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EVALUATION OF LIVE GROWING PIGS OF DIFFERENT GENOTYPES AND SEXES USING COMPUTED TOMOGRAPHY

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UNIVERSIDAD DE ZARAGOZA

Producción Animal y Ciencia de los Alimentos

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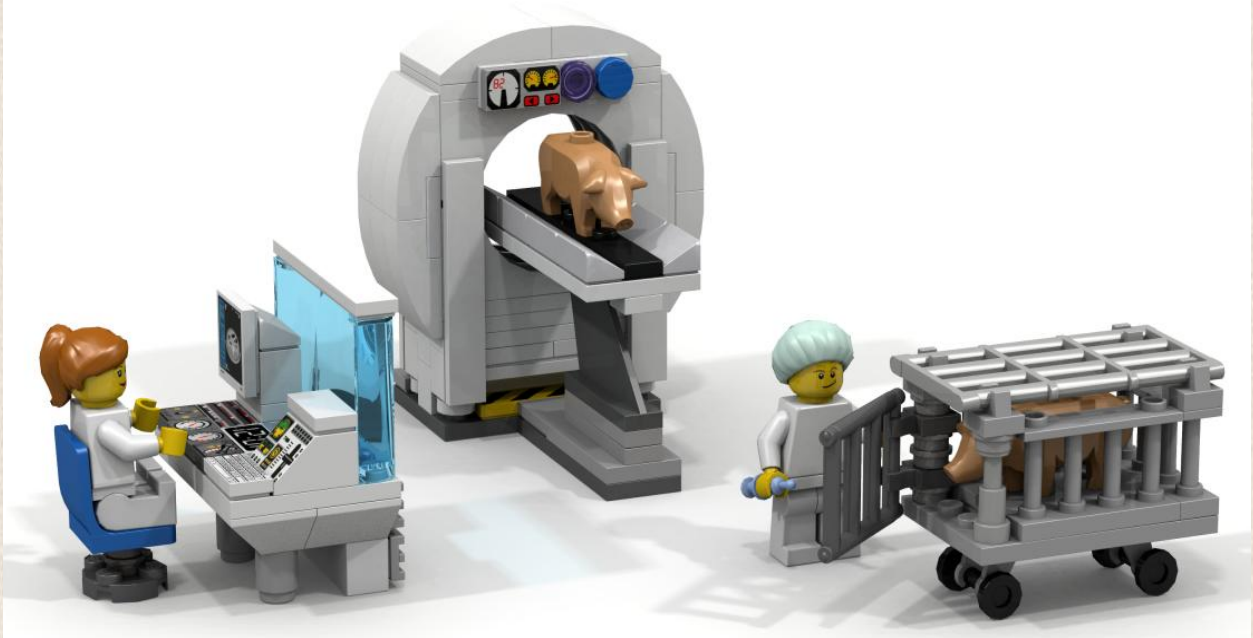
evaluation of live growing Pigs of different genotypes and sexes using computed tomography



Ph. D Thesis
by
Anna Carabús i Flores

Supervisor: Maria Font i Furnols, Ph. D.

Relax. This won't hurt.

Hunter S. Thompson

Evaluation of live growing pigs of different genotypes and sexes using computed tomography.

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Evaluation of live growing pigs of different genotypes and sexes using computed tomography

Anna Carabús i Flores

MARIA FONT I FURNOLS, Ph. D. researcher of the Product Quality Program and director of the Carcass Quality Subprogram at IRTA,

CERTIFIES

This Thesis called "Evaluation of live growing pigs of different genotypes and sexes using computed tomography", written by Anna Carabús i Flores, MSc. Agriculture Engineer, has been carried out under my direction and in fulfillment of the Thesis Project approved on the February 2nd 2011 and it accomplishes with the requirements to qualify for the International Mention and for the degree of Doctor of Philosophy of the University of Zaragoza.

In Monells, June 23th 2015

Maria Font i Furnols, Ph. D.

Als meus pares,

a la tieta Enriqueta

i a l'àvia Ana

(in Catalan)

“Pig farming is a wonderful mixture of scientific precision and massive ignorance”

C. Clark (1998) International Pigletter 18 (3):13

Acknowledgments
Agradecimientos
Agraïments

I would like to dedicate this page to say **THANK YOU** to all the people that have helped me through this "adventure". I know it will sound like a cliché but I really think I will not find the words to express my gratitude for all the people I have met during the last 4 years and, somehow, have helped me. But, as this is about feelings, let me say it in different languages.

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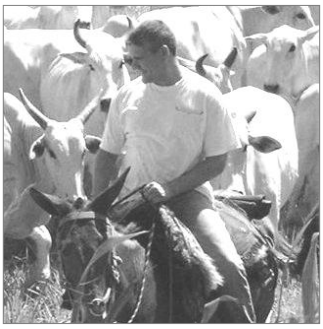
MIL VEGADES GRÀCIES!

Contents

Prologue

by Roberto Sainz, Ph. D.

Professor at the University of California, Davis



Globally, about 70% of agricultural producers rely upon livestock for at least part of their livelihood. Pigs make up a significant proportion of this total. The global swine population stands around 800 million pigs, of which about 18% are in the European Union. These animals provide 112 million metric tons of carcass equivalent, so that pork represents over 36% of the total meat consumed around the world. Swine production system can range from large-scale, highly industrialized farms to small, low-input back yard or communal pig production. The scope and diversity of pig production around the world creates opportunities and challenges for the industry. Pig producers in developed countries typically apply standard production techniques, including animal genotypes, housing and feeding systems. These commercial operations make use of the latest technologies to ensure proper husbandry, animal well-being, and meeting consumer demands. These include state of the art feeding programs, health management, and genetics. The introduction of non-surgical castration, for example, can improve productivity and meat quality, while minimizing stress and potential adverse health outcomes. Likewise, the use of non-invasive imaging techniques such as computed tomography enables evaluation and improvement of meat yield in live animals, for genetic improvement and development of individualized feeding standards, without the need for harvest and dissection. The experimental work described in this thesis included computed tomography scans of growing swine of different ages, sexes, and breeds. Those data were validated against actual carcass dissections, and then used to fit the growth curves of muscle fat, and bone in these different classes of swine. These analyses extracted novel and interesting information from the data, and generated new knowledge about allometric growth in swine. The results have the potential to make significant positive impacts on all segments of the swine industry, improving animal management and well-being as well as product quality, benefitting pork producers and consumers.

Summary

Knowledge of the composition of animal bodies and animal tissue growth is very important for the characterization of the effect of a genotype, the sexual condition, the management or to analyze the feed efficiency and adjust the diet to growth states, because fat and lean composition are dependent on intrinsic and extrinsic factors. The application of computed tomography (CT) to living animals allows analyzing, non-invasively, the evolution of the body composition of a single animal through its growing period. Subsequently, growth and development of the different body tissues can be modeled, without the necessity to slaughter the animal. The Ph. D. Thesis at hand investigates the evolution of the composition of pig bodies from different genetic types (experiment 1) and sexual conditions (experiment 2). Experiment 1 was performed on 90 pigs of three genetic types (all of them were commercial and very used in the swine industry), while experiment 2 was performed on 92 animals with four different sexual conditions (females (FE), entire males (EM), castrated males (CM) and immunocastrated males (IM)). The animals were scanned by CT at 30, 70, 100 and 120 kg live weigh. One subsample for each genetic type and sexual condition (n=5/genetic type and n=4/sexual condition) was slaughtered at the different target weights and were fully or partially dissected. The rest of the animals (animals of the study) were evaluated with the CT at each target weight and, once they reached 120 kg, they were slaughtered. Knowledge gained from slaughtered and dissected animals was used to formulate prediction equations for body and pieces composition. They were then applied to the animals of the study. Predictions were performed independently for each genetic type (Chapter 4) or generalized for all the genetic types and sexual conditions of this work (Chapter 6). Both equations produce good results for the prediction of body composition (Chapter 8). Presenting the individual predictions depending on the genetic type reduces the error (RMSE between 0.011 and 0.886). However, the global equation allows generalizing the predictions for a bigger number of animals, thus, it has preference if the population is mixed or if high level of accuracy is not required. If high accuracy is needed, for instance for genetic companies, individual equations specifically developed for each genetic type are prefered. Results show that tissues grow different depending on the genetic type and sexual condition (Chapter 5 and 7). Tissue that shows the highest allometric coefficient was for fat, corresponding to the fastest deposition. From the different genotypes, LA was the one that shows the fastest deposition of fat (Chapter 5). With respect to the sexual condition, CM and IM exert the highest deposition value for the fat, with EM and FE showing the lowest (Chapter 7). Lean tissue behaves in the opposite way as fat. The IM and CM had a very similar behavior with respect to the deposition speed of fat and lean, even IM behave as EM until the study animals received the second dose of the immunocastration vaccine. In conclusion, CT can be very useful for the meat industry due to its ability to predict quality parameters, as well as carcass composition, at early growth stage. This technique can thus bring economic benefits for the whole livestock industry and meat chain.

Resumen

Conocer la composición corporal en animales vivos y la deposición de los diferentes tejidos durante su crecimiento es de vital importancia para, entre otras cosas, caracterizar el efecto de una genética, la condición sexual, el manejo e incluso analizar la eficiencia alimentaria y adecuar la dieta a cada estadio de crecimiento, ya que la composición en tejido graso y muscular del cuerpo de los animal está influenciada tanto por factores intrínsecos como extrínsecos. La aplicación de la tomografía computerizada (CT) en animales vivos permite analizar, de manera no invasiva, la evolución de la composición corporal de un mismo animal a lo largo del período de crecimiento. Esto permite modelizar el crecimiento y desarrollo de los diferentes tejidos del cuerpo sin necesidad alguna de sacrificar el animal. Esta tesis propone conocer la evolución de la composición corporal de cerdos de distintas genéticas (experimento 1) o sexos (experimento 2). El experimento 1 estaba formado por 90 animales de tres genéticas distintas (todas ellas comerciales y altamente utilizadas en el sector), y el experimento 2 estaba formado por 92 animales de cuatro condiciones sexuales distintas (hembras (FE), machos enteros (EM), machos castrados quirúrgicamente (CM) y machos inmunocastrados (IM)). Los animales se evaluaron con el CT a 30, 70, 100 i 120 kg de peso objetivo. Una submuestra de animales de cada genética y sexo (n=5/genética y n=4/sexo) se sacrificaron a los diferentes pesos objetivo y se disecaron total o parcialmente. El resto de animales (animales de seguimiento), se evaluaron con el CT a cada peso objetivo y, al llegar a 120 kg, se sacrificaron. A partir de los animales sacrificados y disecados, se obtuvieron ecuaciones de predicción, de la composición corporal y de las diferentes piezas, que se usaron en el resto de animales de seguimiento. Las predicciones se hicieron para cada genética independientemente (Chapter 4) o bien generalizadas para todas las genéticas y sexos (Chapter 6). Ambas ecuaciones fueron adecuadas para la predicción de la composición corporal (Chapter 8). En este sentido, presentar las predicciones individuales según la genética reduce el error (RMSE entre 0.011 y 0.886). No obstante, la ecuacion global permite generalizar las predicciones para un mayor número de animales, así pues, es preferible usarla cuando la población está mezclada o cuando el parámetro estimado no requiere un alto valor de precisión. Cuando esta precisión se requiere, como es el caso de compañías genéticas, es preferible utilizar las ecuaciones individuales, específicamente desarrolladas para cada genética. Los resultados muestran que los tejidos crecen de manera diferente según la genética s y el sexo (Chapter 5 y 7). El tejido que mostró el mayor coeficiente alométrico fue la grasa, indicando el índice de deposición más rápido de este tejido. De entre las distintas genéticas, LA fue quien mostró la deposición de grasa más rápida (Chapter 5), mientras que respecto a los sexos, los CM e IM fueron los que tuvieron un índice de deposición de grasa más elevado y más lento en los EM y FE (Chapter 7). El comportamiento de la deposición de magro fue inverso al de la grasa. Añadir que, los IM y CM tuvieron un comportamiento muy similar respecto a la velocidad de deposición de grasa y magro, a pesar que los IM se comportaron como los EM hasta que recibieron la segunda dosis de la vacuna de immunocastración. Finalmente, en las condiciones de realización de este trabajo se puede concluir que el CT puede ser muy útil para la industria cárnica, porque los parámetros de calidad y composición de la canal se pueden conocer a pesos muy tempranos. Como resultado, el uso de esta información puede aportar beneficios económicos para todos los integrantes de la cadena alimenticia.

Resum

Conèixer la composició dels animals vius i la deposició dels diferents teixits durant el seu creixement és de vital importància per, entre d'altres, caracteritzar l'efecte d'una genètica, la condició sexual, el maneig o, fins i tot, analitzar l'eficiència alimentària i adequar la dieta a cada estadi de creixement, ja que la composició del teixit gras i muscular del cos dels animals està influenciada tant per factors intrínsecs com extrínsecs. L'aplicació de la tomografia computeritzada (CT) en animals vius permet analitzar de manera no invasiva l'evolució de la composició corporal d'un mateix animal al llarg del període de creixement. Això permet modelitzar el creixement i desenvolupament dels diferents teixits del cos sense necessitat de sacrificar l'animal. Aquesta Tesi proposa conèixer l'evolució de la composició corporal de porcs de diferents genètiques (experiment 1) i sexes (experiment 2). L'experiment 1 estava format per 90 animals de tres genètiques diferents (totes elles comercials i altament utilitzades en el sector) i, l'experiment 2 estava format per 92 animals de quatre condicions sexuals diferents (femelles (FE), mascles enters (EM), mascles castrats (CM) i mascles immunocastrats (IM)). Els animals es van avaluar amb el CT a 30, 70, 100 i 120 kg de pes viu. Una submostra d'animals de cada genètica i sexe (n=5/genètica i n=4/sexe) es van sacrificar a diferents pesos objectiu, tot seguit se'ls va practicar la dissecció parcial o total. La resta d'animals (animals de seguiment) es van avaluar amb el CT a cada pes objectiu i, un cop arribats a 120 kg, es van sacrificar. A partir dels animals sacrificats i les disseccions, es van obtenir equacions de predicció de la composició corporal de tot el cos i de les seves diferents peces, aquestes equacions es van aplicar als animals de seguiment . Les prediccions es van fer per cada genètica (Chapter 4) o bé generalitzades per genètica i sexe (Chapter 6). Ambdues equacions resultaren ser adequades per a la predicció de la composició corporal (Chapter 8). En aquest sentit, presentar les prediccions individuals segons genètica redueix l'error (RMSE entre 0.011 i 0.886). No obstant, l'equació global permet generalitzar les prediccions per un major nombre d'animals, així doncs, és preferible utilitzar-la quan la població està barrejada o quan el paràmetre estimat no requereix un alt valor de precisió. Quan es requereix aquesta precisió, com en el cas de les companyies genètiques, és preferible utilitzar equacions individuals, específicament desenvolupades per a cada genètica. Els resultats mostren que els teixits creixen de manera diferent segons la genètica i el sexe (Chapters 5 i 7). El teixit que va demostrar un coeficient al·lomètric més alt va ser el teixit adipós (la grassa), indicant un major índex de deposició per aquest teixit. Entre les diferents genètiques, Landrace x Large White (LA), va ser la que va mostrar la deposició de grassa més ràpida (Chapter 5), mentre pel que fa als sexes, aquests varen ser els mascles castrats (CM) i els mascles immunocastrats (IM) i la deposició de greix va ser més lenta en els mascles enters (EM) i les femelles (FE) (Chapter 7). El comportament de la deposició de magre va ser invers al de la grassa. Afegir que, els IM i els CM van tenir un comportament molt similar respecte a la velocitat de deposició de greix i magre, tot i que els IM es van comportar com els EM fins que van rebre la segona dosi de la vacuna. Finalment, en les condicions de realització d'aquest treball es pot concloure que el CT pot ser de gran utilitat per a la industria càrnia perquè els paràmetres de qualitat i composició de la canal es poden conèixer a pesos molt baixos. Com a resultat, l'ús d'aquesta informació pot aportar beneficis econòmics per a tots els integrants de la cadena alimentària.

