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

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

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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

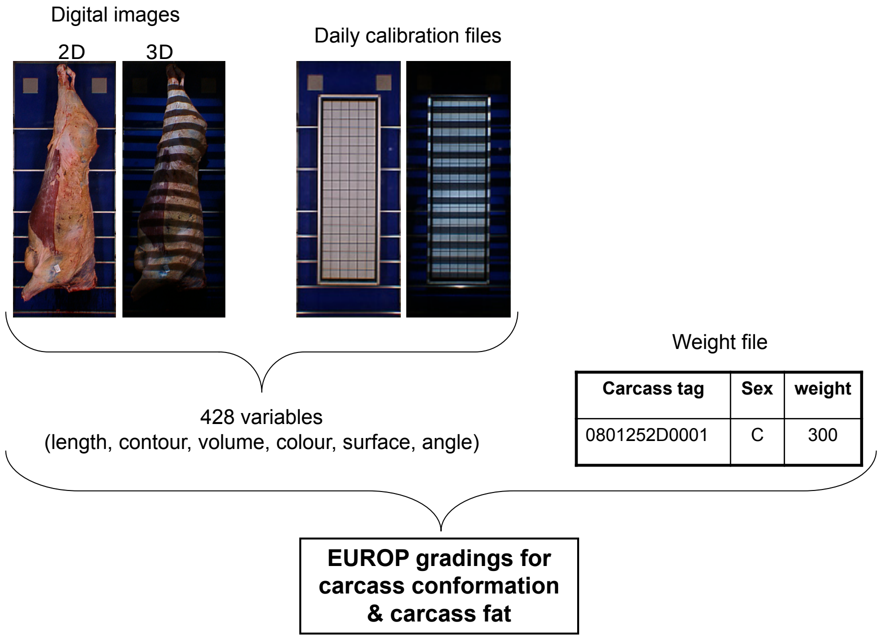
EUROP gradings were based on subjective assessments by highly trained personnel. Boggaard et al. (1996) presented some limitations of European beef carcass grading operated by expert classifiers: bias can occur between groups of carcasses, classifiers' judgment can vary over time, and differences can 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).



Carcass tag	Sex	weight
0801252D0001	C	300

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.

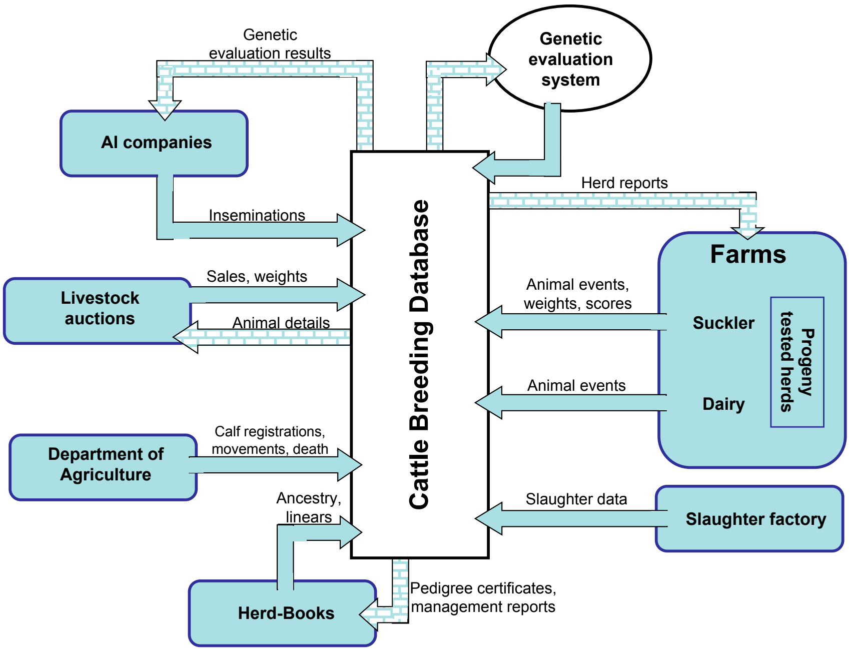


Figure 2. Data and information flow around the ICBF database.

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).

