformation	EUROP carcass fat	Total meat	Total fat	Total bone	LVC	MVC	HVC	VHVC
Carcass weight		0.35 (0.05)	−0.20 (0.07)	0.39 (0.05)	−0.32 (0.07)	−0.14 (0.05)	0.40 (0.07)	0.32 (0.06)	0.43 (0.05)	0.45 (0.07)
EUROP carcass conformation	0.07		−0.05 (0.07)	0.55 (0.04)	−0.34 (0.07)	−0.84 (0.02)	0.44 (0.07)	0.53 (0.05)	0.65 (0.04)	0.84 (0.03)
EUROP carcass fat	0.01	0.03		−0.42 (0.04)	0.36 (0.03)	−0.18 (0.06)	−0.26 (0.08)	−0.38 (0.06)	−0.43 (0.04)	−0.28 (0.08)
Total meat	0.05	0.23	−0.39		−0.61 (0.02)	−0.24 (0.05)	0.71 (0.05)	0.78 (0.04)	0.93 (0.02)	0.80 (0.04)
Total fat	−0.03	−0.09	0.35	−0.38		0.13 (0.08)	−0.50 (0.06)	−0.56 (0.05)	−0.58 (0.02)	−0.54 (0.07)
Total bone	−0.01	−0.47	−0.20	−0.18	−0.01		−0.22 (0.07)	−0.23 (0.06)	−0.35 (0.05)	−0.62 (0.05)
LVC	0.04	0.15	−0.16	0.49	−0.26	−0.07		0.45 (0.08)	0.66 (0.05)	0.57 (0.08)
MVC	0.04	0.18	−0.29	0.41	−0.23	−0.08	0.03		0.79 (0.04)	0.86 (0.04)
HVC	0.06	0.33	−0.37	0.52	−0.59	−0.16	0.26	0.32		0.89 (0.03)
VHVC	0.05	0.28	−0.25	0.33	−0.07	−0.31	0.10	0.21	0.36	

LVC = lower value cuts; MVC = medium value cuts; HVC = high value cuts; VHVC = very high value cuts.
[1]Standard errors for phenotypic correlations were all <0.03.

Table 3 *Phenotypic[1] (below diagonal) and genetic (above diagonal; standard error between parentheses) correlations between carcass weight, EUROP score for conformation and fat, and predicted wholesale cut weights in heifers (n = 14 318)*

	Carcass weight	EUROP carcass conformation	EUROP carcass fat	Total meat	LVC	MVC	HVC	VHVC
Carcass weight		0.41 (0.10)	0.17 (0.10)	0.28 (0.08)	0.26 (0.1)	0.10 (0.12)	0.26 (0.08)	0.38 (0.09)
EUROP carcass conformation	0.11		0.39 (0.12)	0.80 (0.05)	0.46 (0.11)	0.87 (0.09)	0.79 (0.06)	0.85 (0.04)
EUROP carcass fat	0.02	−0.01		−0.70 (0.06)	−0.87 (0.05)	−0.40 (0.13)	−0.67 (0.07)	−0.77 (0.05)
Total meat	0.05	0.40	−0.48		0.87 (0.03)	0.75 (0.08)	0.89 (0.03)	0.82 (0.05)
LVC	0.04	0.13	−0.50	0.66		0.47 (0.14)	0.80 (0.06)	0.69 (0.08)
MVC	0.09	0.20	−0.17	0.34	−0.01		0.82 (0.06)	0.82 (0.06)
HVC	0.06	0.33	−0.38	0.56	0.40	0.33		0.82 (0.05)
VHVC	0.14	0.32	−0.50	0.47	0.25	0.15	0.39	

LVC = lower value cuts; MVC = medium value cuts; HVC = high value cuts; VHVC = very high value cuts.
[1]Standard errors for phenotypic correlations were all <0.04.

Table 4 *Genetic correlations (r; standard error between parentheses) between carcass weight, EUROP conformation and fat score as well as predicted wholesale cut weights in steers and heifers*

	r
Carcass weight	0.81 (0.06)
EUROP carcass conformation	0.80 (0.07)
EUROP carcass fat	0.87 (0.07)
Total meat	0.79 (0.06)
Lower value cuts	0.64 (0.12)
Medium value cuts	0.54 (0.14)
High value cuts	0.76 (0.07)
Very high value cuts	0.69 (0.12)

dissections, whereas LVC and MVC in the steers were based on dissection protocols implemented in a research project (Conroy *et al.*, 2009). Although the dissection procedures between steers and heifers were very similar in the hindquarter of the carcass, commercial dissections produced more lean trimmings (potentially sold as minced meat, stir-fry or diced beef, i.e. lower value cuts) in the forequarter compared with the experimental study population (Pabiou *et al.*, 2010). In addition, the accuracy of the prediction equations for wholesale carcass cuts presented by Pabiou *et al.* (2010) was superior in the steers compared with the heifers, especially in the forequarter cuts (LVC and MVC), which could also have influenced the results.

The heritability estimates observed in both the steers and heifers for cold carcass weight were in agreement 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 across 56 studies. Using two distinct purebred populations of Swedish Charolais and Hereford, Eriksson *et al.* (2003) reported heritability estimates of 0.22 (Hereford) and 0.34 (Charolais) for carcass conformation, and of 0.27 (Hereford) and 0.38 (Charolais) for carcass fat grading. Hickey *et al.* (2007), using data from Irish abattoirs, observed a wide range in heritability estimates across eight Irish sub-populations separated according to breed of sire. Heritability for carcass conformation varied from 0.02 (Holstein sired) to 0.36 (Limousin sired) and from 0.00 (Hereford sired) to 0.40 (Simmental sired) for carcass fat score.

Total carcass meat, fat and bone weight

Predicted total meat, fat and bone weight of the steer carcasses in the present study agree with average total meat weight (227 kg), total fat weight (41 kg) and total bone weight (64 kg) reported by Pabiou *et al.* (2010) in 346 dissected steer carcasses. The sum of the wholesale cut weights in the heifers amounting to 101% of the predicted total meat weight is probably because of the overestimation in the prediction of VHVC from VIA, as documented by Pabiou *et al.* (2010). Nevertheless, the average predicted total meat weight of heifers in the present study (175 kg) agrees with average total meat weight of 183 kg in dissected Irish heifer carcasses reported by Pabiou *et al.* (2010).