List of Publications

The following list contains the Journals publications resulting from this Doctoral Thesis:

Carabús A, Gispert M, Brun A, and Font-i-Furnols M 2015. Image analysis techniques to study de composition of live pigs: an overview. Spanish Journal of Agricultural Research. Submitted. (JCR, impact: 0.703, 2nd quartil, category Agriculture, Multidisciplinary)

Author's contribution: Writing the paper, with contributions from the other authors.

**Included in Chapter 1*

Font-i-Furnols M, **Carabús A**, Pomar C and Gispert M 2015. Estimation of carcass and cuts composition from computed tomography images of growing live pigs of different genotypes. Animal 9 (1) 166-178. (JCR, impact: 1.784, 1st quartil, category Agriculture, Dairy and Animal Sciente)

Author's contribution: The experimental study (scanning of the animals and visual image analysis), with the help of the other authors. Contribution in the writing of the paper.

**Included in Chapter 4*

Carabús A, Gispert M, Brun A, Rodríguez P and Font-i-Furnols M 2014. *In vivo* computed tomography evaluation of the composition of the carcass and various cuts of growing pigs of three commercial crossbreeds. Livestock Production Science 170, 181-192. (JCR, impact: 1.171, 2nd quartil, category Agriculture, Dairy and Animal Sciente)

Author's contribution: The experimental study (scanning of the animals, visual image analysis and statistics), with the help of the other authors.

Writing the paper, with contributions from the other authors.

**Included in Chapter 5*

Carabús A, Sainz RD, Oltjen JW, Gispert M and Font-i-Furnols M 2015. Predicting fat, lean and the weight of primal cuts of pigs of different genotypes and sexes using computed tomography. Journal of Animal Science 93: 1-10. (JCR, impact: 1.920, 1st quartil, category Agriculture, Dairy and Animal Sciente)

Author's contribution: The experimental study (scanning of the animals, visual image analysis and statistics), with the help of the other authors. Writing the paper, with contributions from the other authors. This paper was selected as a late-breaking abstract at the ASAS 106th Annual Meeting, July 2014, Kansas City, MO (USA).

**Included in Chapter 6*

Carabús A, Sainz RD, Oltjen JW, Gispert M and Font-i-Furnols M 2015. Growth of total fat and lean and the primal cuts in relation to estimated mature weight in pigs of different sexual conditions, assessed using computed tomography. Animal. Submitted. (JCR, impact: 1.784, 1st quartil, category Agriculture, Dairy and Animal Sciente)

Author's contribution: The experimental study (scanning of the animals, visual image analysis and statistics), with the help of the other authors. Writing the paper, with contributions from the other authors.

**Included in Chapter 7*

Carabús A, Gispert M and Font-i-Furnols M 2015. Keys to select a prediction model for carcass composition from computed tomography images. Agricultural Systems. Submitted. (JCR, impact: 2.906, 1st quartil, category Agriculture, Multidisciplinary)

Author's contribution: Writing the paper, with contributions from the other authors.

**Included in Chapter 8*

The following list contains the Dissemination Journals publications resulting from this Doctoral Thesis:

Carabús A, Fulladosa E, Garcia-Gil N, Gispert M y Font i Furnols M 2011. Aplicaciones de la tomografía computerizada en el campo de producción y tecnología de alimentos. Eurocarne núm. 202, pg. 60-68.

Author's contribution: Writing the paper, with contributions from the other authors.

**Included in Chapter 1*

Carabús A, Gispert M, Brun A, Francàs C, Tibau J y Font i Furnols M 2012. Evaluación, in vivo, de distintos cruces genéticos porcinos a 30 kg mediante tomografía computerizada. Eurocarne núm. 206, pg. 108-114.

Author's contribution: Writing the paper, with contributions from the other authors.

**Not included in this Ph. D. Thesis*

Carabús A, Gispert M, Brun A, Francàs C, Pedernera C, Soler J, Tibau J, Font i Furnols M 2012. Evaluación, in vivo, de distintos cruces genéticos porcinos a 100 kg mediante tomografía computerizada. Eurocarne núm. 212, pg. 104-110.

Author's contribution: Writing the paper, with contributions from the other authors.

**Not included in this Ph. D. Thesis*

Carabús A, Gispert M, Brun A, Font i Furnols M 2015. Estudio del crecimiento de los tejidos en cerdos de diferentes genéticas y sexos analizados in vivo mediante tomografía computarizada. Eurocarne núm. 235, pg. 177-183.

Author's contribution: Writing the paper, with contributions from the other authors.

**Not included in this Ph. D. Thesis*

The following list contains the communications in different Congresses:

In 2014

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Ph. D. Thesis presentation

Live animal evaluation for body composition has been an important research goal in animal agriculture. Recently, there has been a growing interest among researchers for the application of image analysis for livestock animals, particularly swine, sheep and beef. Image analysis involves different techniques which have the potential to accurately estimate carcass body composition (for yield and quality) in live animals. This should benefit the industry, enhancing genetic selection programs and also allowing it to move to a value-based marketing system. A functional value-based marketing system will provide a means of identifying the value of individual animals or carcasses. The swine industry has set a high priority for developing an instrument grading system and computed tomography (CT) has been identified as having the potential for achieving the goal. CT is commonly used in human medicine (Van Ginneken *et al.,* 2010, Jongbloed *et al.,* 2005) in agriculture (Elliot *et al.,* 2010) and in forestry (Schmoldt et al, 1999). At the same time, this technique has been applied in the food industry and has been proved as a very valuable tool. In fruits, it has been used to determine the water content in apples (Tollner *et al.,* 1992), the internal changes in peaches (Barcelon *et al.,* 1997) or the maturity degree in tomatoes (Brecht *et al.,* 1991). It has also been used in livestock animals and their carcasses. In aquaculture, salmon's shape and its fat content were evaluated (Einen *et al.,* 1998); in poultry, the lean production in Broilers was studied (Remingnon *et al.,* 1997); in ovine, sheep's composition were determined (Toldi *et al.,* 2007); in beef, carcass weight was predicted analyzing primal cuts (Prieto *et al.,* 2010) and in swine, CT have been used to study the deposition and distribution of fat (Kolstad, 2001), the composition of live pigs (Luiting *et al.,* 1995) and carcasses (Romvári *et al.,* 2006; Font i Furnols *et al.,* 2008). It has also been used to predict the amount of fat and water in the ham (Fulladosa *et al.,* 2009). As commented, the application of CT in livestock animals is important to determine the body and carcass composition and, in economic terms, it becomes relevant because of the prediction of lean content that can be done non invasively, avoiding carcass dissection (without the necessity of destroying the carcass).

Measurements obtained by CT have a low prediction error, however, the cost to scan a full animal or carcass is high. One way to reduce the cost could be to study specific anatomical points or specific cuts, which it would allow to reduce the amount of image analyzed and, at the same time, the total cost.

This PhD thesis proposes the use of CT images in live pigs, to study their phenotypic differences between genotypes (Experiment 1) and sexual conditions (Experiment 2), from 30 to 120 kg live weight, and to achieve prediction models with high level of accuracy to obtain the weight of the main tissues and cuts. In order to obtain accurate prediction models, in both experiments there were a group of animals scanned at each target weight (30, 70, 100 and 120 kg) and another group (5 of each genotype and 4 of each sexual type) slaughtered and dissected at different target weights. Besides this presentation, this thesis is organized in different chapters. The content of these chapters is as follows:

- Chapter 1 contains an introduction divided in two parts. After presenting the definition of the techniques used to study live animals and other related terms that are used in this work, special emphasis is put in their applications and their contributions to the swine industry

- Chapter 2 presents the main and specific objectives of this Thesis

- Chapter 3 explains the methodology used. It includes the animals selected, the anesthesia applied, the scanning parameters and the statistics elected for each occasion

- Chapters 4, 5, 6, 7 and 8 present the results. Chapter 4 is mainly focused in the slaughtered animals at each target weight of the first experiment and provides different predicting models, comparing them and selecting the most appropriate

- Chapter 5 contains the phenotypic differences between animals of experiment 1 from 30 kg to 120 kg. Moreover, this chapter uses prediction equations obtained in Chapter 4 to provide information of the allometric growth of the main tissues

- Chapter 6 provides prediction equations for the main tissues and cuts of the animals of different genotypes and sexes. These equations are the same for all the animals, meaning no distinction between genotype or sex. Also, two types of equations are shown, depending of the predictor used: CT predictors or potential on farming predictors, which can provide useful information on farming conditions without the necessity of the CT device

- Chapter 7 is mainly focused in the animals of experiment 2. It presents the allometric growth of the main tissues and cuts, using prediction equations of Chapter 6. It also provides the estimation of maturity weight, using Gompertz function, and the relation between the allometric model and the estimated maturity body weight

- Ending with the results, Chapter 8 compares the accuracy of the two main prediction models used in this thesis, the ones presented in Chapter 4 and in Chapter 6, and provides keys to distinguish the best option when different prediction models are suggested

- Chapter 9 presents a general discussion with the results obtained in the previous chapter

- Chapter 10 gives the most relevant conclusions of this Thesis

- Finally, the Annexes include different information, such as the original Spanish paper in its original letter

All the references used in this PhD are included at the end of each chapter. Moreover, chapters 1, 4, 5, 6, 7 and 8 are presented as their paper published or submitted in the scientist journal.

Another way to gather all this concepts together is presented in Figure 1.

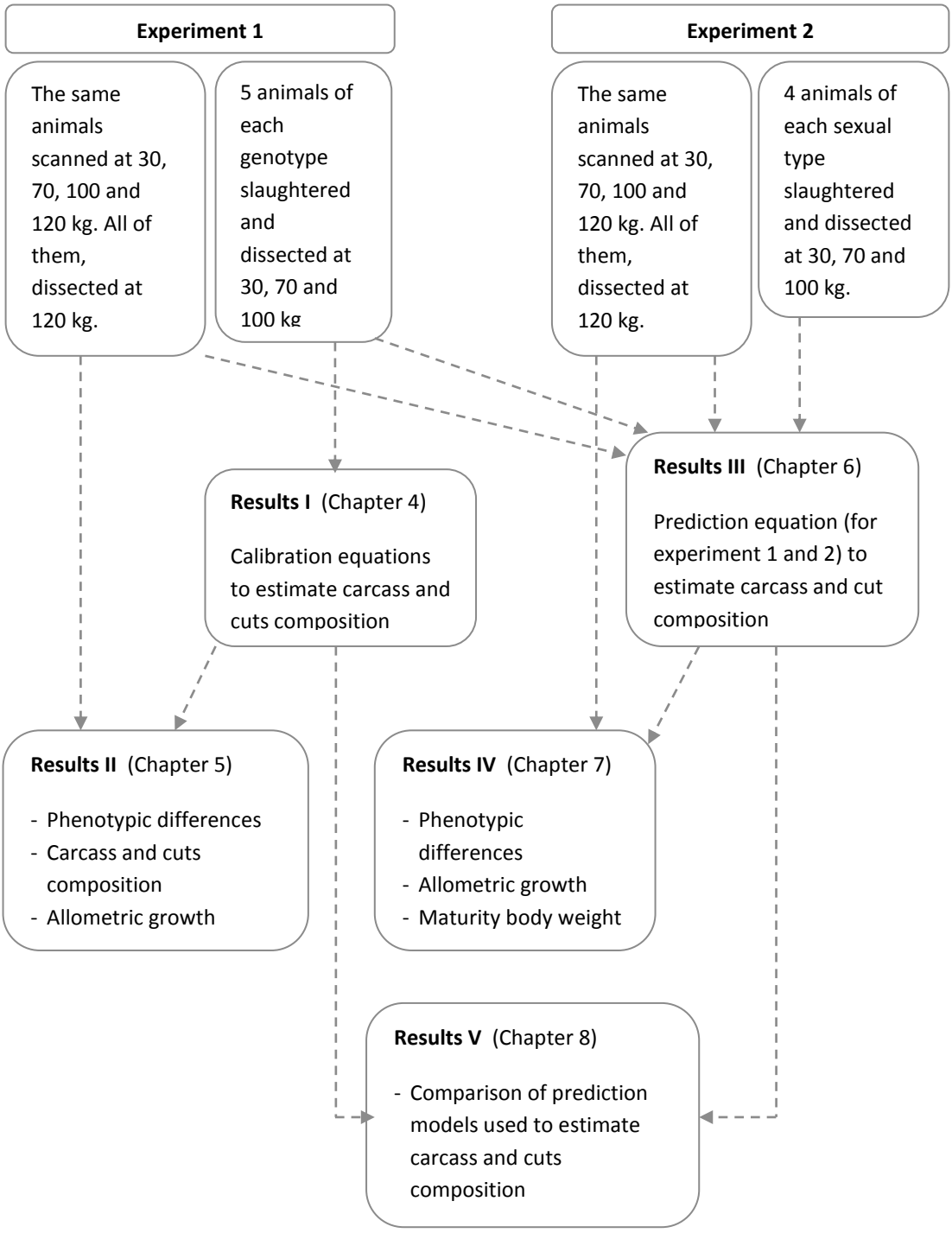

Figure 1. Conceptual diagram that represents the structure of the Thesis

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Chapter 1

Introduction. Part I

The content of this chapter is submitted in the Spanish Journal of Agricultural Research.

This chapter is divided in two parts. Regarding the first part of the chapter, images technologies to evaluate pigs' composition are described first, because these are the research fields that provide conceptual support for the image analysis. Then, the uses of these techniques, as well as the engineering software used to analyze the images, are presented. And finally, the applications of image analysis in the swine industry are reviewed and compared. The second part presents deeper information about computed tomography and its uses in the agrifood industry field.