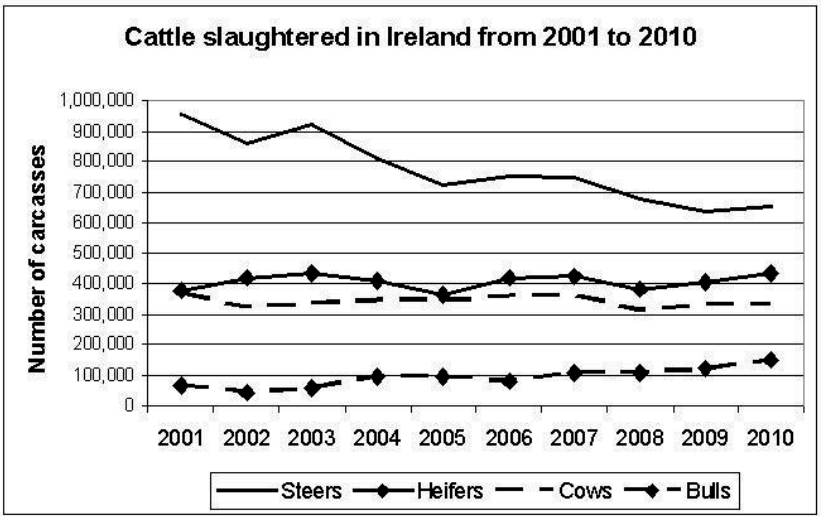


Figure 3. Evolution of cattle slaughtered in Ireland from 2001 to 2010.

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.

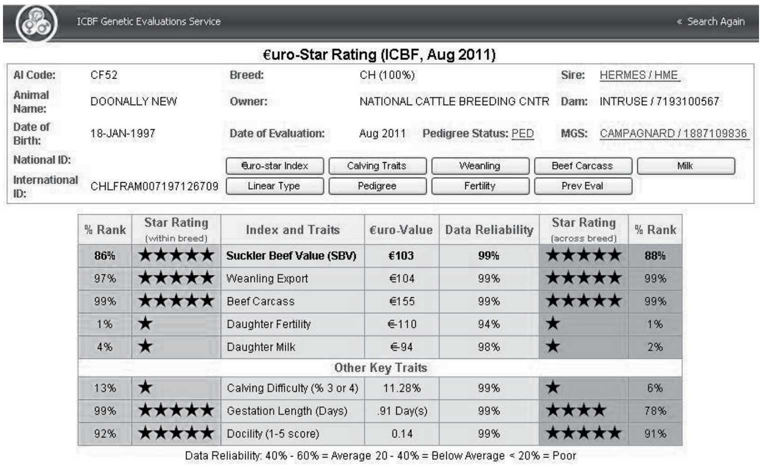
The Suckler Beef Value combines all 4 indexes to reflect the overall profit value of animals. Currently, calving index, weanling export index, carcass index, and replacement index represent 44%, 9%, 35%, and 13%, respectively of the Suckler Beef Value.

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.



€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				

% 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%

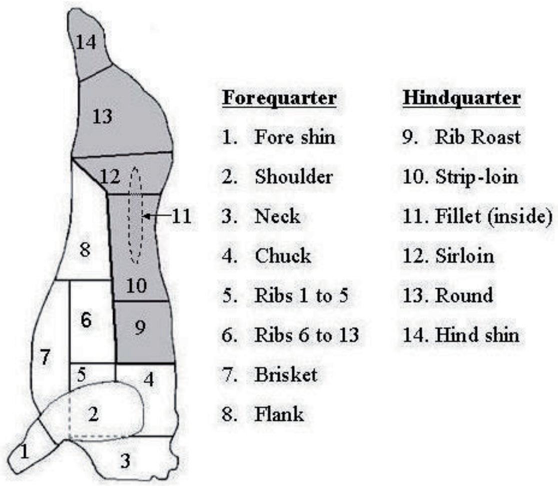


Figure 5. Location of the primal cuts used in Paper I & II.

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).