Heritability for total meat weight in steers in the present study (0.38) was comparable to the average heritability of 0.51 reported in the review by Rios Utrera and Van Vleck (2004) across 13 studies. Pabiou *et al.* (2009) observed heritability for total meat weight of 0.68 and 0.54 in two distinct small populations of steers and heifers, respectively. In the present study, heritability for total meat weight in the heifers was particularly greater (0.72) than those reported in the literature: the maximum heritability reported by Rios Utrera and Van Vleck (2004) was 0.66 when adjusted to a constant age of slaughter. Heritability of total fat weight observed in the steers in the present study (0.14) was lower than the average heritability calculated across nine studies ($h^2 = 0.50$) by Rios Utrera and Van Vleck (2004). The large variation in the heritability estimates of total fat weight across studies is likely to be influenced by the gender under investigation, the breed, the feed system the animals were exposed to, the method of assessing fat content, as well as the data-editing criteria imposed and statistical model used. The heritability estimate of total bone weight in the present study (0.49) was comparable to the average heritability of 0.51 reported by Rios Utrera and Van Vleck (2004) following a summary of seven studies.

The strong genetic associations between EUROP conformation score and the hindquarter cut weights (HVC and VHVC) proved that EUROP scores for conformation were indeed a method to indirectly select for more valuable carcasses. However, the genetic correlations between these cuts and EUROP conformation were less than unity, suggesting that additional genetic gain in carcass value may be achieved by exploiting genetic information on predicted cut yields.

The genetic correlation between EUROP fat score and predicted total fat weight in the steers was 0.36, indicating that all the genetic variation in total carcass fat weight was not captured by EUROP carcass fat score. Indeed, EUROP classification for fat aims to describe the amount of fat on the outside of the carcass and in the thoracic cavity, whereas the predicted total fat weight also includes intra-muscular fat and therefore a correlation of one is not expected.

Wholesale cut weights

In both the steers and heifers, mean wholesale cut weights were comparable to those documented by Pabiou *et al.* (2010) in a population of 346 and 281 steers and heifers, respectively, based on actual carcass dissections. Nevertheless, the coefficient of phenotypic variation in heifers in the present study (LVC: 16%; MVC: 18%; HVC: 18%; VHVC: 17%) was larger than those observed by Pabiou *et al.* (2010; LVC: 13%; MVC: 13%; HVC: 13%; VHVC: 11%). These results suggest greater variation in heifer carcass conformation in the present field study, and are also in accordance with the observation made by Pabiou *et al.* (2010) on the over-representation of well-conformed heifers present in the sample used in their study.

Strong phenotypic and genetic correlations among the wholesale cut weights are somewhat expected, as some of the wholesale cut weights share part of the same muscles in the carcass. Moreover, the eigenvalues summarising the raw phenotypic correlation structure between predicted wholesale cuts in the present study, not adjusted for any confounding effects, were similar to the eigenvalues of the phenotypic correlation matrix between true wholesale cut weights reported by Pabiou *et al.* (2010), also not adjusting for any confounding effects. In the steers, the largest eigenvalue represented 77% of the total eigenvalues of the predicted wholesale cut weights in the present study and 88% of the total eigenvalues for the true cut weights in Pabiou *et al.* (2010). In the heifers, the largest eigenvalue represented 87% of the total eigenvalues of the predicted wholesale cut weights in the present study and 86% of the total eigenvalues for the true cut weights in Pabiou *et al.* (2010). This indicates the ability of the predicted wholesale cut weights to recover the variation in carcass composition.

There is a paucity of heritability estimates in the literature for wholesale carcass cut yields in cattle. Furthermore, because of the cost of undertaking carcass dissections, previous studies reporting heritability estimates used relatively small populations ($n = 503$, Cundiff *et al.* (1969); $n = 257$, Brackelsberg *et al.* (1971); $n = 413$ to 635, Pabiou *et al.* (2009)). In those studies, heritability estimates for wholesale cuts were generally moderate to high. Using carcass dissection data on 413 steers, Pabiou *et al.* (2009) documented heritability estimates for primal cut weights ranging from 0.03 to 0.73 for the primal cut components of LVC (fore- and hind-shins, ribs, flank, brisket, neck, lean trimmings), from 0.79 to 0.83 for the primal cut components of MVC (shoulder, chuck), from 0.67 to 0.86 for the primal cut components of HVC (sirloin, round) and from 0.14 to 0.49 for the primal cut components of VHVC (fillet, strip loin, rib roast). Using carcass dissection data from 635 cross-bred heifers, Pabiou *et al.* (2009) also reported heritability estimates for primal cut weights ranging from 0.28 to 0.74 for the primal cut components of LVC (lean trimmings, ribs, flank, brisket), from 0.41 to 0.61 for the primal cut components of MVC (blade, chuck), from 0.42 to 0.55 for the primal cut components of HVC (sirloin, round) and from 0.40 to 0.62 for the primal cut components of VHVC (fillet, strip loin, rib roast).

Genetic correlations between genders

The genetic correlations between the same wholesale cuts in either steers or heifers were not unity (Table 4), suggesting that they could be under different genetic control. Even for carcass weight, a trait that was actually recorded and not predicted, the genetic correlation deviated substantially from unity. Robertson (1959) suggested that traits with a genetic correlation above 0.80 could be treated as the same trait with little loss of information. Using data on post-weaning gain in five breeds of Swedish beef cattle, Stålhammar and Philipsson (1997) reported a pooled genetic correlation of 0.60 between genders, and concluded that the traits should be treated separately in the genetic evaluation of males and females. Näsholm (2004) observed genetic correlations between genders for weight at 4 months of age greater than 0.89 and suggested that weight traits in male and female lambs may be governed by the same genes. However, in the present study, the genetic correlations between the same carcass cut weight in both genders were (i) weakest for wholesale cut weights where the prediction equation accuracies were also the poorest in heifers (LVC: $R^2 = 0.65$; MVC: $R^2 = 0.70$; Pabiou *et al.*, 2010), and where the dissection techniques differed most between steers and heifers (Pabiou *et al.*, 2009 and 2010) and (ii) the strongest for total meat weight and HVC where the prediction equation accuracy was also the highest in heifers (total meat weight: $R^2 = 0.84$; HVC: $R^2 = 0.85$; Pabiou *et al.*, 2010). This suggests that stronger genetic correlations between steers and heifers might be achievable if the accuracy of the prediction equations for heifers was improved, as well as the difference in cutting methodology standardised. However, differences in genetic and phenotypic variances between genders should be accounted for in a genetic evaluation, and ideally the traits should therefore be treated separately in a multi-trait genetic evaluation.