Image analysis techniques to study the composition of live pigs: a review

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This chapter deals with:

- Recent advance in image processing analysis for live pigs
- Advantages and disadvantage between devices, variables and measurements analyzed
- Results and application of image analysis in the swine industry

Highlights

Imaging techniques are useful for determining the body composition of live pigs
Obtained precision and accuracy depen on the technique, the protocol, device and image analysis software
Imaging technologies can improve feeding, breeding and processing

Abstract

Image analysis techniques are increasingly being applied to livestock animals. This paper overviews recent advances in image processing analysis for live pigs, including ultrasound, visual image analysis by monitoring, dual-energy x-ray absorptiometry, nuclear magnetic resonance imaging and computed tomography. The advantages and disadvantages of different devices, the variables and measurements analysed, the predictions obtained using these measurements and their accuracy are discussed in the present paper. The correlations between image processing techniques for evaluating pig body composition are demonstrated. Computed tomography and nuclear magnetic resonance yield useful results for the estimation of the amount of fat and lean mass, but the accuracy of these techniques for predicting intramuscular fat is not acceptable and must be improved. Ultrasound is not sufficiently accurate when high precision in estimating pig body composition is necessary but can provide useful information in agriculture to classify pigs for breeding purposes or before slaughter. Improvements in factors, such as the speed of scanning, cost and image accuracy and processing, would advance the application of image processing technologies in livestock animals.

Keywords
body composition, ultrasound, visual image analysis, dual-energy x-ray absorptiometry, computed tomography, magnetic resonance image

Introduction

An ideal technique for the measurement of body growth and composition in livestock animals is non-invasive, non-destructive, accurate, easy to perform and applicable to a wide range of ages and body weights (BWs). Non-invasive techniques allow tissue changes in the same animal to be followed to study development over different stages. However, invasive techniques, such as serial slaughter of collaterals or descendant animals and dissections, continue to be used to determine body composition or calibrate various devices. Based on image analysis, Font-i-Furnols *et al.* (2015) and Carabús *et al.* (2015) analysed serial slaughter data from 30 to 120 kg for gilts of different genotypes and pigs of different sexes, respectively, and obtained prediction equations for body composition based on computed tomography images. In these studies, serial slaughter was used for device calibration and was replaced by *in vivo* estimations once the equations were validated. However, in others works, such as those by Gjerlaug *et al.* (2012) and Lambe *et al.* (2013), dissections were not used, and information was obtained directly from image analysis without the application of a prediction equation. Thus, *in vivo* estimations can be performed using non-invasive technologies based on image analysis. The five main non-invasive technologies are ultrasound (US), visual image analysis by monitoring (VIA), dual-energy x-ray absorptiometry (DXA), magnetic resonance imaging (MRI), and computed tomography (CT). Image processing techniques have been developed rapidly. These technologies are reliable and can quantitatively characterise complex sizes, shapes and densities of tissue in live animals. However, these five technologies are very different, and although they can be used for the same purpose, each one has different specifications that are described in detail in the present paper. The purpose of this paper is to provide an overview of the technologies and associated methodologies for studying pig composition *in vivo*, describe how these techniques work and their main applications and, finally, to present certain of the most relevant results obtained in growing pigs using these devices.

Technologies to evaluate pig composition

These technologies can be divided into two groups: invasive and non-invasive technologies. Invasive technologies are reviewed only briefly because this paper is focused on non-invasive technologies.

Invasive techniques

Invasive technologies can be reversible (such as biopsy, after which the affected zone is regenerated) or irreversible (such as serial slaughtering).

Serial slaughtering is the most-used invasive technique to study pig body composition. Pigs are slaughtered at different growth stages, followed by full or partial dissections and sampling. Serial slaughtering provides information about pig carcass composition to enable improvements in the efficiency of the production systems at any point of the meat chain. Serial slaughtering has also been used to identify differences in growing pigs based on genetics (Fisher *et al.,* 2003) or sexual conditions (Schinckel *et al.*, 2008). For example, Fisher *et al.* (2003) compared Landrace, Pietrain

and Meishan pigs using five serial slaughters. Pietrain had the widest ham and shoulder, lowest subcutaneous fat content and highest lean content, whereas Landrace had the longest body in relation to age of slaughter, consistent with the results obtained by Carabús *et al,* (2011) using a non-invasive technique, CT. Serial slaughtering has also been used to study body tissue and chemical body composition in relation to empty body weight or carcass weight. Schinckel *et al.* (2008) observed that although maximal protein deposition and BW growth were not likely achieved between 30 and 60 kg of BW, substantial differences in nutrient requirements existed between genetic populations and sexes. Serial slaughtering has also been used to examine the development of primal cuts and differences among genotypes in lean weight of the primal carcasses cuts and the growth of organs (Gu *et al.,* 1992). Serial slaughtering and subsequent dissection and cutting are the most common methods to determine the physical composition of the body. As an invasive technique, serial slaughtering enables the study of growth in a pig population but cannot be performed on the same animal in different stages, and thus non-invasive techniques are more relevant. However, serial slaughtering can be used to calibrate non-invasive devices when studying pig body composition. Once the device is calibrated, serial slaughtering is only needed to confirm the calibration equation periodically.

Biopsy *in vivo* is another invasive technique that provides relevant information about tissue composition. Bosch *et al.* (2009) performed 1 to 3 biopsies of the *longissimus dorsi* (LM) in Duroc pigs at different stages of growth. The information obtained by biopsy was used in combination with other measurements to estimate intramuscular fat content and fatty acid composition in *in vivo* and *post mortem* samples of pigs.

Non-invasive techniques

In animal science, a non-invasive technique permits the study of an animal without piercing any tissue. Several non-invasive techniques are commonly used in live pigs. A common feature of most non-invasive techniques for body or carcass composition measurements is a reliance on electromagnetic or mechanical energy, which can pass completely or partially through body or carcass tissue, such as muscle, adipose tissue and bone (Scholz *et al.,* 2015).

VIA is the acronym for visual image analysis by monitoring, also known as video image analysis and computed aided design (CAD). VIA can include one or more cameras to acquire 2D images or video images. This technique was developed in the USA specifically for objective beef carcass evaluation in the early 1980s (Cross *et al.,* 1983). VIA has also been extensively used to classify carcasses into payment categories and to improve the consistency of SEUROP classification compared to visual appraisal (Allen and Finnerty, 2000; Craigie *et al.,* 2012). However, the application of VIA to live animals has been more limited. Doeschl-Wilson *et al.,* (2005) used it to describe pig growth in terms of size and shape and concluded that the analysis of shape data combined with composition data from dissected carcasses was significantly related ($P<0.05$) to carcass composition at all growth stages and that this relationship varied among genetic populations. This technique is useful in agricultural applications, and no human-animal interaction is required. However, the information provided solely concerns the external portion of the body,

and no internal image of the pig is obtained. The proximity of electrical outlets for non-portable cameras, the proper positions of cameras (without death nooks), the light intensity and the cleanliness and dust control of the farm are major factors to consider when using this equipment.

US enables the acquisition of internal images for use in body composition evaluation. There are two models for ultrasonic imaging: A-mode (amplitude modulation) and B-mode (brightness modulation). A-mode is the simplest type of US. A single transducer scans a line through the body, and the echoes are plotted on screen as a function of depth. In B-mode US, more commonly known as 2D mode, a linear array of transducers simultaneously scans a plane through the body that can be viewed as a two-dimensional image on screen. Ultrasonic image analysis has been performed in live animals or carcasses to measure fat thickness and assess the quality of meat (Fortin *et al.,* 2003). Backfat thickness, muscle width and area are indirect measurements of body composition typically obtained with the US device. Additional factors to consider are the cost of the equipment, the length of battery life for portable units, and the proximity of electrical outlets for non-portable units. For portable machines, batteries are scheduled to operate continuously for ~3 hours, and most US evaluations require approximately 1-2 minutes per image acquisition (Newcom *et al.,* 2002; Mörlein *et al.,* 2005; Bahelka *et al.,* 2009; Maignel *et al.,* 2010; Lakshmanan *et al.,* 2012). US has also been used to study intramuscular fat in live pigs (Newcom *et al*., 2002).

DXA is an improved form of X-ray technology that is used mainly to measure bone density (Figure 1). The determination of body and carcass composition by dual X-ray absorptiometry is based on the different X-ray attenuation coefficients at low and high X-ray spectral levels for soft tissue and bone mineral. DXA provides a 2D scan image of the whole body or region of interest. In addition, the image can be analysed as a whole or regionally by semi-automatically or manually defining regions of interest (Mitchell *et al.,* 2002). In addition to the amounts of soft lean or fat tissue and bone mineral content, DXA also provides a measure of bone mineral density (d/cm^2). Different generations of DXA machines use either pencil or fan-beam technology. A whole body scan with a rather slow but very accurate pencil-beam scanner can take 35 minutes, whereas a whole body scan with a cone-beam scanner takes less than 3 minutes (Scholz *et al.,* 2015).

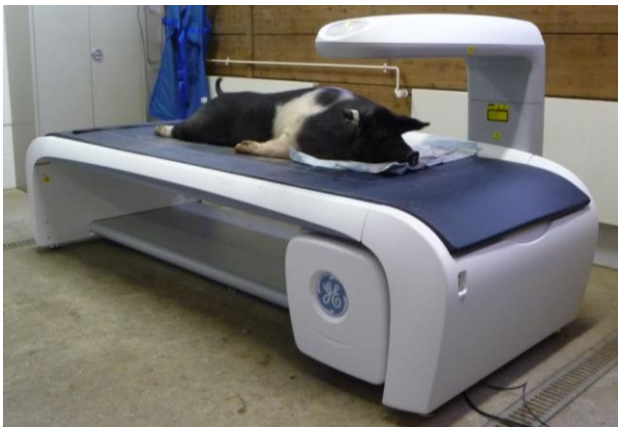

Figure 1. Scanning of a live pig by DXA. Photo courtesy of Armin M. Scholz from Ludwig Maximilian University of Munich.

CT is a non-invasive technique that permits internal images of the patient, in this case, livestock animals (Figure 2), to be obtained. CT is one of the best techniques for studying the body composition of live pigs (Kolstad, 2001). CT is based on the attenuation of X-rays passing through the body. The attenuation is the difference between the emitted X-ray and the X-ray received by the detector and is expressed in Hounsfield (HU) values in a matrix of voxels (3D pixels) presented in the grey or HU scale, which represents colours from black (low density) to white (high density) (Figure 3a). The object of interest is measured in a simple manner from many angles (360º), and thus the density of an individual voxel is not affected by the densities of the neighbouring voxels. Thus, structures of high and low density can be resolved, even if they are close to other structures. The distribution of the attenuation of an X-ray is mathematically calculated as a projection of reconstruction (Cann, 1988) and is presented by the software of the device as a 2D image. Although the image is presented in 2D, the width of the X-ray used permits the calculation of the density and the real volume. As CT provides 3D images, the measurements obtained with this device are good predictors of body composition in live pigs (Luiting *et al.,* 1995) and pig carcasses (Font-i-Furnols and Gispert, 2009). However, due to the emission of X-rays, the equipment must be isolated in a room with leaded walls, and during scanning, the operator is normally in another room close to the device with a leaded window to visualise the scanning while it occurs.

An additional factor to consider is the cost of the equipment, which is 300,000 to 600,000 € (Kongsro *et al.,* 2009), although there is market for used devices from human medical facilities. Another factor is the radiation exposure, which is a major concern for humans and animals. Finally, CT equipment can be portable (Daumas and Monziols, 2011), *i.e.*, placed inside a truck, which is very useful for working under farming conditions, or non-portable, *i.e.*, fixed in a room.

Figure 2. Scanning of a pig by computed tomography at 30 and 120 kg at IRTA's installations.

MRI, magnetic resonance imaging, is a non-invasive diagnostic method that has been used in humans, domestic animals and, recently, livestock animals and carcass evaluation. The basic principle of this method relies on the properties of atomic nuclei with an odd number of protons

or neutrons (or both), which absorb and reemit radio waves when placed in a powerful magnetic field. Tissues containing water molecules are used to create a signal that is processed to form an image of the body. Each tissue returns to its equilibrium state after excitation by the independent processes of T1 (spin-lattice) and T2 (spin-spin) relaxation. The intensity of the emitted signal is related to the number of protons present in a given volume. T1 and T2 are both very important and are constant values that depend on the studied tissue (and temperature). To generate a good MRI image, different tissues must be classified according to these constants. Either a T1 weighted image (the contrast between tissues is based on T1 differences) or T2 weighted can be generated. MRI acquisitions are generally quite long, and T2 weighted acquisitions are longer than T1 weighted acquisitions. Thus, if T1 weighted acquisition enables sufficient contrast, the T2 weighted acquisition is not performed due to the long sequence required. Spin echo and gradient echo are the methods used to excite protons. The main difference between these methods is that the gradient echo sequence creates a chemical shift between water and fat, thereby improving the contrast between them. Gradient echo is generally used in "fat-suppression" sequences (Monziols *et al.,* 2006). Spin echo is a more classic excitation method in which no chemical shift is induced, and the signal observed is directly linked to the T1 or T2 weighting. MRI has substantial potential for livestock evaluation and as a non-invasive technique for estimating the composition of pigs with different live weights (Mitchell *et al.,* 2001; Kremer *et al.,* 2013). Moreover, as a radiation-free device, there are no concerns for the use of MRI in humans and animals, and its price, approximately 100,000€, is considerably lower than that of CT (Kremer *et al.,* 2013). However, due to the magnetic field, more time is required for acquisition compared to other devices, and portable devices are not possible. Table 1 presents the main advantages and disadvantages of these techniques and devices.

Table 1. Advantages and disadvantages of non-invasive techniques applied in animal science

Equipment	Information	Advantages	Disadvantages
CT	Density Shape	3D images Fast Possibility of a portable device Internal images Superior bone tissue contrast compared to MRI	Anaesthesia or sedation required Ionising radiation Most expensive device
DXA	Density Shape	Fast Internal images Superior bone tissue contrast compared to MRI Intermediate price	2D images Anaesthesia or sedation required Ionising radiation (lower than CT)

MRI	Density Shape	No ionising radiation Internal images 3D images Superior soft tissue contrast compared to CT	No metals allowed due to magnetic field Slow image acquisition Anaesthesia or sedation required Portable device not possible Expensive device
VIA	Shape	Anaesthesia or sedation not required Useful in farm conditions Real-time image in movement Video recording possible Cheaper than CT, DXA and MRI	2D images Only external view, no tissue contrast
Ultrasound	Density	Anaesthesia or sedation not required Real-time image in movement Video recording possible Fast Portable device Useful in farm conditions Cheaper than CT, DXA and MRI	2D images Poor tissue contrast

HOW do these techniques work?