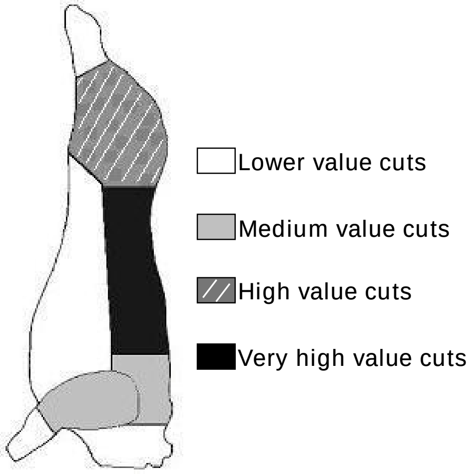


Figure 6. Location of the predicted wholesale cuts used in Papers II, III, & IV.

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.

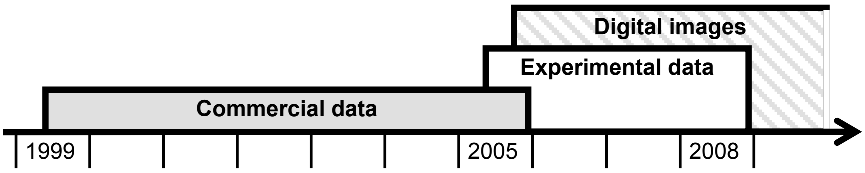


Figure 7. Different data recording periods for carcass cut data and digital images used in Paper II.

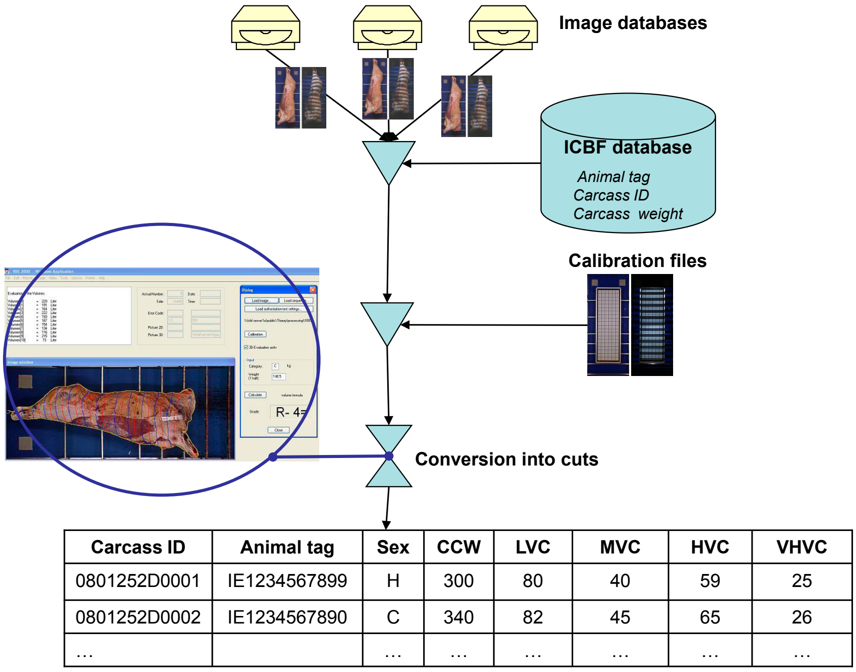
Multivariate analyses studied in Paper II were based on 281 heifers (commercial data), 346 steers, and 74 bulls (experimental data). Images have been collected by ICBF across 25 slaughter houses and stored on hard drives since July 2005. Images were recorded in *tif* format and the approximate size per 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:

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

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*

			EW	Selection index			
Trait	h^2	σ^2_P	(€/unit)	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				✓	✓