Adjustment of cut weights for carcass weight

In the present study, carcass weight was included as a covariate in the model for the estimation of genetic parameters for the carcass cuts. This approach was undertaken so that the wholesale carcass cut weights were expressed relative to a constant carcass weight. This was preferred over the expression of each carcass cut weight as a proportion of total carcass weight because of the associated disadvantages of selecting on a ratio trait (Gunsett, 1984). Nevertheless, heritability estimates for wholesale carcass cut weight as a proportion of total carcass weight were obtained but are not reported because estimates were similar to those when the dependent variable was wholesale carcass cut weight but carcass weight was included as a covariate in the model. Similar results were also observed in the early findings of Benyshek (1981). However, genetic correlations between proportion of wholesale cut weight and carcass weight were either very weak (genetic correlation between medium value carcass cut weights as a proportion of carcass weight and carcass weight was −0.03 in steers) or strong (genetic correlation between low value carcass cut weights as a proportion of carcass weight and carcass weight was 0.78 in steers). When adjustment for carcass weight was undertaken through the inclusion of carcass weight as a covariate in the model, the genetic correlations between the wholesale cut weights and carcass weight were less variable, ranging from 0.32 (correlation between MVC and carcass weight) to 0.45 (correlation between VHVC and carcass weight) in the steers, and from 0.10 (correlation between MVC and carcass weight) to 0.38 (correlation between VHVC and carcass weight) in the heifers. This also suggested that, at constant carcass weight, heavier animals tended to have more HVC and VHVC.

The other rationale for estimating (co)variance components relative to a constant carcass weight, as opposed to simply estimating carcass cut weights, is to facilitate transparency in the breeding objectives used by farmers. When the wholesale cut weights were unadjusted for carcass weights, the genetic correlations between the wholesale cut weights and carcass weight were very strong, varying from 0.89 to 0.99 across the steers and heifers (results not shown). With the approach used in the present study, the economic benefit of heavier carcasses or carcasses with a greater proportion of higher value cuts can be easily elucidated, thereby aiding in the explanation and acceptance of the breeding objective.

Conclusions

This study is the first to report genetic parameters for wholesale carcass cut weights in cattle predicted from digital images of individual carcasses. Clear genetic variation in carcass cut weights, at a constant carcass weight, exists. Coupled with the obvious contribution of such traits to the overall profitability of beef production systems, and the now routine access to the carcass images on all animals slaughtered in Ireland, it has become feasible to breed for improved carcass value.

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IV

Genetic relationships between carcass cut weights predicted from video image analysis and other performance traits in cattle

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Abstract

The objective of this study was to quantify the genetic associations between a range of carcass related traits including wholesale cut weights predicted from Video Image Analysis (**VIA**) technology, and a range of pre-slaughter performance traits in commercial Irish cattle. Predicted carcass cut weights comprised of cut weights based on retail value: Lower Value Cuts (**LVC**), Medium Value Cuts (**MVC**), High Value Cuts (**HVC**), and Very High Value Cuts (**VHVC**), as well as total meat, fat and bone weights. Four main sources of data were used in the genetic analyses: price data of live animals collected from livestock auctions, live-weight data, and linear type collected from both commercial and pedigree farms as well as from livestock auctions, and weanling quality recorded on-farm. Heritability of carcass cut weights were ranged from 0.21 to 0.39. Genetic correlations between the cut traits and the other performance traits were estimated using a series of bivariate sire linear mixed models where carcass cut weights were phenotypically adjusted to a constant carcass weight. Strongest positive genetic correlations were obtained between predicted carcass cut weights and carcass value (min $r_{g(MVC)}$ = 0.35; max $r_{g(VHVC)}$ = 0.69), and animal price at both weaning (min $r_{g(MVC)}$ = 0.37; max $r_{g(VHVC)}$ = 0.66) and post-weaning (min $r_{g(MVC)}$ = 0.50; max $r_{g(VHVC)}$ = 0.67). Moderate genetic correlations were obtained between carcass cut weights and calf price (min $r_{g(HVC)}$ = 0.34; max $r_{g(LVC)}$ = 0.45), and weanling quality (min $r_{g(MVC)}$ = 0.12; max $r_{g(VHVC)}$ = 0.49), and linear scores for muscularity at both weaning (hindquarter development: min $r_{g(MVC)}$ = -0.06; max $r_{g(VHVC)}$ = 0.46), and post-weaning (hindquarter development: min $r_{g(MVC)}$ = 0.23; max $r_{g(VHVC)}$ = 0.44). The genetic correlations between total meat weight were consistent with those observed with the predicted wholesale cut weights. Total fat and total bone weights were generally negatively correlated with carcass value, auction prices, and weanling quality. Total bone weight was, however, positively correlated with skeletal scores at weaning and post-weaning. These results indicate that some traits collected early in life are moderate to strongly correlated with carcass cut weights predicted from VIA technology. This information can be used to improve the accuracy of selection for carcass cut weights in national genetic evaluations.

Introduction

The main source of revenue for beef farmers, either directly or indirectly, is carcass value. In Europe, carcass price is traditionally derived from the EUROP grading for conformation and fat (European Council regulations 1208/81 and 2930/81) obtained from human assessment or mechanical grading machines. Using Irish data, Pabiou et al. (2011a) defined four groups of wholesale cut weights based on retail value: Lower Value Cuts (**LVC**), Medium Value Cuts (**MVC**), High Value Cuts (**HVC**), and Very High Value Cuts (**VHVC**), as well as three groups of overall cut weights: total meat weight, total fat weight, and total bone weight. Pabiou et al. (2011a) then showed that these four wholesale carcass cut weights can be accurately predicted from carcass images generated at slaughter by the mechanical grading machines used to predict the EUROP scores for conformation and fat. Pabiou et al. (2011b) proceeded to show that significant genetic variation in these predicted wholesale carcass cuts at constant carcass weight existed implying the genetic selection for such traits is possible.

Phenotypic information on digital images, and therefore predicted wholesale carcass cut yields, are however only available at slaughter in Ireland at approximately 24 (heifers) to 28 (steers) months of age (Pabiou et al. 2011a). This has implications for the accuracy of selection of potential parents for subsequent generations. Indirect genetic selection using readily accessible phenotypes, measured early in life and genetically correlated with the goal trait (i.e., wholesale carcass cuts), may be used to increase the accuracy of selection at a younger age, and therefore increase annual genetic gain. Phenotypes routinely collected in Ireland that could possibly be used as early genetic predictors of wholesale carcass cut yields include individual animal auction price, live weight, and visual assessment of live animals at weaning and post-weaning.

The objective of this study was, therefore, to quantify the genetic associations between wholesale cut weights predicted from video image analysis (**VIA**) and a range of performance traits currently being recorded on cattle in Ireland. Results from this study will be useful in quantifying the accuracy of selection for wholesale carcass cuts achievable using a multi-trait selection index including readily available traits measured early in life.