First step: Preparation of the animal

Anaesthesia or sedation of pigs is not required for VIA and US measurement, but stable readings can only be obtained when the animal is not moving, unless the reason for the study is to examine animal movement (Kongsro, 2013). By contrast, anaesthesia or sedation is required for DXA, MRI and CT. First, the pigs must be fasted for several hours. The examination then begins with weighing of the pigs to calculate the dose of anaesthetic or sedative. A combination of two or more products is generally used to anaesthetise pigs. Kolstad *et al.* (2001) used Azaperon (4 mg/kg LW) followed by Phentotal sodium (5 mg/kg LW). Giles *et al.* (2008) used Yohimbine (10 mg/ml), and Carabús *et al.* (2014) sedated animals intramuscularly with azaperon (0.1 mg/kg BW) and anaesthetised them with ketamine (0.2 mg/kg BW) and propofol (0.22 mg/kg BW,

intravenously in the ear). Propofol was only administered at heavy weights. Sedation without the use of anaesthetic is also possible. Aasmundstad *et al.* (2014) used only an intramuscular injection of azaperone. It is also possible to use several type of gases (such as isoflurane), although in this case a mask must be placed on the pig's face, which is not always convenient. The time required to acquire a CT image depends on the device used and is shorter for newer devices. CT is faster than MRI, which requires more time per image for magnetic resonance. Consequently, the doses of anaesthetic or sedative will depend on the time required for scanning, the type of device and the number of images required per animal.

Other major factors when working with DXA, CT and MRI and live animals is that an extra room close to the device is needed to perform the anaesthesia or sedation. Moreover, the decrease in body temperature due to anaesthesia must be compensated by providing a heating system, blankets or other options to avoid possible future health problems.

Second step: Measurement procedure

US. Although anaesthesia is not required, the animal must be fixed by cage or by human restriction. Moreover, it is very important to keep the animal calm, and this technique must be performed by trained technicians. Once the animal is fixed, a specific gel that improves light conductivity is applied to the region to be examined. Depending on the type of US device used, the results are presented automatically as an image on a portable screen (Figure 3a) directly or as the value of the measurements obtained (subcutaneous fat, loin eye area, etc.).

VIA. Anaesthesia and conductive gel are not required for VIA. A fixed position of the animal or human-pig interaction are not required. The animals are monitored. This system provides images of the pigs by video or photo camera from which measurements can be obtained manually or using specific software.

MRI. To perform MRI, the pig must be calm and immobile, which is primarily achieved by the use of anaesthesia or sedatives. In contrast to VIA and US, at least one staff member must have veterinary knowledge to control the anaesthesia or sedation procedure. Once the animal is anaesthetised or sedated, it is placed on the diagnostic table of the device and can be handled by a PVC cradle, special inflatable plastic or blankets (Mitchell *et al.,* 2001). No metal object is allowed due to the magnetic field created. It is very important to check the pig's ear tag and verify that it does not contain metal; otherwise, the exam will not be performed properly. An MRI or CT scan usually starts with a so-called scout to define the zone studied and the positions and directions of the slices selected. The positions of the scans are determined by anatomical points selected by the operator. It is also possible to scan a specific anatomical region or the whole pig. Figure 3b shows an image of a loin obtained by MRI. MRI parameters depend on each device and the requirements of the study. Important parameters include the T1 and T2 constants, the sequence used (spin or echo), the time of repetition, the time between two consecutive radiofrequency pulse signals or between successive excitations (TR), the time between echoes, between the middle of the exciting radiofrequency pulse signal and the middle of spin echo production (TE), the flip angle, matrix dimension and the slice thickness. Kremer *et al.* (2013) used

a protocol consisting of a T1 weighted spin echo sequence (TR of 380 ms, TE of 15 ms, flip angle 90), a field of view of 461x461 mm with an image matrix of 256x256 pixels, and a transversal slice thickness of 15 mm with a distance factor of 0.25. For a T1-weighted sequence with a TR of 300 ms and a TE of 17 ms, the fat tissue pixels have rather high signals intensities, whereas the non-fat pixels have lower signal intensities (Scholz *et al.,* 2015). However, this pattern differs for cold objects (Monziols *et al.,* 2006).

DXA. Like MRI, this technique requires a calm, immobilised pig, and the anaesthesia or sedation protocol is very similar. However, less time is required for scanning compared to MRI. The measurement of body composition by the DXA system is based on the differential attenuation of low and high-energy X-rays. The fat, lean and bone content are determined for each pixel of a total body scan. The most important parameters when using a DXA device are the radiation source, the voltage (also known as photo peaks, which are the differential attenuation between low and high voltage), the scan speed and the longitudinal section distance.

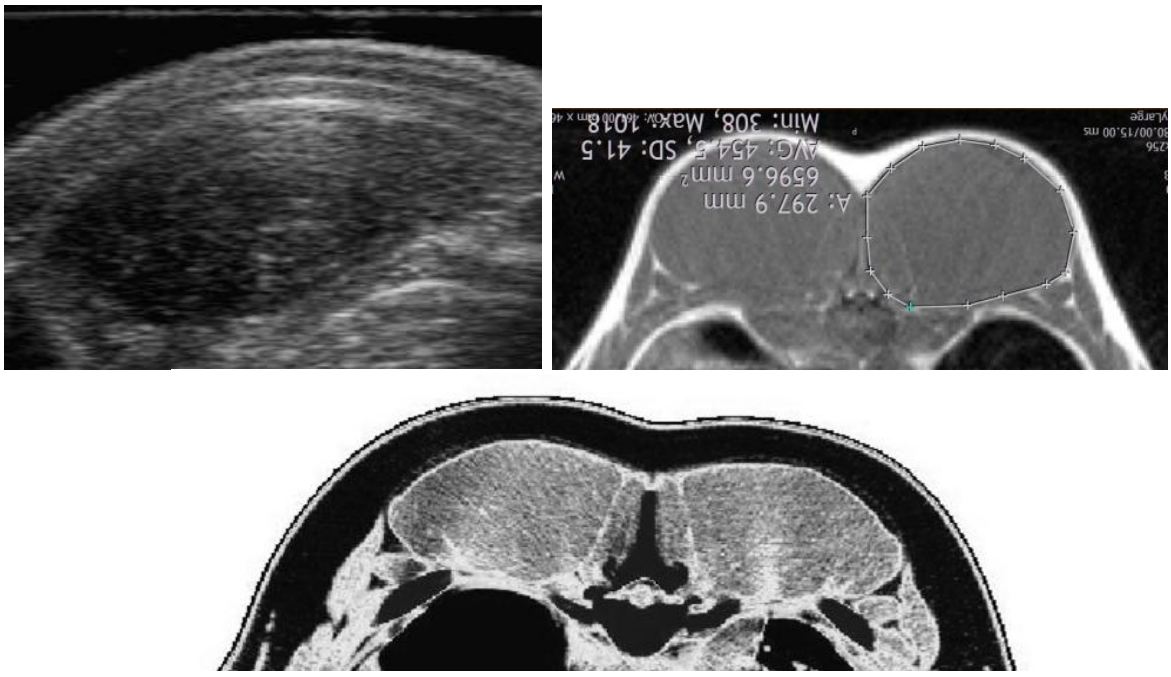

Figure 3. Comparison of the image resolution of a pig's loin: US (a), MRI (b), and CT (c). Photo 3b courtesy of Armin M. Scholz from Ludwig Maximilian University of Munich.

The basic theory and methodology for measuring body composition by DXA is similar to that for dual-energy photon absorptiometry (DPA), which has been described in detail by Peppler and Mazess (1981) and Gotfredsen *et al.* (1984). The whole body composition estimation is available immediately after the scan is completed. A regional analysis to quantify the 2D tissue distribution requires manual manipulation time, depending on the number and anatomical characteristics of the regions of interest (Scholz *et al.,* 2015).

CT. Like the two last techniques, the use of CT for livestock animals requires anaesthetic or sedatives. CT parameters differ on the device and the purpose of the exam. The important instrumental settings for CT are the type of acquisition image (axial or helicoidal), the voltage, the intensity, the matrix dimensions and the slice thicknesses. The instrumental settings used by Carabús *et al.* (2014) were 140 kV, 145 mA, pixels matrix of 512x512, axial, and two different slice thicknesses: 7 or 10 mm. Konsgro (2013) used two different energy levels of 80 kV and 140 kV, pixel spacing of 0.933 × 0.933 mm and 5-mm slice thickness and their combination to study intramuscular fat in live pigs. The accuracy and definition of the image will vary depending on these parameters.

As in MRI, the temperature of the object is important; a cold carcass and a live body will not present the same signal intensities, even for the same animal.

Third step. Image analysis procedure

Image analysis can be performed with varying degrees of automation, and an important issue is the software used. As for the majority of technology devices, explicit software is required to analyse an image. Each device typically includes its own software, but researchers usually require more information than that generally provided. Software used in published works include Visual Pork (Bardera et al., 2012), ATAR (Animal Tomogram Analysis Routines)-STAR (Mann *et al.,* 2013), Osirix (Rosset *et al.,* 2004), Dicom Works 1.3.5, and Lunar 4.7e (Kremer *et al.,* 2013). More information about software is available at www.costfaim.wikispot.org. Images can be analysed in three different ways: using phenotypic measurements, such as linear measurements, areas or volumes; using segmentation based on the application of algorithms to classify each voxel according to its density; or using the volume distribution by HU value.

Phenotypic measurements of specific regions such as the 3^{rd}-4^{th} last rib or P2 in livestock animals have been studied extensively for three main reasons. First, these measurements in live pigs are good predictors of carcass composition, that is, the measurements obtained from the image are related to the lean content of the carcass, and the scientific community uses these measurements for prediction. Second, the meat industry use these measurements in carcasses to estimate the lean meat content. Third, measuring the same region in live pigs or carcasses allows the results of different experiments to be compared.

Segmentation uses the differences between HU values or colours in grey-scale to classify tissues as lean, fat and bone. However, segmentation demands special attention when using measurements obtained from pixels or voxels because there is not an agreed standard for segmentation based on HU values and segmentation depends on the specific equipment, its calibration and researcher preference. Differences in CT protocols may lead to variations of HU values of up to 20% (Scholz *et al.,* 2015). Image segmentation can be divided into different approaches. Thresholding is the method used in the majority of experiments involving DXA, CT, MRI and live animals. Thresholding segmentation is based on assumptions of specific mass attenuation coefficients for different body or carcass tissues, calculated as HU. The histogram shape-based method analyses the peaks, valleys and curvatures of the smoothed histogram. Histograms have been used and studied extensively in CT of growing pigs. Font-i-Furnols *et al.* (2015) used histograms to segment fat, lean and bone tissue in live pig images using

the volumes of fat, lean and bones obtained by the sum of voxels distributed with values of HU between -149 and 0, 1 and 150, and 151 and 1400, respectively. Chang *et al.* (2011) reported HU values between -20 and -200 for visceral and subcutaneous fat in minipigs, and Gjerlaug-Enger *et al.* (2012) distinguished fat, lean and bones based on HU values of -200 to 0, 0 to 200 and greater than 200, respectively. Image segmentation is the last step if the imaging technique provides sufficient information to obtain the parameters of interest.

However, external factors such as environmental temperature during CT scanning or the animal's internal temperature can affect the tissue density and, consequently, the pixel values. Variations of temperature and differences in the acquisition parameters of each device underlie the lack of global segmentation for all devices. According to Scholz *et al.,* (2015), differences in the calculation of CT densities for lean meat result in different lean meat weights for similar lean meat volumes, complicating the harmonisation of acquisition parameters among different countries or among various CT scanners.

The third method of image segmentation is the development of prediction equations using the distribution of volume or voxels by HU value as predictors, with or without additional linear or area measures obtained directly from images (Carabús *et al.,* 2015; Font-i-Furnols *et al.,* 2015). In this case, a fourth step is needed as explained below.

US. US can provide areas, perimeters and linear measurements in addition to intramuscular fat content. The technician uses the machine to measure the area of the loin eye, its depth and how much fat is deposited over the loin eye. Different locations and measurements have been reported (Table 2). McKeith *et al.* (2010) studied loin muscle area, loin muscle depth, and backfat depth at the 10^{th} rib and last rib from commercial finishing pigs.

VIA. External linear measurements, perimeters and areas can be obtained from a 2D image, and reconstruction is feasible, including volume measurements, when an extra image is added. However, most of the information obtained is related to shape (White *et al.,* 2004; Doeschl-Wilson *et al.,* 2005) and behaviour and evaluation of gait analysis (Kongsro, 2013). No internal images are obtained.

DXA, MRI and CT. Linear measurements, perimeters and areas are obtained by these three devices. The volumes at any point and between any points can also be obtained by MRI and CT. Although DXA generally produces 2D images, 3D reconstruction images are also possible (Humbert *et al.,* 2012); however, even though the three devices allow the same types of measurements, the image resolution differs among the devices and depends on the tissue analysed, its density and the target. Thus, DXA is more specific for dense tissues with low hydration, such as bones. CT has adequate resolution for dense and medium-dense tissues. While MRI does not differ substantially from CT, MRI has better resolution and provides detailed results for soft tissues (Szabo *et al.,* 1990). Table 2 presents examples of measures obtained using the different technologies.

Table 2. Measures obtained at several positions using non-invasive techniques in live pigs.

Device	Number of images	Width (mm)	Measurement in each image	Position	Source
CT	20-25	50	Areas of fat Areas of lean Non-fat visceral components Areas of bone Areas deposited within tissues	From the femur to the first vertical vertebra	Kolstad, 2001 Lambe *et al.,* 2013
CT	10	5	Volumes / Histograms	From the last rib to coronal direction	Kongsro and Gjerlaug-Enger 2013
CT	Whole body	7 and 10	Volumes		Font-i-Furnols *et al.,* 2015
CT	Whole body	8	Areas Fat density Muscle density Bone density		Lambe *et al.,* 2013
MRI	33-52 (depending on animal weight)	16 or 32	Volume of fat Volume of lean	From parotid gland to the rind of the ham	Mohrman *et al.,* 2005
MRI	4 repetitions at the same point	15	Loin eye area Fat area from the previous measurement	13^{th} and 14^{th} ribs	Kremer *et al.*, 2013
Ultra-sound	3		Backfat Loin muscle area Loin muscle depth	10^{th} rib Last rib	McKeith *et al.,* 2010
Ultra-sound	1		Backfat	P2	Doeschl-Wilson *et al.,* (2005)

DXA	2D all over the body		Soft lean tissue mass Soft lean tissue mass percentage Fat tissue mass Fat tissue mass percentage		Kremer *et al.,* 2013
DXA	14	57.6	Fat tissue mass percentage Lean tissue mass percentage	Front leg / thoracic region Abdominal region Back leg region	Mitchell *et al.,* 2002
VIA	1		Linear measures Areas measures Body length	Above view of all of the animal but the head	Doeschl-Wilson *et al.,* 2005

Fourth step: Predictions.

Prediction is the last step (not always necessary) and transforms the data from the image analysis into variables of interest for the pig sector (kg of fat, lean meat percentage, etc.) by applying previously developed prediction equations. Accurate precision of the prediction is important to obtain reliable results. Thus, the technique used must be well calibrated, and previous calibration or validation using dissections is occasionally necessary.

Predictions are acquired from different sources, including the measurements obtained from the devices (backfat, loin muscle area, volumes, segmentation, etc.) and external data such as body weight, genotype, sex, diet, health status, and farm density. To obtain a reasonable prediction, the prediction equation must be accurate, as indicated by a high coefficient of determination (R^2) and a low error (root mean square error- RMSE). Examples of predictions obtained from pig image analysis for the carcass characteristics of live pigs are presented in Table 3.