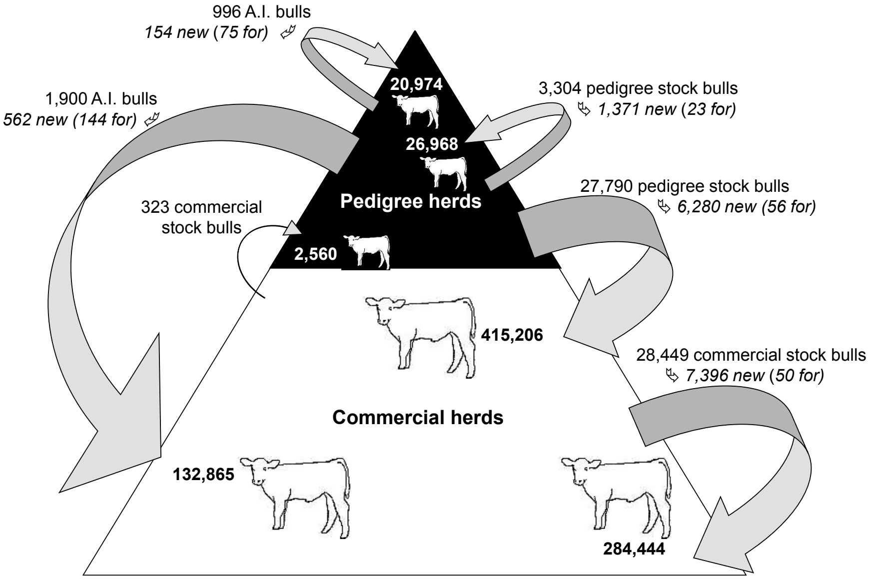
[1] *Calving subindex : calving ease, calf mortality, and gestation length.*

[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.



New = bulls without progeny in 2009 and with progeny in 2010
for = bulls registered outside Ireland

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

		Experimental data		Commercial data	
Primal cut weight (kg)		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).

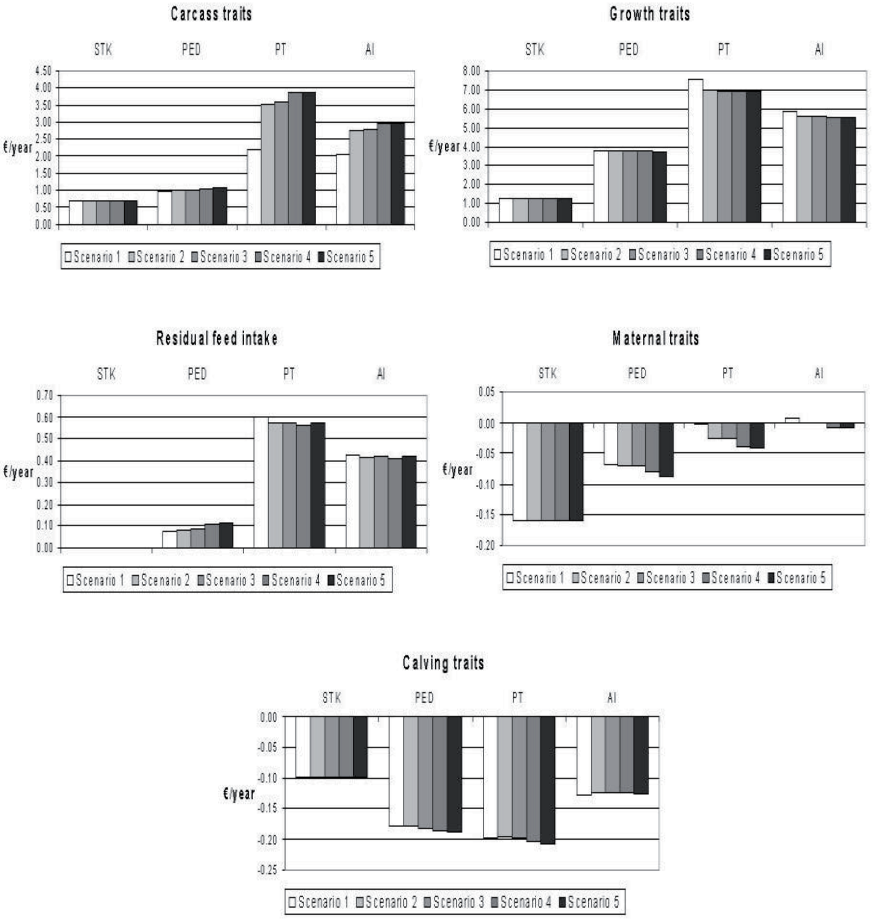


Figure 11. Annual gains in calving, maternal, growth, residual feed intake, and carcass traits calculated across the different candidates, traits, and scenario explored.

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 12th 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 6th 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.

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