Materials and Methods

The data originated from four sources: 1) predicted carcass cut weights and carcass value collected from abattoirs, 2) animal price data collected from livestock auctions, 3) live-weight and linear type traits collected from commercial and pedigree farms as well as from livestock auctions (live-weight only), and 4) weanling quality scores subjectively assessed by commercial and pedigree farmers. The data consisted of routinely collected records of crossbred animals; the main breed proportions represented in teh crossbred animals were Charolais, Friesian, Holstein, Limousin, Angus, Simmental, Hereford, and Belgian Blue.

Predicted carcass cut weights and carcass value

Prediction methods used to predict carcass cut weights from video image analysis have been previously described in detail by Pabiou et al. (2011a). Predicted carcass cut weights were available on steers and heifers and consisted of i) predicted wholesale cut weights based on their respective market value: Lower Value Cuts (**LVC**), Medium Value Cuts (**MVC**), High Value Cuts (**HVC**), and Very High Value Cuts (**VHVC**), and ii) predicted overall cut weights: total meat weight, total fat weight, and total bone weight. Predicted wholesale cut weights were calculated for both steers and heifers, whereas total fat, and bone weights were only calculated in steers (Pabiou et al., 2011a). Appendix A Figure 1 shows the location of LVC, MVC, HVC, and VHVC on a live animal. Accuracy of prediction (R^2) for LVC, MVC, HVC, and VHVC was 0.92, 0.86, 0.93, and 0.84, respectively in steers, and 0.65, 0.70, 0.85, and 0.72, respectively in heifers (Pabiou et al., 2011a).

Predicted carcass cut weights from 568,831 steers and 356,216 heifers slaughtered between 2005 and 2010, from 22 Irish abattoirs were available. Animals slaughtered before 300 days of age (i.e., 10 months), as well as steers and heifers slaughtered older than 1,800 days (i.e., 60 months) and 1,087 days (i.e., 36 months) of age, respectively, were discarded. Animals without a recorded sire or from an unknown herd were also discarded.

In Ireland, payment for carcasses is based on carcass weight and gender, adjusted, within factory, for EUROP conformation and fat grade. Carcass value (€ per animal) was available for all carcasses, and to account for potential large variations in market trends across time, carcass values were standardised to a common residual variance within contemporary group as described by McHugh et al. (2011) for animal price.

Herd-year-season of slaughter contemporary groups were defined, within sex, using the iterative algorithm of Crump et al. (1997). The algorithm is based on grouping animals together, within herd, that are slaughtered in close proximity of time. Initially, records taken within 60 days were joined together. Subsequently, if the number of records within a contemporary group was less than 5, they were merged with a contemporary group adjacent in time if the start date of this group and the end date of the adjacent group were less than 120 days apart.

Carcass value records contemporary groups with no variation in carcass value were set to missing. This edit was applied to discard data where a flat price for a group of cattle was negotiated between the individual farmer and the abattoir. The edited dataset comprised of 110,308 predicted carcass cut weight records (79,744 steers and 30,564 heifers), as well as 106,612 records with carcass value records (79,075 steers and 25,537 heifers; Table 1).

Animal market price

A total of 4,207,051 animal market price records (overall animal price rather than price per kg) from 3,552,089 animals sold at 74 livestock auctions in Ireland between the years 2000 to 2010, were extracted from the Irish Cattle Breeding Federation (**ICBF**) database. Livestock auction venues are present across Ireland and are the locations where most cattle are purchased.

Table 1. *The different pre-slaughter datasets to be merged with the carcass cut weight dataset (n = 110,308 records): number of records, contemporary groups (CG) size, number of sires in common with the carcass cut dataset*

Trait	Maturity group	Age group (days)	Number of animals with records	Number of CG	Number of common sires with carcass cut dataset
Carcass Value		> 300	106,612	11,883	10,049
Price	Calves	2 to 84	36,754	1,898	1,280
Price	Weanling	150 to 300	17,681	661	368
Price	Post Weanling	300 to 600	33,620	1,283	606
Live weight	Weanling	150 to 300	34,637	2,990	781
Live weight	Post Weanling	300 to 600	72,180	4,217	1,287
Calf Quality	Weanling	150 to 300	81,815	7,824	1,848
Linear scores[1]	Weanling	150 to 300	Min: 26,539 Max: 31,692	2,353	2,550
Linear scores[1]	Post Weanling	300 to 600	Min: 38,699 Max: 38,703	3,916	3,397

[1]Includes 7 different traits.

The data were divided into three distinct maturity categories as described in detail by McHugh et al., (2010): calves, weanlings, and post-weanlings. The edits implemented were those described by McHugh et al. (2010). Calves were defined as animals born from dairy cows (i.e., dam breed proportion > 66% dairy) sold between 2 days of age and 12 weeks of age. No live weight information was available on these animals and only calves sold between €2 and €450 were included. Weanlings were defined as animals sold between 150 and 300 days of age as beef animals (i.e., dam breed proportion > 66% beef). Weanling auction data were limited to animals weighing between 150 and 600 kg and sold for between €200 and €1,200. Post-weanlings were also defined as beef animals sold between 301 and 600 days of age. Post-weanlings auction data were limited to animals weighing between 200 and 1,000 kg and sold for between €200 and €1,500.

Irrespective of maturity category, animals were discarded if price per animal (euro, €), herd of origin, or sire were unknown. When age of dam at calving was less than 18 months, the data were discarded; similarly, within parity, when age of dam at calving was greater than 22 months from the median age, the data were also discarded. Only price data from animals sold individually at auctions were considered, and for animals sold through livestock auctions more than once in their lifetime, only the first recorded date in time was kept. Animals included also had to have at least 66% of the breed composition known. In order to account for potential large variation in market trends across time, auction prices were standardised to a common residual variance within contemporary group as described by McHugh et al. (2011).

In order to account for differences in rearing/finishing practices on farm as well as day and location of sale effects, two distinct contemporary groups were defined in each of the three maturity groups: i) herd-year-season of auction sale, and ii) auction-date of sale. Herd-year-season of auction sale contemporary groups were defined using the iterative algorithm of Crump et al. (1997), parameterised by the minimum and maximum span of a group for auction sale date of 10, and 182 days, respectively, as well as a minimum number of 5 records per group. Only animals from contemporary groups (i.e., herd-year-season and auction-date) with at least 5 animals were considered for further analysis. Following all edits, the calf dataset contained 36,754 calves with price distributed across 1,898 auction date-of-sale contemporary groups (Table 1). The weanling and post-weanling datasets included 17,681 and 33,620 animals with price, respectively, and included 661 and 1,283 auction date-of-sale contemporary groups, respectively (Table 1).

Live-weight

A total of 1,360,900 live-weight records from 1,244,869 animals, aged between 150 and 600 days of age, from 81,400 herds, between the years 2000 to 2010, were available. Live weights were collected from livestock auctions as well as from commercial and pedigree farms. On average over the 2000 to 2010 time period, live-weight from auctions represented more than 85% of the total live-weights collected.