Table 3. Coefficient of determination (R^2) of body composition characteristics using measurements obtained with non-invasive techniques in live pigs as predictors.

Dependent variable	**Device**	**Independent variable used for prediction**	**R^2**	**Source**
Intramuscular fat	CT	Volume of squared region of interest from the loin region	0.53	Kongsro & Gjerlaug-Enger, 2013

Lean meat %	CT	Volume of lean / Total volume + Ham perimeter + Ham superior + Subcutaneous fat + Loin superior subcutaneous fat thickness + Loin lateral subcutaneous fat thickness + Diagonal muscle thickness + Loin area	>0.95	Font-i-Furnols *et al.,* 2015
Ham weight	CT	Total volume + Loin superior subcutaneous fat	>0.95	Font-i-Furnols *et al.,* 2015
Fat in the ham	CT	Volume of fat + Ham superior subcutaneous fat + Fat area of the ham	>0.95	Font-i-Furnols *et al.,* 2015
Fat in the 4 main cuts	CT	Volume of fat + genotype + sex	0.99	Carabús *et al.,* 2015
Lean in the 4 main cuts + tenderloin	CT	Volume of lean + genotype + sex	0.99	Carabús *et al.,* 2015
Carcass weight	CT	Loin perimeter + BW + genotype + sex	0.99	Carabús *et al.,* 2015
4 primal cuts weight	CT	Loin area + BW + genotype + sex	0.99	Carabús *et al.,* 2015
% of carcass fat	CT	BW + fat density + different areas	0.92	Lambe *et al.,* 2013
Fat weight	MRI	Volume of backfat	0.95	Mitchell *et al.,* 2002
Liver weight	MRI	Volume of liver	0.90	Mitchell *et al.,* 2002
Fat weight	DXA	Equivalent measurements for fat from DXA	0.99	Pomar & Rivest, 1996
Protein weight	DXA	Equivalent measurements for protein from DXA	0.99	Pomar & Rivest, 1996

Fat-free lean	US	Backfat at the last rib + loin muscle area + BW	0.82	McKeith *et al.,* 2010
Intramuscular fat at the 10th rib	US	Backfat linear measurement + loin muscle area + loin muscle depth + BW	0.49	McKeith *et al.,* 2010
Intramuscular fat at the last rib	US	Backfat linear measurement + loin muscle area + loin muscle depth + BW	0.52	McKeith *et al.,* 2010
Carcass weight	VIA	Via shape	0.54	Doeschl-Wilson *et al.,* 2005
Carcass weight	VIA	Via shape + BW	0.62	Doeschl-Wilson *et al.,* 2005
Carcass weight	VIA + US	Via shape + backfat linear measurement	0.66	Doeschl-Wilson *et al.,* 2005

Utility of these techniques for livestock animals

Non-invasive techniques have a number of applications:

- Breeding and selection: effect of genetic and sex type
- Nutrition: effect of diet
- Health: veterinary diagnostic
- Medicine: animal as a model for human research
- Slaughter plant: carcass and cuts composition
- Processing plants: cutting optimisation and cuts composition (virtual butcher)

This paper primarily provides an overview of the first two applications.

Effect of genetic type evaluated by image analysis

At slaughter weight, carcass characteristics differ depending on genetics (Gispert *et al.,* 2007). Kolstad *et al.* (1996) compared Landrace and Duroc growing pigs fed at maintenance. Landrace pigs contained more internal fat (2.28 vs 2.20 kg) and less inter/intramuscular fat (1.90 vs 2.26 kg) at the start of the maintenance feeding period than the Duroc pigs. Margeta *et al.* (2007) used MRI to study the influence of MHS-genotype and feeding regime on the growth and development of muscle and fatty tissue in the whole body as well as in hams of hybrid pigs and concluded that

different feeding regimes and MHS genetic statuses of pigs do not significantly influence the growth of muscle and fatty tissue in hams. The stage of maturity is a primary reason for reported genotype-dependent differences in carcass composition, and the effects are more pronounced when pigs of different mature weights are compared at the same weight than at the same age. There is some evidence that breeds differ in the relative growth rates of tissue in discrete anatomical regions, independent of degree of maturity (Fortin *et al.*, 1987). Information on sow lines carrying genes for prolificacy (Fisher *et al.*, 2003) is very valuable for breeding companies. Gjerlaug-Enger *et al.* (2011) used CT to calculate genetic parameters for the growth rate of muscle, carcass fat, bone and non-carcass tissue from birth to 100-kg live weight of Landrace and Duroc genotype pigs. Mitchell *et al.* (2002) used DXA to determine the feasibility of predicting total body composition of live pigs of three different genotypes based on a single cross-sectional measurement. Carabús *et al.* (2011) used CT to study the phenotypic characteristics of three different genotypes at 30, 70, 100 and 120 kg. The Pietrain cross type exhibited a greater amount of ham, which is useful information for companies that use Pietrain pigs for their lean potential. As an example of an application not involving meat, Kongsro (2013) applied CT in live pigs to diagnose osteochondrosis, its heritability and genetic correlations to weight gain in specific age intervals, useful information for breeding companies. Ley (2013) declared CT "part of the routine genetic selection programs in modern times" (Scholz *et al.*, 2015). Modern CT permits the acquisition of more than 1100 slices per live pig in less than a minute (Gjerlaug-Enger *et al.*, 2012). Accordingly, testing 24 boars per day is a routine application at Topigs-Norsvin facilities in Norway. The information from the 1100 slices per potential breeding boar is processed to determine body composition phenotypes such as lean meat, fat, bone, primal cuts, live and carcass weight (Scholz *et al.*, 2015).

Evaluation of the effect of sex by image analysis

Giles *et al.* (2008) used CT to study the differential growth and development of pigs and determined that differences in the weights of body components by sex were minimal at the starting 30 kg target BW but increased with increasing target BW (up to 150 kg). Doeschl-Wilson *et al.* (2005) used VIA to evaluate the relationship between the body dimensions of live pigs and their carcass composition by sex and identified significant differences in the regression results between boars and gilts. Mitchell *et al.* (2001) used MRI in live pigs, including females and entire males. Four different experiments were performed, with the main objective of predicting carcass composition. The results of the different experiments were compared to identify the most accurate prediction of fat and lean content obtained by analysing the fat and muscle values of a specified number of slices within the ham and loin regions.

European interest in animal welfare and the prospect of legislation in several countries limiting the current practice of surgical castration without anaesthesia have encouraged the swine industry to reconsider its traditional approach to the control of boar taint and investigate alternatives (Gispert et al, 2010). One alternative is the immunocastration vaccine, and thus the immunocastrated male must be considered as another sexual condition to be studied. Regarding immunocastration, Carabús *et al.* (2015) used CT to evaluate growing pigs of different sexes,

including females, entire males, castrated males and immunocastrated males, and different live weights. Females exhibited significantly greater loin width than entire males, immunocastrated males and castrated males (211.7 mm *vs.* 209.63 mm *vs.* 203.2 mm and 201.7 mm). Castrated males presented greater subcutaneous fat of the loin and ham compared to the others sexes. Castrated males and entire males exhibited different subcutaneous lateral ham fat growth rates, whereas the growth rates of females were similar to those of castrated and immunocastrated males. Immunocastrated males were significantly leaner than castrated males.

Nutrition: Evaluation of the effect of diet by image analysis

Meat composition, growth rate and feed conversion are directly related to dietary composition. Lambe *et al.* (2013) studied the effects of feeding pig diets with different protein and amino acid levels on compositional changes during the growing-finishing period (40-115 kg) using CT scanning (at 60, 85 and 115 kg live weight).

Different factors such as genotype, sex or feeding regime are typically studied together to optimise the use and potential of these non-invasive technologies. Kuseć *et al.* (2006) used MRI to study the effect of the MHS (malignant hyperthermia syndrome) gene on intensive and restrictive feeding and observed significantly higher feed intake, daily gain and feed conversion ratio in pigs maintained under intensive feeding conditions compared with restrictive feeding regime. The growth of muscle tissue in pigs was not influenced by the feeding regime. The intensive feeding was designed to ensure optimal or possibly enhanced muscle growth capacity of hybrid pigs, but the study indicated that the restricted feeding regime supported the muscle growth just as effectively, which is very valuable information for nutrition companies. Non-invasive technologies have been used more often as a tool in live pigs for breeding and selection applications than for the study of diet itself. Some of these studies are presented in Table 4.

The application of non-invasive techniques in farming pigs is useful and adequate to study animal growth, in other words, to model their growth, because the same animal can be evaluated several times during its growth. Non-invasive techniques enable growth to be modelled depending on the genotype, sex, diet and many other factors. Modelling the growth of a certain group of pigs from birth to death and studying the same animals in each period is one of the best applications of modelling functions to predict BW, mature BW, fat weight, muscle weight, etc. at a certain future weight or to study the deposition speed of cuts and tissues, as suggested by the allometric function.

Several functions are available for the description of growth, including Brody's function, the logistic function, the allometric function, the Gompertz function, the von Bertalanffy function, and the four-parameter Richards function, which combines aspects of all of the above growth functions into a single function. Growth functions are not the topic of the present paper but certainly exploit many of the advantages of non-invasive techniques.

Table 4. Field of applications of image analysis in live pigs and main objectives.

Source	n	Device	Objective	Field of application
Doeschl-Wilson *et al.,* (2005)	25	VIA	To describe pig growth in terms of body size and shape	Breeding and sex type
Kolstad, (2001)	141	CT	To examine the development of different fat depots using restricted feeding	Breeding and nutrition
Kusec *et al.,* (2006)	68	MRI	To investigate growth characteristics of barrows of two genotypes in two different feeding regimes	Breeding and nutrition
Romvári *et al.,* (2004)	10	CT	To describe changes in the tissue composition of the belly during the fattening period	Nutrition
Kolstad *et al.,* (1996)	92	CT	To examine breed and sex differences in fat distribution prior to and changes in fat distribution during the maintenance period	Breeding, sex and nutrition
Luiting *et al.,* (1995)	32	CT	To determine the body composition at the maintenance feeding period	Nutrition
Giles *et al.,* (2008)	54	CT	To quantify and mathematically describe the differential growth and development of body components of live pigs	Breeding
Doeschl-Wilson *et al.,* (2005)	144	VIA	To determine if VIA shape indices derived from digital images of live pigs can provide useful information about carcass composition	Breeding
Lambe *et al.,* (2013)	108	CT	To determine the effect of low protein in the diet	Nutrition
Mitchell *et al.,* (2002)	212	DXA	To determine pig composition	Breeding
Kremer *et al.,* (2013)	77	MRI/DXA	To determine pig composition	Breeding

In summary, US, VIA, MRI, DXA and CT are the most popular techniques for image acquisition in livestock animal evaluation. Whereas VIA is usually used to capture external attributes, MRI, US, CT, and DXA can be used to inspect internal structure. However, the accuracy of the images and

the predictions obtained differ among techniques. Predictions with the highest resolution are generated from CT and MRI, followed by DXA, VIA and US. CT presents superb results for the estimation of the amount of fat and lean mass, but its accuracy to predict IMF is not acceptable and requires improvement. US is not sufficiently accurate in estimating the body composition of pigs if highly precise information is needed for research purposes. However, the information obtained can be used in farming conditions to successfully classify pigs before slaughter. For livestock animals, portable devices must also be considered, which excludes MRI. Moreover, the time required for image acquisition differs greatly among devices, with MRI the slowest. However, a combination of different devices could yield improved results. Swine farmers have been using US imaging for several years to detect maternity traits, subcutaneous amount of fat or muscle depths. Combining a less-expensive device such US or VIA as a first selector with a second device such as CT or MRI to obtain 3D images in the selected animals could minimise the sample studied and, consequently, reduce the cost. Moreover, according to Scholz *et al.* (2015), the combination of phenotypic data obtained from non-invasive techniques with genome data could provide deeper information and knowledge of the growth and body composition of farm animals (Aasmundstad *et al.*, 2013).

Conclusions

Image analysis has applications in the livestock field. However, some devices are expensive, and to satisfy the demand for cost-effective techniques, inexpensive multipurpose image processing systems that yield higher-accuracy predictions must be developed. Portable devices make technology feasible for farming conditions and easier to obtain income by renting the device, particularly if the device is expensive, such as CT. Improving the processing speed of the scan or image analysis by technicians and integrating specific image processing algorithms would improve the value of the technology. Cheaper and faster solutions have enabled image processing in live animals to assume and maintain an important role.

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Introduction. Part II.

The content of this chapter is published as a dissemination paper in the Spanish journal Eurocarne.
The original paper is presented, as published (in Spanish) in Annex 1.

As explained before, the Chapter 1 is divided in two parts. The first part of the Chapter is part of a scientific paper presented in the Spanish Agricultural Research journal, while the second part is a divulgation paper presented in Eurocarne (Spanish journal). Once all the devices are presented, it is necessary to explain, deeply, the one used in the present Ph. D. Thesis, the computer tomography (CT). This second part presents the main applications of CT and a huge number of possibilities for the agrifood industry.

Applications of computed tomography in the production field and food technology

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This chapter deals with:

- Main uses and applications of computed tomography in livestock animals and food industry

What is computed tomography about?

X-rays are electromagnetic waves that can penetrate solid matter and, as they do so, lose parts of their original energy. These energy differences can be projected onto an image. Computed tomography (CT) produces cross-sectional digital images of an object by combining X-ray projections (Kalender, 2005; Seeram, 2009).

The application of CT in the production and technology fields for food is based on the different attenuation that X-ray produce on the biological tissues, depending on its density. CT tomograms thus reveal different tissues and biological structures. The technology is very useful because it is non invasive.

Applications of computed tomography

The CT device is very common in human medicine for the diagnosis diseases (Jongbloed *et al.*, 2005). It is also useful in agriculture (Elliot *et al.*, 2010) and forestry (Schmoldt *et al.*, 1999). In addition, the technology has been applied in agrifood and has proven itself as valuable tool to estimate food composition. In the field of fruit studies, studies using CT revealed the water content of apples (Tollner *et al.*, 1992), internal changes in peaches (Barcelon *et al.*, 1997) or the maturity degree of tomates (Brecht *et al.*, 1991). Other research has focused on livestock animals and their carcasses. In aquiculture, salmon fat content has been evaluated (Einen *et al.*, 1998); in poultry, the chest production of broilers has been measured (Remignon *et al.*, 1997); sheeps have been evaluated *in vivo* (Toldi *et al.*, 2007) and in carcass (Johansen et al, 2007); pigs have also been studied for their fat deposition and distribution (Kolstad, 2001), composition of living bodies (Luiting *et al.*, 1995) and carcasses (Font i Furnols *et al.*,2008). The application of CT to animals is very important to determine the composition of the body and, in economic terms, its results are relevant to prediction of the lean fraction of meat (live animals and their carcasses, both) without the necessity to dissect the animal. CT has also been used to determine intramuscular fat (Font i Furnols *et al.*, 2009) and fatty acid composition of the meat (Nieto *et al.*, 2010). It further allows to follow salt diffusion during curing meat, as well as to quantify the salt and water content in dry cured hams at different stages of the refinement process (Fulladosa *et al.*, 2010; Santos-Garcés *et al.,* 2011).

Evaluation of body composition in live animals

Knowledge of the composition of live animals, as well as the evolution and deposition of different tissues during their growth, is crucial for the optimization of the final product. It is generally assumed that variation in body's composition plays an important role in growth of pigs. This information, referred to the quality of the product, should increase the communication within the different actors of the meat chain, from farmers to consumers. (Cross and Whittaker, 1992; Kirton and Purchas, 1996). It is well known that at a similar weight, carcasses of pigs with different genotypes exert different characteristics (Gispert *et al.,* 2007) that already appear at 30 kg (Carabús *et al.,* 2011). , obtaining a high variability of carcass depending on its fat's dephs, loin's area, ham's proportion and lean content. One of the best ways to study the body's composition of live animals is using a CT, because the tissues have different densities that permit distinction and quantification in the images obtained (Figure 1). Theses images are evaluated with specific software, such as VisualPork (Boada et al., 2009), with advanced statistical techniques, such as regressions by partial squared minimums or PLS or their combination.

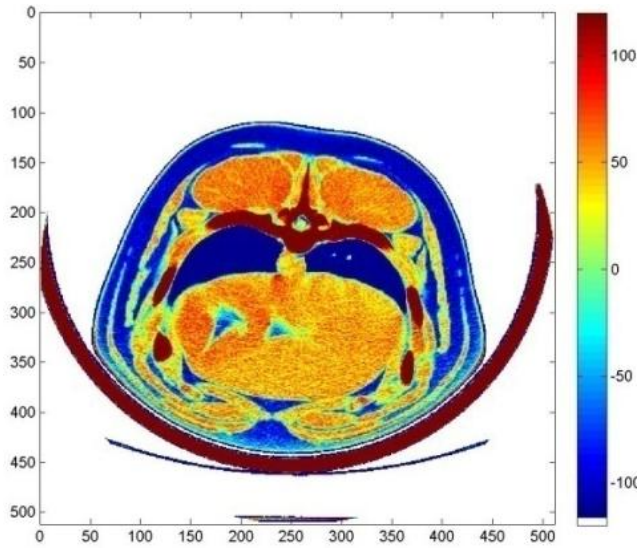


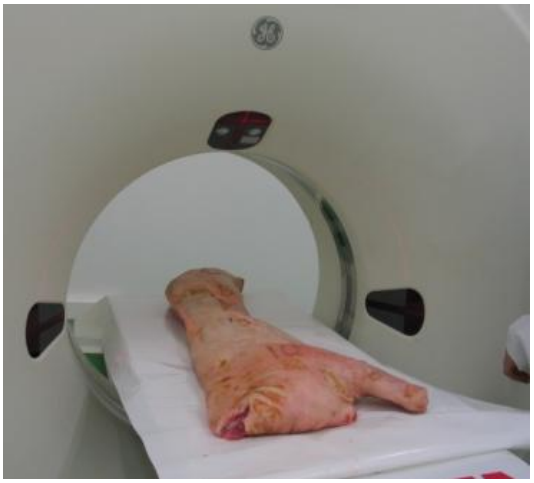
Figure 1. Tomogram of the loin

In vivo evaluation of live animals allows observing the effect of a diet, that is, how and when different tissues are deposited, the effect of vaccines on the growth, carcass and meat characteristics. Moreover, allometric coefficients can be obtained from the different characteristics of a body's or carcass' composition, depending on the genotype, sex and feed. Prior to the development of these technologies, the evolution of the composition of a body from a single animal was difficult to determine during its growth. The technique used (and still in use) was to take measurements from the loin's zone using ultrasounds. CT, in contrast, permits a global analysis of the whole animal.

Carcass caracterization

Lean tissue content is used to classify carcasses. For this reason, much research has focused on prediction of this content (Font i Furnols et al., 2001; Gispert y Font i Furnols, 2003). The

slaughterhouses estimate the lean content with devices using ultrasound (Autofom, Ultrafom y Ultrameater), reflectance (Fat-o-Meat'er, HennessyGradingProbe and Captador Grasa-Magro) vision (VCS2000 and Imagemeater) or lineal measures obtained in the medium line of the carcass. In order to to predict the lean content best, these devices require work-intensive calibration: Cuts and dissection using the reference simply method (Walstra y Merkus, 1995) or full dissection of at least 120 carcasses. The prediction error of the estimation needs to be less than 2,5% ((CE) nº 1234/2008). Jopson et al. (1995) as well as Glasbey y Robinson (1999, 2002) suggested the use of CT as alternative method when dissection is needed (Figure 2 and 3). From data obtained in the EU-EUPIGCLASS project, Dobrowolski et al., (2004) recommended the use of CT as reference method for estimation of lean tissue percentage. Recently, new legislation ((CE) nº 1234/2008) permits this technique . Measurements obtained with CT have a low prediction error (Judas et al., 2007; Font i Furnols et al. 2008), but scanning of whole carcasses is expensive. Costs can be cut by reducing the number of images produced (Teran et al., 2009), e.g. by scanning only specific anatomical parts of the carcass (Figure 4) or main cuts (Figure 5).



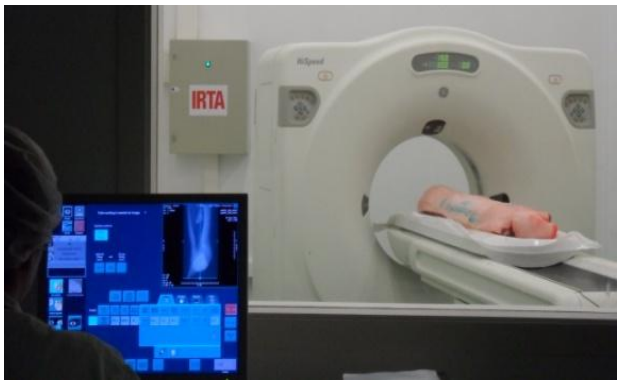
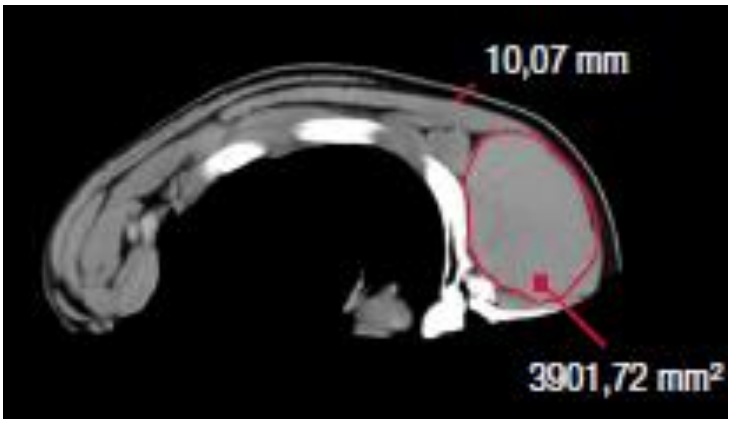


Figure 2 and 3. Half carcass in a CT (left) and during the scanning process (right).



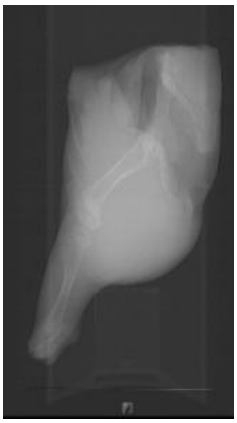


Figure 4 and 5. Tomogram of the loin and measurements obtained (left) and tomogram of the ham (right). Photos courtesy of IRTA.

Applications to the final product

CT can also be used as support for the design and development of new processes and products, to evaluate the quality of the final product, and also for the analysis of internal structures of food. Figure 6 is an example of the images that can be obtained using this technology. It illustrates how internal structures may be observed in a non-invasive way, for example the “eyes” of the cheese depending on the process it has been subjected, the maturity degree of fruits or the structure of a banana.

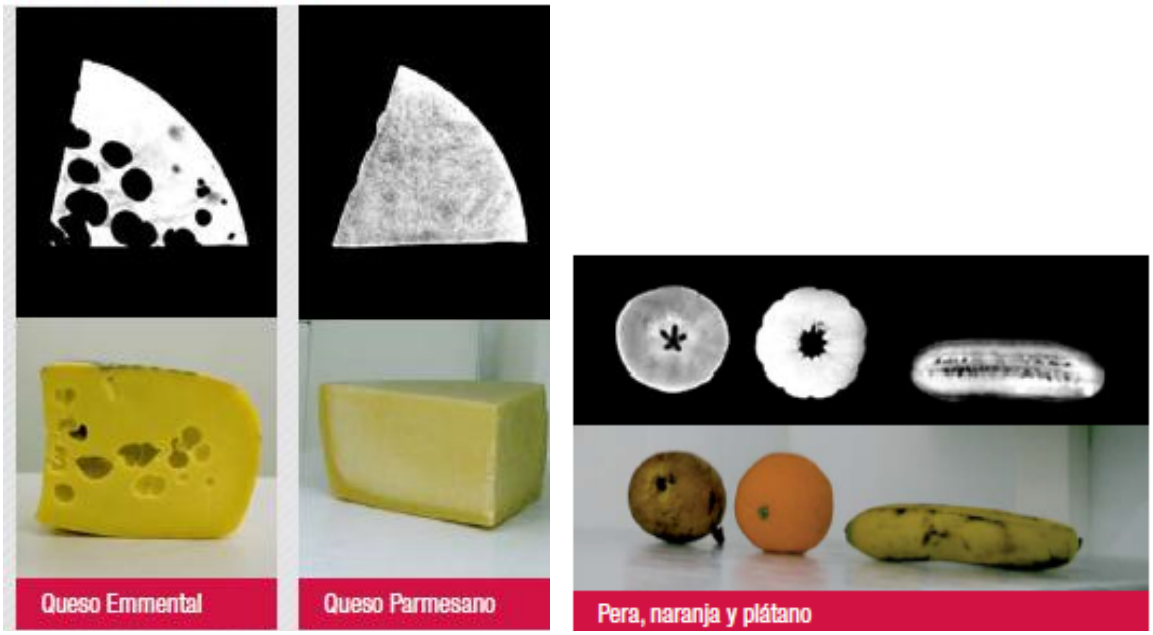


Figure 6. Internal structure of different food. Photos courtesy of IRTA.

CT also is of special interest to study the salting and curing process in meat. The high density of the salt ions increase the attenuation values of the CT. Na^+ and Cl^- ions have a higher density that the main components of the meat (C, H, N, O), which allows to distinguish salt from other components. For that reason, this non-invasive technology allows to study salt and water diffusion, and also their distribution, in the same piece or during the refinement process (Figure 7). Moreover, models have been developed to predict the amount of salt and water in the cured ham with an error between 0,3% and 1,5% (Fulladosa et al., 2010; Santos-Garcés et al., 2011).

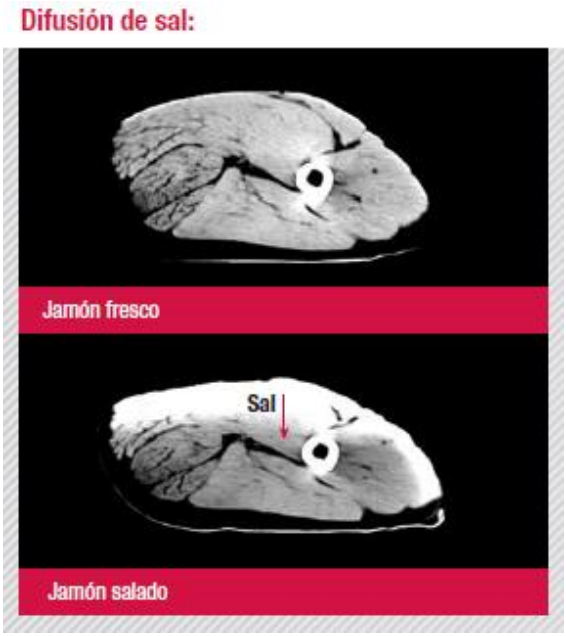


Figure 7. Image of a fresh ham and a salty ham, where the salt movement to the center of the product can be observed. Na and Cl-rich areas increase attenuation of X-rays and are shown brighter in CT pictures. Photos courtesy of IRTA.

Thus, as explained above, CT has the potential to optimize the food processes, particularly for the study of the slating process in cured ham (Figure 8).

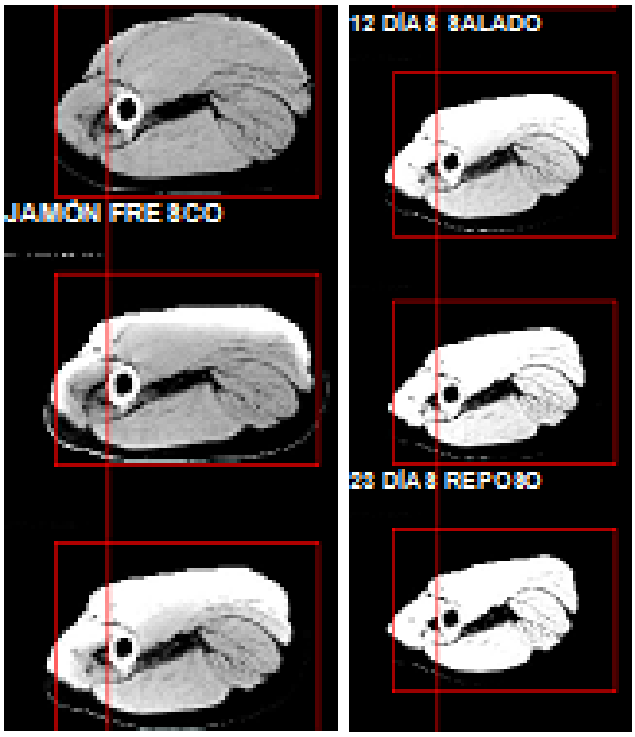


Figure 8: Images from CT of the same cured ham during the salty process at different times. Photos courtesy of IRTA.

Images for the salt and water distribution of the whole section (Figure 9) permit to obtain deeper information than the ones obtained by chemical analysis, since the piece is not destroyed and it is analyzed completely rather than in a specific point.

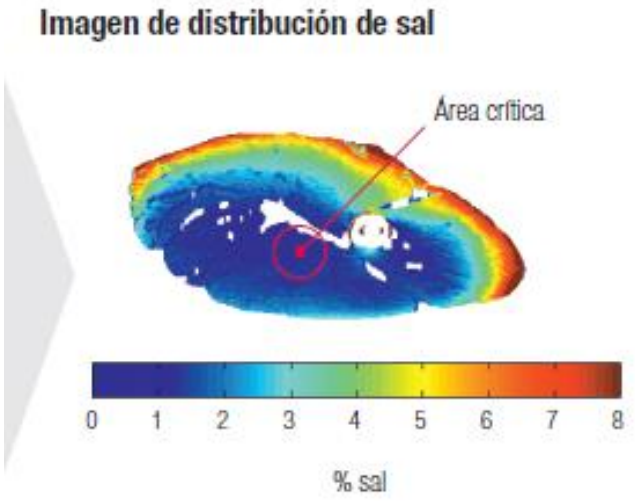


Figure 9. Distribution of salt and water in a section of a dry cured ham. Photos courtesy of IRTA.