The dataset was divided into weanling and post-weanling records as no live weight data were available on calves. Across both data sources, animals were discarded if herd of origin or sire were unknown. When age of dam at calving was less than 18 months, the data were discarded; similarly, within parity, when age of dam at calving was greater than 22 months from the median age, the data were also discarded. Since some animals can be weighed more than once within maturity group, only the first recorded date in time was considered. Weanlings were defined as progeny of beef cows (i.e., dam breed proportion > 66% beef) aged between 150 and 300 days of age and weighing between 150 and 600 kg. Post-weanlings between 301 and 600 days of age and weighing between 200 and 1,000 kg and were from both dairy and beef cows.

Contemporary groups data were defined as herd-year-season of weighing and were generated using the Crump et al. (1997) algorithm, parameterised by the minimum and maximum span of a group for weighing date of 10, and 182 days, respectively, as well as a minimum of 5 records per group. Following all edits, 34,637 weanlings with live weight records across 2,990 contemporary groups and 72,180 post-weanlings with live weight records across 4,217 contemporary groups were available for subsequent analysis (Table 1).

Weanling quality

As part of a national scheme (state aid N 140/2007), weanling quality was to be subjectively scored on a scale of 1 (poor) to 5 (excellent) by beef farmers to describe the overall quality of their weanling animals. In 2007, the state aid N 140/2007-Ireland 'Animal Welfare, Recording, and Breeding Scheme for Suckler Herds' from the European Commission approved the technical and financial framework for the scheme in Ireland to operate from the years 2008 to 2012.

In the present study, 1,710,263 weanling quality scores were available from 43,869 commercial farms across Ireland between the years 2008 and 2010. Weanlings visually scored outside the age of 150 to 300 days were excluded from the analysis (n = 351,799). Animals without a known sire (n = 69,311) as well as animals with less than 66% of their breed composition known (n = 774,845) were discarded from the analysis.

Contemporary groups were defined as herd-date of scoring using the Crump et al. (1997) algorithm, parameterised by the minimum and maximum span of a group for scoring date of 10, and 182 days, respectively, as well as a minimum of 5 records per group. Contemporary groups containing less than 5 animals (n = 328,866), and contemporary groups with no variation in weanling quality scores (n = 103,627) were discarded from further analysis. Following all edits, 81,815 animals with weanling quality scoring from 7,824 contemporary groups were included in the analysis (Table 1).

Linear type traits

Linear scoring is a visual assessment of an animal's morphology and is routinely undertaken in Ireland by 32 independent linear scorers on both commercial and pedigree beef herds. Seven different traits are currently used in the Irish beef genetic evaluation, and include the muscularity traits (Appendix A Figure 2.1) of loin development, hindquarter development, width at withers, and width behind withers, as well as the skeletal traits (Appendix A Figure 2.2) of length of back, length of pelvis, and height at withers. Linear score data were available on 180,320 beef animals, aged between 150 and 1,087 days, in 8,082 herds between the years 2000 and 2010. Each linear trait was standardised within scorer by year to a common variance within trait. Information on all 7 traits was not available on all animals.

Animals were discarded if herd of scoring or sire were unknown. Animals were split into two groups according to age at scoring: weanling scored between 150 and 300 days of age, and post-weanling scored between 301 and 600 days of age. Within each maturity group, herd-year-season of scoring contemporary groups were generated using the Crump et al. (1997) algorithm (parameterised by the minimum (10 days) and maximum (182 days) span of a group for date, and the minimum number of records (n = 5) per group) and only contemporary groups with at least 5 records were considered. Following all edits, up to 31,692 and 38,703 animals with linear scores were available for further analysis in the weanling and post-weanling maturity group, respectively (Table 1).

Statistical analyses

Phenotypic and genetic variance components were estimated separately for all traits using animal linear mixed models in DMU (Madsen et al., 2007). The univariate model can be described as:

$$\mathbf{Y = Xb + Za + e} \qquad \mathbf{[1]}$$

where **Y** is a vector of performances, **b** is a matrix of fixed effects, **a** is a vector of random genetic animal effects, and **e** if a vector of residuals; **X** and **Z** are the associated incidence matrices. Where live-weight at weaning was the dependent variable, a random maternal genetic component (i.e., dam of animal) was also included in the model. The univariate model with maternal effect was therefore:

$$\mathbf{Y = Xb + Za + Wm + e} \qquad \mathbf{[2]}$$

where Y is a vector of performances, b is a matrix of fixed effects, a is a vector of random genetic animal effects, m is a vector of dam of animal genetic effect, and e is a vector of residuals; X, Z and M are the associated incidence matrices. When no maternal genetic component was included in the model, the direct heritability was represented by the ratio of the animal variance to the sum of the animal and residual variance. When the model contained a maternal genetic component the direct (h^2_d) and maternal (h^2_m) heritabilities were computed as:

$$h_d^2 = \frac{\sigma_d^2}{\sigma_d^2 + \sigma_m^2 + \sigma_{dm} + \sigma_e^2}$$

$$h_m^2 = \frac{\sigma_m^2}{\sigma_d^2 + \sigma_m^2 + \sigma_{dm} + \sigma_e^2}$$

where σ_d^2 *= direct genetic variance;*

σ_m^2 *= maternal genetic variance;*

σ_{dm} *= covariance between direct and maternal traits;*

σ_e^2 *= residual variance.*

Genetic correlations between carcass cut weights and each of the associated traits (i.e., carcass value, auction price, live weight, weanling quality score, and linear scores) were estimated using a series of bivariate sire linear mixed models (DMU; Madsen et al., 2007) accounting for all relationships among sires. Genetic correlations between carcass value and auction prices, as well as between weanling quality and linear scores were also estimated. The model description was similar to model [1] but expanded to be multi-trait: vector **a** was replaced by matrix **s** of sire genetic effects, and genetic and residual (co)variance matrices between the traits were estimated. When live-weight at weaning was one of the dependent variables, the model also included a random maternal genetic component (i.e., maternal grand-sire of animal) for this trait.

Fixed class effects included in all models were sex of the animal (male or female), age of the dam when the animal was born (<3 years, 3 to 5 years, 6 to 8 years, and >8 years), birth type (i.e., whether the animal was born singleton or from a multiple birth), as well as the contemporary groups defined specifically for each trait in the analysis.