CT can also be used to design a new processes for post salty products. In products with a low content of salt it is necessary to adapt the traditional processes depending on the final content of salt in the most critical points of the product (Figure 9). In this sense, CT has been used for many companies to adapt the process conditions in dry cured ham with a low content of salt, taking into account the microbiological stability. The extensions of the post-salty stage to low temperature to acquire, in the most critical part of the product, an identical content of salt as the standard product permits to reduce defects in the final product.

Innovation, application and assessment

This technology is available for the agrifood industry and allows to

- Increase productivity
- Design of new processes
- Optimization of traditional processes
- Study of internal defects of the product
- Study of the internal structures and textures of all kind of solid food
- Estimation of intramuscular and marbling in meat
- Support to design processes for low content of salt products
- Evaluation and characterization of carcasses and their cuts
- Calibration of classification devices for pigs's carcasses
- Evaluation of live pigs to study the effect of genotype, sex or diet and the deposition of tissues among the growing period.

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Chapter 2

Objectives

The main objective of this PhD Thesis is to study the evolution of fat and lean tissues of live pigs from different genetic types and sexual conditions from 30 to 120 kg by means of computed tomography images. To do that, as the number of pigs used is big, the work is divided in two groups, from now on, Experiment 1 (pigs of different genetic types) and Experiment 2 (pigs of different sexual conditions). Thus, in order to get the final result, different objectives are planned for both experiments:

1) To study the relationship between cross-sectional CT images obtained in live growing pigs and dissection measurements (Chapters 4 and 6)

2) To estimate carcass composition and cuts composition using CT predictors (Chapters 4 and 6) or potencial on-farm predictors (Chapter 6)

3) To evaluate variations in the body composition of pigs at the live weights of 30, 70, 100 and 120 kg by analyzing live pigs with CT (Chapters 5 and 7)

4) To determine the allometric growth of the main body parts in relation to their weight and their lean, fat and bone contents (Chapters 5 and 7)

5) To compare and discuss the goodness of equations developed in order to know which one is better for each occasion and necessity (Chapter 8)

Chapter 3

Material and methods

Animals

Two experiments were performed for this Thesis. The first experiment took place between December 2011-June 2012 and included 90 gilts of different genotypes. The ones that were scanned at all the target body weights were raised individually, while the ones that were slaughtered and dissected after scanning were raised in group. The second experiment took place between December 2012-June 2013 and included 92 pigs of different sexual condition.

The first set (Exp. 1) included 90 gilts of three different genotypes (GEN): 30 (Duroc x (Landrace x Large White)) (DU), 30 (Pietrain x (Landrace x Large White)) (PI) and 30 (Landrace x Large White) (LA). There were no parental relationships within the breeds as Landrace and Large White pigs came from different companies. The second set (Exp. 2) included 92 (Pietrain x (Landrace x Duroc)) pigs, all of them from the same company, and of different sexual conditions (SEX): 24 each of females (FE), entire males (EM), castrated males (CM) and 20 immunocastrated males (IM). Improvac® (Zoetis, Spain) was injected at 12 and 18 weeks of age. Pigs were reared at IRTA experimental farm in Monells (Girona).

All the pigs were fed a commercial diet according to a two-phase feeding program (10.24 and 10.08 MJ net energy, 18% and 17% crude protein and 0.91% and 0.90% digestible lysine, for the first and second phases, respectively) on an *ad libitum* basis. Pigs were weighed weekly and CT scanned at 30, 70, 100 and 120 kg target body weight (TBW). After each scan (thus, at each TBW), subsets of five pigs of each GEN and four of each SEX were transported to the experimental abattoir, stunned with CO_2, slaughtered following standard commercial procedures and dissected (Figure 1). After chilling for 24 hours (h) to 48 h, carcasses were cut and dissected. The same stunning and slaughter procedure was applied to all the pigs that reached 120 kg, then the experiments were finished.

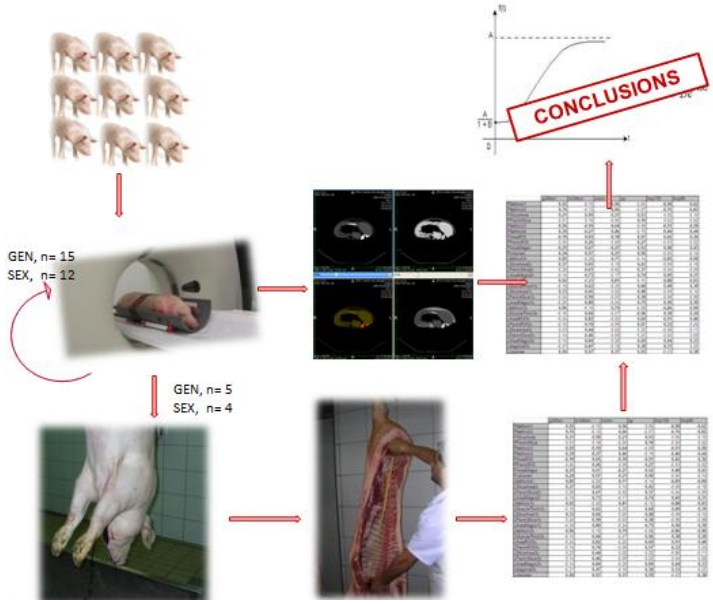

Figure 1. Scheme of the of the experiment

Computed tomography

Animals were fully scanned with a General Electric HiSpeed Zx/I tomograph, located in IRTA-Monells (Girona), and the instrumental settings were: 140 kV, 145 mA, matrix 512x512, axial, 7 mm thick (30 kg TBW) and 10 mm thick (70, 100 and 120 kg TBW). A custom-built half-tube cradle (PVC, Ø 0.30 m, length: 1.2 m for 30 kg pigs and Ø 0.46 m, length: 1.8 m for 70, 100 and 120 kg pigs) was used to hold the pigs in the prone position during scanning. Pigs had free access to water but not solid feed for a minimum of 8 h before scanning. Pigs were sedated intramuscularly with azaperone (0.1 mg/kg BW), ketamine (0.2 mg/kg BW) and intravenously in the ear with propofol (0.22 mg/kg BWi) to minimize disturbances in the CT images. Intravenous sedation was only used at 100 and 120 kg TBW. Only one EM from Exp. 2 died during the procedure and was not replaced. After scanning, the animals were returned to the IRTA experimental farm until their last scan, when they were transported to the abattoir. All procedures were approved by the ethics committee of IRTA.

Slaughter and dissection

For Exp.1, five animals of each GEN were slaughtered at 30, 70 and 100 kg TBW and 15 animals at 120 kg TBW (Table 1). Carcasses were kept refrigerated at 2ºC for 24 to 48 h until dissected. The left side of each carcass was prepared and cut following the European Union reference method (Walstra and Merkus, 1995). Thereafter, four primal cuts plus tenderloin were weighed and manually dissected. Lean, subcutaneous fat including the skin, intermuscular fat, and bone were separated with a knife by trained technicians, and the weights of all these tissues were recorded to obtain the total amounts of fat, lean and bone in the primal cuts, considering the tenderloin weight as lean. For Exp. 2, four animals of three 3 SEX (FE, EM and CM) at 30 kg TBW, four animals of each SEX (FE, EM, CM and IM) at 70 and 100 kg TBW and 12 animals of each SEX (FE, EM, CM and IM) at 120 kg TBW were slaughtered (Table 2). Carcasses were also cut following Waltra and Merkus (1995) procedure. Due to lack of skilled labor, only the weights of the tissues of the four primal cuts, subcutaneous fat including the skin of the 4 primal cuts and dissection of the ham (subcutaneous fat including the skin, intermuscular fat, lean and bone) were used. So, for Exp. 2 the total amounts of fat and lean needed to be estimated.

Table 1. Animals of different GEN scanned (----) and slaughtered (O) at different weights

n	30 kg	70 kg	100 kg	120 kg
45 (15 of each GEN)	----	----	----	O
15 (5 of each GEN)	----	O		
15 (5 of each GEN)		----	O	
15 (5 of each GEN)			----	O

Table 2. Animals of different SEX scanned (----) and slaughtered (O) at different weights

n	30 kg	70 kg	100 kg	120 kg
48 (12 of each SEX)	----	----	----	O
12 (4 of FE, EM and CM)	----	O		
16 (4 of each SEX)		----	O	
16 (4 of each SEX)			----	O

FE: Female, EM: Entire male, CM: Castrated male

Image analysis - CT predictors

Acquisition of volume. The entire body of the pig was scanned to obtain the total number of voxels. Density measurements based on the Hounsfield scale (in Hounsfield units [HU]) were obtained from CT images using the VisualPork software package, which was developed for that purpose by the University of Girona and the IRTA (Bardera *et al.,* 2012; Boada *et al.,* 2009). The cradle was removed from all the images, but the viscera remained. The frequencies of voxels between −1000 and +1400 HU were converted into volumes. Hounsfield volume distributions were studied further to determine the limits for fat, muscle, and bone tissues. The HU value of 0 was selected as the separation between muscle and fat. Thus, the partial volume estimated between −149 and −1, between 0 and 140, and between 141 and 1,400 HU were associated with fat, muscle and bone volume, respectively, and were used as independent variables in the regression analysis. Volumes between −1,000 and −150 HU, which belong mainly to the less dense parts of the viscera, were considered only in calculating the total volume.

Acquisition of phenotypic measurements. Although the entire body of the pig was scanned, CT phenotypic measurements were manually obtained in a reduced set of images. The measurements were determined from six different tomograms. The anatomical location of the tomograms and the parameters evaluated for each one are presented in Table 3 and in Fig. 2

Components predicted

Equations, using CT predictors, were derived to predict the following variables obtained by dissection: total amounts of fat (subcutaneous and intermuscular fat of the four primal cuts) and lean (lean of the four primal cuts + tenderloin), as well as the weights of ham, shoulder, belly, loin and its subcutaneous fat and also lean and bone of the ham.

Table 3. Anatomical location of the measurements taken from each tomogram

Tomogram	Location	Measurements
Shoulder **(Fig. 1a)**	Cross section -SS- (Pork.org, 2005)	Subcutaneous fat thickness (mm) in the middle of the vertebral column and perpendicular to the skin (A) Area (mm^2) of the whole shoulder (B) Perimeter (mm) of the shoulder (C)
Loin **(Fig. 1c)**	Between: 6^{th}-7^{th}last rib 11^{th}-12^{th}last rib 14^{th}-15^{th}last rib 3^{rd}-4^{th}lumbar vertebrae	Subcutaneous fat thickness (mm) in the middle of the vertebral column and perpendicular to the skin (D) Maximum width (mm) of the right loin (E) Lateral fat thickness (mm) of right loin eye perpendicular to the skin, at the bottom and in the right side of the loin (F) Right loin eye area (mm^2) (G) Right loin perimeter (mm) (H) Maximum length of the 2 loins (mm) (I)
Ham **(Fig. 1b)**	Cross section -N- (Pork.org, 2005)	Maximum vertical height (mm) of the ham (J) Subcutaneous fat thickness (mm) at the top of the ham and perpendicular to the skin (K) Area of the ham's subcutaneous fat (mm^2) (L) Ham's width (mm) above the bones (M) Lateral fat thickness (mm) at the previous level (N) Area of the ham (mm^2) (O) Perimeter --- Perimeter (mm) of the whole ham (P)

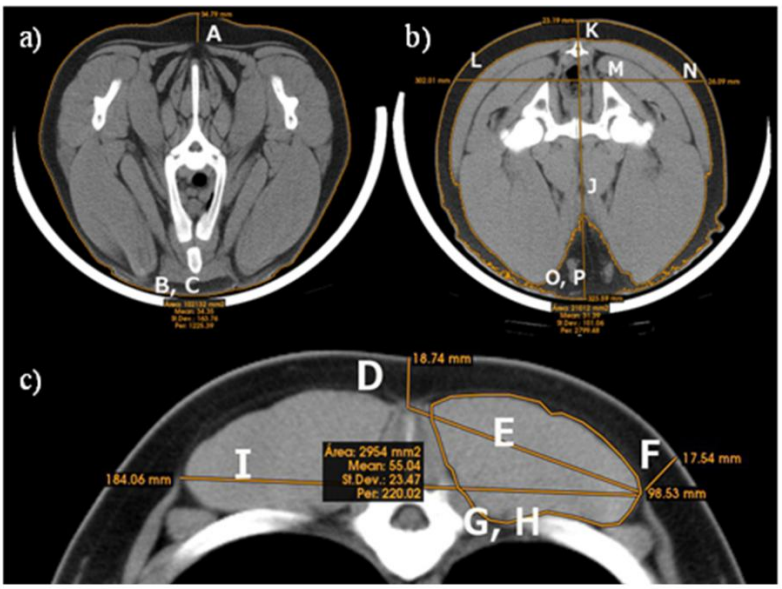

Figure 2. Measures obtained from CT images in the shoulder (a), in the ham (b) and in the loin (c).

Statistical analyses

Statistical analysis were performed using SAS software (version 9.2, SAS Institute Inc, Cary, NC, USA).

Differences between phenotypic measurements. In Chapters 5 and 7, a MIXED procedure with repeated measures was used to determine whether significant differences between treatments existed. The model included GEN or SEX (depending on the experiment), TBW and their interaction as the fixed effects. The type of covariance matrix used in the model was selected for each parameter analysed as those that presented the lowest value of the Akaike's information criterion (AIC) or the corrected Akaike's information criterion (AICC). Tukey's test was used to compare the least-squared mean valued at the 0.05 significance level.

Prediction equations. In Chapters 4 and 6 the REG procedure was used to determine the best predictors for the regression equations. In Chapter 4, four different regression approaches were performed: 1) Linear regressions using CT volumes or CT ratios of volumes as predictors, 2) Quadratic regressions using the previous CT volumes or ratios and their squared value as predictors, 3) Allometric equations (linearized as log$Y$ = log$a$ + b.log$X$) and 4) Linear regressions using CT volumes, ratios of volumes and direct physical measurements. In Chapter 6, the same equation for GEN and SEX was used to predict carcass and cuts composition. To do that, linear and non-linear regressions were performed and the models included the values from dissection as the dependent variables, and CT predictors as independent variables for animals of different GEN or SEX. Then, the MIXED procedure was used to detect differences in regression parameters among GEN or SEX. The model included GEN or SEX as a class and the predictors obtained from the REG procedure. Even if the GEN or SEX effect was significant, the equations selected were those that presented lower variance than the variance within GEN or SEX and TBW. The accuracy and precision of each equation were evaluated from the R^2 and the Root Mean Square Error (RMSE). Moreover, to investigate lack of fit of equations for both data sets, without distinction of GEN or SEX, the Mean Square Error of Prediction (MSEP) was decomposed into mean bias, slope bias and random error. Ideally, most of the error should reside in the random component of MSEP (Tedeschi, 2006). If the proportion of random error for any of the groups was lower than 0.70, another regression was performed using different predictors. Furthermore, when necessary to standardize the variance, the dependent and independent variables were transformed into natural logarithms.