Covariates tested and included in all models included heterosis and recombination loss which were calculated as $1 - \sum_{i=1}^{n} sire_i \cdot dam_i$ and $1 - \sum_{i=1}^{n} \frac{sire_i^2 + dam_i^2}{2}$, respectively where $sire_i$ and dam_i were the proportion of breed i in the sire and dam, respectively. Additionally, age at trait measurement was included in all models as a covariate. When the dependent variable was carcass value, LVC, MVC, HVC, VHVC, total meat weight, total fat weight, or total bone weight, then carcass weight was also included in the model as a covariate. When the dependent variable was either weanling or post-weanling auction price, a covariate for live weight at the time of sale was also included in the model.

Pedigree of animals (univariate models) and sires (bivariate models) was extracted from the ICBF database, and back-pedigrees were traced back at least four generations of ancestors, where available. Relationships among animals or sires were accounted for using a relationship matrix where unknown ancestors were included as phantom groups of the following breeds: Charolais, Friesian, Holstein, Limousin, Angus, Simmental, Hereford, Belgian Blue, French hardy breeds (Salers and Aubrac), other beef breeds (Piemontese, Parthenaise, Blonde d'Aquitaine, and Shorthorn), and unknown breed in both the steers and heifer pedigree files.

Results

Summary statistics

The measured carcass weight reported at slaughter was 349 kg for steers and 296 kg for heifers; the average predicted carcass weight for steers (i.e., sum of the averages predicted total fat weight, predicted total bone weight, and predicted wholesale cut weight) was 337 kg (Table 2). Average auction price increased consistently with age from €134 in calves to €589 and €664 in weanlings and post-weanling, respectively; average carcass value was €938. The coefficient of genetic variation for calf auction price (15%) was three times larger than the coefficient of genetic variation for weanling and post-weanling auction price. Average live weight at weaning and post-weaning was 315 kg and 430 kg, respectively.

Table 2. *Presentation of the data: number of records (N), mean, phenotypic standard deviation (STD), heritability (h^2), standard error of heritability (s.e.), and coefficient of genetic variation (CVg) for carcass cut weights, carcass and animal value, live weight, weanling quality, and linear scores at weaning and post-weaning*

Trait	N	Mean	STD	h^2 (s.e.).	CVg
Total meat weight	110,308	217	7.89	0.42 (0.02)	2%
Total fat weight	79,744	43	10.54	0.14 (0.01)	9%
Total bone weight	79,744	77	3.03	0.49 (0.02)	3%
Lower value cut weight	110,308	88	4.07	0.22 (0.02)	2%
Medium value cut weight	110,308	41	1.78	0.26 (0.02)	2%
High value cut weight	110,308	57	3.33	0.39 (0.02)	4%
Very value high cut weight	110,308	24	1.44	0.21 (0.01)	3%
Carcass value	106,612	938	21.73	0.35 (0.02)	1%
Auction price calves	36,754	134	30.58	0.43 (0.03)	15%
Auction price weanlings	17,681	589	60.77	0.49 (0.05)	7%
Auction price post-weanlings	33,620	664	57.09	0.38 (0.03)	5%
Live weight weanlings	34,637	315	40.08	0.27 (0.03)^d	7%
				0.14 (0.02)^m	5%
Live weight post-weanlings	72,180	430	63.79	0.25 (0.01)	7%
Weanling quality	81,815	3.57	0.61	0.32 (0.02)	10%
Linear scores at weaning age					
Height at withers	31,690	5.28	0.88	0.34 (0.03)	10%
Length of back	31,602	6.05	0.89	0.24 (0.02)	7%
Length of pelvis	26,456	5.88	0.87	0.2 (0.02)	7%
Width at withers	26,456	7.81	1.04	0.2 (0.02)	6%
Width behind withers	31,604	7.24	1.03	0.19 (0.02)	6%
Loin development	31,691	7.99	1.10	0.24 (0.02)	7%
Hindquarter development	31,687	8.21	1.05	0.26 (0.02)	7%
Linear scores at post-weaning age					
Height at withers	38,700	6.08	0.96	0.31 (0.02)	9%
Length of back	38,654	6.79	0.95	0.22 (0.02)	7%
Length of pelvis	37,775	6.52	0.91	0.17 (0.02)	6%
Width at withers	37,775	8.25	1.08	0.19 (0.01)	6%
Width behind withers	38,654	7.63	1.06	0.12 (0.01)	5%
Loin development	38,700	8.14	1.08	0.19 (0.02)	6%
Hindquarter development	38,696	8.27	1.05	0.22 (0.02)	6%

d=direct; m= maternal

Heritability

Heritability of the individual wholesale cut weights varied from 0.21 (VHVC) to 0.39 (HVC) (Table 2). Heritability of auction price increased from 0.43 in calves to 0.49 in weanlings, then decreased to 0.38 in post-weanlings. Heritability of live weight (direct effect) was similar in both weanlings (0.27) and post-weanlings (0.25). The estimated heritability of weanling quality measured subjectively by individual farmers without any specific training was 0.32. Heritability of linear scored traits were similar across the two maturity groups and varied from 0.12 to 0.34.

Genetic correlations

Strong positive genetic correlations existed between HVC, VHVC, and carcass value, while negative correlations existed between carcass value and both carcass fat and bone weight (Table 3). Genetic correlations between carcass cut weights and auction price collected on live animals increased in magnitude from calves ($0.34 \leq r_g \leq 0.45$), to weanlings ($0.37 \leq r_g \leq 0.66$), to post-weanling ($0.50 \leq r_g \leq 0.67$). Strong positive genetic correlations were also observed between carcass value and calves auction prices (0.48), weanling auction prices (0.79), and post-weanling auction prices (0.52).

In both weanlings and post-weanlings, genetic correlations between live-weight and the carcass traits (overall and wholesale cut weights) were close to zero (Table 4). Genetic correlations between maternal weaning weight and carcass cuts were also close to zero.

Weanling quality, as scored by farmers, was positively correlated with total meat weight and the wholesale cut weights ($0.12 \leq r_g \leq 0.49$), and negatively correlated with total fat weight and total bone weight (Table 4).

Irrespective of age at scoring, skeletal linear traits (i.e., height at withers, length of back, and length of pelvis) were positively correlated with total bone weight ($0.27 \leq r_g \leq 0.68$). Total meat weight, LVC, MVC, HVC, VHVC was positively correlated with muscle linear traits (width at withers, width behind withers, loin development, and hindquarter development), with the exception of MVC in weanlings.

Strong positive genetic correlations existed between weanling quality and muscle linear scores: width at withers (0.76), width behind withers (0.73), loin development (0.74), and hindquarter development (0.68). Genetic correlations between weanling quality and length of pelvis, length of back, and height at withers were 0.29, 0.60, 0.41, respectively.

Table 3. *Genetic correlations (standard errors in brackets) between carcass cut weights (at constant carcass weight) and carcass value (at constant live weight), auction prices for calves, weanlings (at constant live weight) and post-weanlings (at constant live weight), live weight, and weanling quality.*

Trait		Total meat weight	Total fat weight	Total bone weight	Lower value cuts weight	Medium value cuts weight	High value cuts weight	Very high value cuts weight
Carcass value		0.45 (0.03)	-0.38 (0.05)	-0.72 (0.03)	0.38 (0.05)	0.35 (0.04)	0.52 (0.03)	0.69 (0.03)
Calves auction price		0.26 (0.07)	-0.23 (0.09)	-0.35 (0.07)	0.45 (0.08)	0.38 (0.07)	0.34 (0.07)	0.38 (0.07)
Weanling auction price		0.49 (0.11)	-0.39 (0.16)	-0.45 (0.13)	0.41 (0.14)	0.66 (0.10)	0.37 (0.11)	0.55 (0.12)
Post-weanling auction price		0.68 (0.08)	-0.67 (0.12)	-0.32 (0.13)	0.61 (0.11)	0.50 (0.11)	0.65 (0.08)	0.67 (0.10)
Live weight at weaning	*Direct*	-0.13 (0.10)	-0.10 (0.14)	0.10 (0.12)	-0.03 (0.12)	-0.34 (0.11)	-0.07 (0.10)	0.01 (0.12)
	Maternal	-0.01 (0.11)	-0.13 (0.15)	0.10 (0.13)	-0.16 (0.13)	0.07 (0.12)	-0.01 (0.11)	-0.01 (0.13)
Live weight at post-weaning		0.08 (0.08)	-0.12 (0.12)	0.09 (0.09)	-0.07 (0.10)	0.14 (0.08)	0.04 (0.08)	-0.02 (0.10)
Weanling quality		0.39 (0.08)	-0.31 (0.12)	-0.30 (0.10)	0.33 (0.10)	0.12 (0.09)	0.28 (0.08)	0.49 (0.09)

Discussion

The potential use of VIA in a national breeding program, due primarily to the existence of genetic variation in predicted carcass cut weights, was proposed by Pabiou et al. (2011a). However, because it is necessary to wait until the animal is slaughtered, accurate estimates of genetic merit for carcass cut weights are not available early in the lifetime of potential parents. Therefore, the motivation for this study was to quantify the strength of genetic associations between routinely available measures of performance in Irish cattle and predicted carcass cut weights.

General statistics and variance components

The heritability estimates in the present study were similar to those reported by Pabiou et al. (2011b) in a smaller population sample of Irish steers and heifers. The heritability estimates for animal price were greater than those reported by McHugh et al. (2011) in a smaller dataset of Irish cattle, attributable to the greater genetic variance estimated in the present study. Heritability estimates for live weight at weaning and post-weaning estimated in the present study were consistent with those documented by McHugh et al. (2011). Heritabilities for linear scores at weaning and post-weaning were also consistent with McHugh et al. (2011).

The heritability of weanling quality score (0.32) and its coefficient of genetic variation was similar than the respective measures of the individual linear scores, assessed by experienced and trained classifiers. Despite the lack of any formal training of farmers on scoring this trait, it is obvious that perception of quality at weaning age is relatively consistent across farmers.

Table 4. *Genetic correlations (standard errors in brackets) between carcass cut weights (at constant carcass weight) and linear traits recorded at weaning and post-weaning age.*

Trait	Total meat weight	Total fat weight	Total bone weight	Lower value cuts weight	Medium value cuts weight	High value cuts weight	Very high value cuts weight
Linear scores at weaning age							
Height at withers	-0.25 (0.11)	0.08 (0.17)	0.68 (0.10)	0.09 (0.14)	-0.58 (0.11)	-0.09 (0.12)	-0.06 (0.14)
Length of back	-0.22 (0.12)	0.23 (0.17)	0.51 (0.13)	-0.12 (0.15)	-0.51 (0.12)	-0.09 (0.13)	-0.10 (0.15)
Length of pelvis	-0.26 (0.15)	0.02 (0.21)	0.44 (0.17)	-0.28 (0.18)	-0.56 (0.14)	-0.20 (0.15)	-0.20 (0.18)
Width at withers	0.32 (0.14)	-0.34 (0.20)	-0.28 (0.17)	0.44 (0.16)	-0.38 (0.15)	0.25 (0.15)	0.63 (0.14)
Width behind withers	0.13 (0.13)	-0.17 (0.19)	-0.37 (0.16)	0.18 (0.16)	-0.33 (0.14)	0.10 (0.13)	0.43 (0.15)
Loin development	0.29 (0.15)	-0.11 (0.21)	-0.46 (0.17)	0.26 (0.17)	-0.47 (0.15)	0.09 (0.15)	0.50 (0.15)
Hindquarter development	0.42 (0.10)	-0.28 (0.16)	-0.41 (0.12)	0.32 (0.13)	-0.06 (0.12)	0.38 (0.11)	0.46 (0.12)
Linear scores at post-weaning age							
Height at withers	-0.08 (0.10)	-0.27 (0.14)	0.59 (0.09)	-0.02 (0.12)	0.11 (0.11)	0.01 (0.10)	-0.17 (0.12)
Length of back	-0.06 (0.11)	-0.23 (0.16)	0.27 (0.13)	0.03 (0.13)	-0.12 (0.12)	0.06 (0.11)	-0.04 (0.13)
Length of pelvis	-0.17 (0.12)	-0.28 (0.16)	0.51 (0.12)	-0.18 (0.14)	0.02 (0.13)	0.00 (0.12)	-0.10 (0.14)
Width at withers	0.44 (0.10)	-0.37 (0.15)	-0.19 (0.13)	0.49 (0.12)	0.16 (0.12)	0.46 (0.10)	0.46 (0.12)
Width behind withers	0.32 (0.12)	-0.29 (0.17)	-0.30 (0.14)	0.39 (0.13)	0.11 (0.13)	0.40 (0.11)	0.39 (0.13)
Loin development	0.38 (0.10)	-0.29 (0.15)	-0.24 (0.13)	0.53 (0.11)	0.10 (0.12)	0.35 (0.10)	0.42 (0.12)
Hindquarter development	0.45 (0.09)	-0.33 (0.14)	-0.33 (0.12)	0.37 (0.12)	0.23 (0.11)	0.38 (0.10)	0.44 (0.11)

Genetic correlations

The majority of the correlations estimated in the present study are in line with expectations. The moderate to strong positive genetic correlations between carcass value and both VHVC and HVC, and the fact that these were stronger than with LVC and MVC agrees with the objective of the current beef EUROP carcass classification (Council Regulation (EEC) No 1208/81 of 28 April 1981) for conformation to describe "the development of carcasses profiles, in particular the essential parts (round, back, shoulder)". Pabiou et al. (2011b) also observed positive genetic correlations between predicted wholesale cut weights and EUROP grading for conformation ranging from 0.44 (LVC) to 0.84 (VHVC). This was also reflected in the positive correlation between carcass value and total meat weight but a strong negative correlation between carcass value and bone weight, the latter reflecting the contribution of bone weight to differences in carcass kill out.

As expected, prices paid for cattle at livestock auctions are good predictors of future carcass quality as evidenced by the positive genetic correlations between auction price with total meat weight and carcass cut weights, especially HVC and VHVC. The genetic correlation between auction price in weanlings and carcass value (0.79) indicates that purchasers' preference at livestock auction is mainly based on potential carcass return. Post-weaning, a slight weakening of the genetic correlations between auction price and carcass value (0.52) compared to their respective genetic correlations at weaning was observed. This indicates that purchasers' preference at auction is still based on potential carcass return, but could be more influenced by other factors like purchasing replacement cattle. The majority of calves are sold at livestock auctions prior to compulsory health testing at 42 days of age (McHugh et al., 2010). Nonetheless, calf price, although limited to progeny from dairy cows and thus influencing primarily the estimated breeding values of sires (or their relatives) used on dairy cows is nonetheless a very useful early predictor trait of carcass cut yields especially since these data are available at no additional cost. Weanlings from beef cows are on average sold at 8 months of age and therefore also provide a useful, albeit slightly later in life, genetic predictor of carcass quality with no additional cost of collecting the data.

Not all animals, however, are sold during their life-time or even sold through the livestock auctions. Weanling quality, on the other hand, can potentially be scored by all commercial and pedigree farmers on all weanlings and its high heritability, coupled with its ample genetic variation and moderate genetic correlations with carcass quality, clearly indicate that it is a useful trait for inclusion in a multi-trait genetic evaluation for carcass quality. The strong positive genetic correlations observed between the muscle linear traits and weanling quality ($r_g \geq 0.71$) suggest they are measuring relatively similar genetic characteristics in the animals, despite being measured by trained assessors (i.e., linear scores) or individual farmers (i.e., weanling quality). Currently, Irish farmers receive a small financial incentive to record weanling quality (as well as other information). However, the recording of weaning quality (and the other traits) may still persist, for some animals at least, even without the financial incentive in the future, if farmers see their recorded data contributing to genetic evaluations and thus genetic gain.

The weak correlations between carcass cut weights and live weight were expected because of the adjustment of the carcass cut weights to a constant carcass weight in the present study. Renand et al. (1985) also observed weak genetic correlations between weaning weight and carcass muscle percentage (-0.08) and carcass fat percentage (0.11) in a model adjusting for slaughter weight. Without the adjustment to a constant carcass weight in the present study, the genetic correlations between carcass cut weights and live weight at weaning were 0.37, 0.38, 0.21, and 0.32 for LVC, MVC, HVC, and VHVC, respectively, and 0.49, 0.48, and 0.50 for total meat weight, total fat weight, and total bone weight, respectively.

Genetic correlations between carcass cut weights and muscle linear scores were, as expected, positive, and moderate to strong since linear scores for muscularity describe the amount of muscle present on the live animal. The genetic correlations between the carcass cut weights and muscle linear scores were consistent across both weaning and post-weaning for LVC, HVC, VHVC, but noticeably weaker for MVC especially at weaning. The linear score traits used in the present study all describe the physical structure and composition of the animals hindquarter; no linear scores were available in this study that properly describe the volume of the shoulders (Appendix A Figure 1, Figure 2.1, Figure2.2). At post-weaning, the genetic correlations between the linear scores and MVC (-0.12 to +0.23) were weaker than the genetic correlations of linear scores with the other cut traits (LVC, HVC, and VHVC) but to a lesser extent than those taken at weaning. This may reflect the importance of age in the development of the muscle on the animal. Results from Teuscher et al. (2006) on changes in muscle structure with breed and age also suggested that difference in muscle size (defined by the muscle cross-sectional area) within and between breeds (Angus, Galloway, Holstein-Friesian, and Belgian Blue) become significantly more apparent after 12 months of age. This implies that linear scores at post-weaning age should be a better indicator of carcass cut weights, and results from this study generally support this hypothesis.

Conclusions

This study clearly shows a benefit in increasing the accuracy of selection on carcass cut weight from exploiting data on routinely available measures of performance in Irish cattle such as auction price and weanling quality scored by farmers. Other recorded phenotypes such as linear scores at weaning and post-weaning are also useful predictors of carcass cut weights, but with potentially higher recording costs, albeit the linear scores are usually recorded on the selection candidates themselves which may increase the accuracy of selection but also reduce the generation interval. Carcass quality in the Irish national evaluation, which is currently based on the EUROP scores for carcass, should now be replaced with a multi-trait genetic evaluation for carcass cut weights predicted from VIA, which includes other performance traits such as linear scores, auction price and weaning quality.

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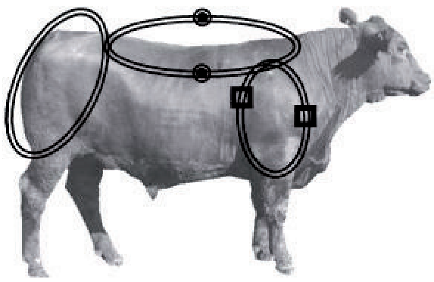
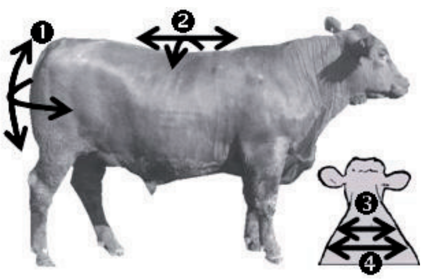
Appendix A



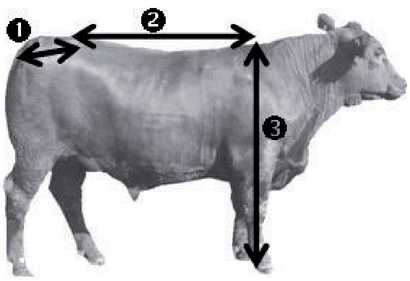
=⊙= Very high value cuts; === High value cuts (excluding tail); =□= Medium value cuts; Rest of animal (excluding feet and head): Lower value cuts

Figure 1. Location of the carcass cut weights on a live animal.



❶ Hindquarter development; ❷ Loin development; ❸ Width at withers; ❹ Width behind withers

Figure 2.1: Location of the muscle linear traits on a live animal.



❶ Length of pelvis; ❷ Length of back; ❸ Height at withers

Figure 2.2: Location of the skeletal linear traits on a live animal.