Allometric growth. In Chapters 4, 5 and 7 the allometric equation $Y = aX^b$ *was chosen to model the growth of the main cuts and tissues.* The equation was linearized as follows:

$$\log Y = \log a + b * \log X$$

where Y is the weight of the tissue, and X is the live weight or the weight of the cut, depending of the variable analysed; a is an intercept and b is the allometric growth coefficient that describes the relationship between the two body constituents. A unity of the allometric growth is assumed if b = 1; then, Y grows at the same proportional rate as X; if b >1, Y grows proportionately faster

than *X*, and the opposite is true if *b* < 1. To determine the allometric coefficients for each GEN or SEX, a MIXED procedure was applied, including GEN/SEX as a fixed effect, the natural log of BW as the covariate within GEN/SEX, and the repeated subject was the animal (ID). Tukey's test was used to compare the least-square mean values at the 0.05 significance level.

Estimation of mature body weight (MBW). In Chapter 7*,* the MBW of each group of pigs of Exp 2 was obtained using the Gompertz equation (Gompertz, 1825):

$$Y(t) = a.\, e^{(-be)^{(kt)}}$$

where *Y* is the BW, *t* is the time period generally expressed in days or weeks (expressed in days in the present study), *a* is an asymptote equivalent to MBW, *b* sets the displacement along the *x* axis (time; translates the graph to the left or right), *k* sets the growth rate (*y* scaling) and *e* is Euler's number. The function is simple, sigmoidal in shape, and fits a range of growth data well (Kyriazakis *et al.,* 1991, Ferguson *et al.,* 1994). It adequately describes the more rapid growth in the early stages of life and the decline in growth in the later stages. The parameters are empirically derived, but may have biological meaning attributed to them, such that comparisons can be made between different animals of different SEX. A three stage procedure was adopted for the estimation of MBW. Initially, it was necessary to establish biological minimum and maximum values for the parameters *a*, *b* and *k* from the literature (Vincek *et al.,* 2012), forcing the MBW estimates to fall between these two values of *a*. Then the NLIN procedure was applied to fit the Gompertz equation, using ID as a repeated measure. Once an average MBW (parameter *a*) and consequently parameters *b* and *k* were obtained for each SEX, the average group *b* and *k* values were used to find the individual MBW for each animal. To study the relationships between the allometric models and the MBW a MIXED procedure was used, using %MBW (100*BW/MBW) as a covariate. The selected variables were studied as a percentage of the total weight of the four main cuts and the BW was presented as a percentage of the MBW at scanning.

Comparison of the prediction equations. The criterion selected to compare both models for each parameter predicted was decomposing and studying the error into: (1) error due to central tendency (ECT), (2) error due to regression (ER) and (3) error due to disturbances or random effects (ED) (Gispert *et al.,* 2000, Tedeschi 2006). The decomposition was carried out as follows:

$$MSE = ECT + ET + ED$$
$$ECT = (\bar{\hat{Y}} - \bar{Y})^2$$
$$ER = (S_P - r \times S_O)^2$$
$$ED = (1 - r^2) \times S_O^2$$

where $\bar{\hat{Y}}$ are the mean of the predicted values, $\bar{Y}$ the mean of the observed values, S_P the standard deviation of the predicted values, S_O the standard deviation of the observed values, and r is the coefficient of correlation between predicted and observed values. ECT, ER and ED are expressed in proportion, thus, their sum is one. The bias between dissection and predictions

presented in Chapter 4 and 6 was analyzed and the standard deviation was obtained as a measure of lack of precision, also considering all three GEN together and individually, by each GEN separately. Moreover the coefficient of model determination (CD), which is the ratio of the total variance of observed data to the squared of the difference between predicted and mean of the observed data was calculated for both predictions.
It is calculated as follow (Tedeschi, 2006):

$$CD = \frac{\sum_{i=1}^{n}(Y_i - \bar{Y})^2}{\sum_{i=1}^{n}\left(\hat{Y}_i - \bar{Y}\right)^2}$$

where Y_i is the observed *i*th value, $\bar{Y}$ is the mean of the observed values and $\hat{Y}_i$ is the predicted *i*th value. The CD statistic represents the proportion of the total variance of the observed values explained by the predicted values (Loague and Green, 1991).

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Chapter 4

Results I

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Estimation of carcass composition and cut composition from computed tomography images of live growing pigs of different genotypes

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This chapter deals with:

- Comparison of predicting models
- Selection of Hounsfield volume distribution among air, fat, lean and bone

Abstract

The aim of the present work was 1) to study the relationship between cross-sectional computed tomography (CT) images obtained in live growing pigs of different genotypes and dissection measurements and 2) to estimate carcass composition and cut composition from CT measurements. Sixty gilts from three genotypes (Duroc x (Landrace x Large White), Pietrain x (Landrace x Large White), and Landrace x Large White) were CT scanned and slaughtered at 30 kg (n=15), 70 kg (n=15), 100 kg (n=12) or 120 kg (n=18). Carcasses were cut and the four main cuts were dissected. The distribution of density volumes on the Hounsfield scale (HU) were obtained from CT images and classified into fat (HU between -149 and -1), muscle (HU between 0 and 140) or bone (HU between 141 and 1400). Moreover physical measurements were obtained on an image of the loin and an image of the ham. Four different regression approaches were studied to predict carcass and cut composition: linear regression, quadratic regression and allometric equations using volumes as predictors, and linear regression using volumes and physical measurements as predictors. Results show that measurements from whole animal taken *in vivo* with CT allow accurate estimation of carcass and cut composition. The prediction accuracy varied across genotypes, body weight and variable to be predicted. In general linear models, allometric models and linear models which included also physical measurements at the loin and the ham produced the lowest prediction errors.

Keywords: computed tomography; live growing pig; carcass composition; cut composition; prediction equations.

Implications

Pig carcass composition and cut composition are determinant parameters in the optimization of the production chain. The knowledge of these characteristics with the minimum error in live pigs during growth would be useful in breeding and nutritional programs to improve the overall

economic performance of pig carcasses and to ensure an optimized production to obtain the desired product according to producers and industry demands. This paper shows the feasibility of computed tomography for this purpose and the errors of prediction obtained according to different statistical approaches.

Introduction

Pig growth and body composition are essential components of pig profitability. Weight and composition of gain change in pigs during the growing and finishing periods is determined mainly by the genetic potential and supply of nutrients (Kolstad *et al.*, 1996; Kouba *et al.*, 1999; Lambe *et al.*, 2013). Knowledge of changes in tissue composition at whole-carcass and primal-cut levels would allow the optimization of slaughter, satisfy niche market demands, and improve the economic efficiency of pork production systems. This information is required as the economic value of pig carcasses is related to the composition of primal cuts rather than the composition of the whole carcass (Marcoux *et al.*, 2007).

Serial slaughtering has traditionally been used to study the body composition of pigs during growth (Fisher *et al.*, 2003; Landgraf *et al.*, 2006). However, another method used X-ray computed tomography (CT), a non-destructive and non-invasive technique that measures the density of the tissues and allows the body composition of animals to be estimated easily (Kolstad *et al.*, 1996; Barchia *et al.*, 2010; Lambe *et al.*, 2013); thus serial slaughtering may no longer be required. Nevertheless, serial slaughtering is still needed to establish the relationship between CT data (*i.e.* total lean volume) and cutting (joints separation) and dissection (separation of the different tissues of the joints) data and to obtain prediction equations for the weight and composition of main cuts. Several studies have demonstrated that CT is an excellent tool for estimating carcass tissue composition in either pig carcasses (Judas *et al.*, 2006; Font i Furnols *et al.*, 2009; Picouet *et al.*, 2010) or live animals (Kolstad *et al.*, 1996; Kolstad, 2001). However, to the best of our knowledge, the estimation of cut composition from the CT scanning of live animal has not yet been reported. The aim of the present work was 1) to study the relationship between cross-sectional CT images obtained in live growing female pigs of different genotypes and dissection measurements and 2) to estimate carcass composition and cut composition from CT measurements.

Materials and methods

Animals and scanning procedure

The study used a total of 60 female pigs from three different genotypes, namely Duroc × (Landrace × Large White), Pietrain × (Landrace × Large White), and Landrace × Large White, respectively referred to in this paper as DU×(LD×LW), PI×(LD×LW), and LD×LW. Within each genotype, the pigs were assigned randomly to a target live weight of 30 kg (*n* = 15, five per genotype), 70 kg (*n* = 15, five per genotype), 100 kg (*n* = 12, four per genotype), or 120 kg (*n* = 18, six per genotype). The animals were reared individually on the IRTA experimental farm in Monells, Spain. Feeds were provided *ad libitum* according to a two-phase feeding program and contained

10.24 and 10.08 MJ net energy/kg, 18.00% and 17.02% crude protein, and 0.91% and 0.90% digestible lysine fed basis during the first and second phases, respectively. The feeds were formulated to satisfy or exceed the a priori estimated animal requirements using commercial standards. The second feeding phase started at approximately 25 kg body weight. When the pigs reached their assigned target weight, they were fasted for a minimum of 8 h and then transported to the IRTA New Technologies Centre (Monells, Spain), where they were anaesthetized (by intramuscular injection of azaperone at 0.1 mg/kg, ketamine at 0.2 mg/kg, and if necessary, propofol at 0.22 mg/kg), placed in a PVC cradle, and scanned using a CT device (HiSpeed Zx/I; GE Healthcare). Scanning was done following the protocol used in carcass evaluation (Font i Furnols et al., 2009) with some modifications: axial acquisition, 140 kV and 145 mA, 512 × 512 matrix, 7 mm-thickness (at the 30 kg target weight) or 10 mm-thickness (at the 70, 100, and 120 kg target weights) and displayed field of view (DFOV) between 300 and 460 mm, adapted to the size of the pig. The experiment was approved by the IRTA Ethics Committee.

Slaughter and dissection

After scanning, the pigs were transported to the experimental abattoir and slaughtered following standard procedures (after having been previously stunning with CO_2 when animals had recovered consciousness from scanning). The carcasses were kept refrigerated at 2ºC until they were processed. The left side of each carcass was prepared and cut following the European Union reference method (Walstra and Merkus, 1995) between twenty-four and forty-eight hours after slaughter. Thereafter, four primal cuts (ham, shoulder, belly, and loin) plus tenderloin were weighed and manually dissected. Lean, subcutaneous fat including the skin, intermuscular fat, and bone were separated with a knife by trained technicians, and the weights of all these tissues were recorded. All tenderloin weight was considered as lean. Descriptive statistics of these variables are provided as supplementary Table S1. Carcass lean meat percentage was calculated by dividing the overall amount of dissected meat from each primal cut plus tenderloin by the total weight of these five cuts. A factor of 0.89 was applied in accordance with Commission Regulation (EC) No. 1249/2008 to obtain the lean meat percentage of the whole carcass from the four main cuts.

Image processing

The distribution of density volumes based on the Hounsfield scale (in Hounsfield units [HU]) was obtained from CT images using the VisualPork software package, which was developed for that purpose by the University of Girona and the IRTA (Boada *et al.*, 2009; Bardera *et al.*, 2012). The cradle was removed from all the images, but the viscera was left. The frequencies of voxels between −1000 and +1400 HU were converted into volumes by means of the DFOV value, the matrix size and the image thickness value, as follows: volume = number of voxels × thickness × $(DFOV/512)^2$. Hounsfield volume distributions were studied further to determine the limits for fat, muscle, and bone tissues. From the volume distribution averaged by the target weight in the border region between muscle and bone, the change in slope after the high decrease in the lean area was selected as a cut-off and was set at an HU value of 140 (supplementary Figure S1). The HU value of 0 was selected as a separation between muscle and fat. Finally, because viscera were

included in the images, a cut-off was necessary to separate fat from tissues with less density, such as the lungs or parts of the intestines. In this case, a change in the curve was found at −149 HU because of the inner methodology of the program for determining the contour of the body, and this value was used as the cut-off. Thus, the partial volumes estimated between −149 and −1, between 0 and 140, and between 141 and 1400 were associated with fat, muscle, and bone volumes, respectively, and were used afterwards as independent variables in the regression analysis. Volumes between −1000 and −150 HU, which belong mainly to the less dense parts of the viscera, were considered only in the total volume. The relative carcass lean meat volume (PLean) was calculated as the ratio between the carcass lean meat volume and total carcass volume. Descriptive statistics of the volumes by slaughter weight and genotype are presented in Table 1.

Table 1. Mean and standard deviation (s.d.) of weights and computed tomography tissue volumes[a] obtained in live pigs of three genotypes at different live weight.

	30 kg (*n* = 15)		**70 kg (*n* = 15)**		**100 kg (*n* = 12)**		**120 kg (*n* = 18)**	
	Mean	**s.d.**	**Mean**	**s.d.**	**Mean**	**s.d.**	**Mean**	**s.d.**
LD x LW [b]								
Live wgt. (kg)	30.0	2.2	71.3	2.5	98.5	1.8	122.0	1.8
VolLean (dm^3)	18.5	1.3	41.1	2.1	50.3	5.5	60.1	4.1
VolFat (dm^3)	6.0	0.7	20.0	1.9	35.3	8.1	45.7	5.5
VolBone (dm^3)	2.2	0.1	4.4	0.2	5.7	0.3	6.7	0.4
TotalVol (dm^3)	28.7	1.9	69.5	3.1	96.2	2.2	117.2	4.3
PLean (%)	64.5	1.1	59.2	2.5	52.4	6.6	51.4	4.0
PI x (LD x LW) [b]								
Live wgt. (kg)	31.4	2.2	67.7	1.8	100.5	1.5	123.1	3.8
VolLean (dm^3)	19.2	1.4	43.1	1.3	57.2	1.5	66.6	5.1
VolFat (dm^3)	6.1	0.6	14.3	2.2	30.0	3.1	39.5	4.0
VolBone (dm^3)	2.1	0.1	4.27	0.1	5.55	0.3	6.6	0.4
TotalVol (dm^3)	29.2	2.1	65.1	2.5	96.8	1.5	117.2	2.0
PLean (%)	65.7	1.5	66.2	2.3	59.1	1.9	56.8	3.5
DU x (LD x LW) [b]								
Live wgt. (kg)	29.3	2.3	68.8	2.2	100.8	3.2	123.8	3.4
VolLean (dm^3)	18.3	0.6	41.0	3.6	53.3	2.9	63.3	2.4
VolFat (dm^3)	5.4	1.3	17.4	2.9	33.0	2.5	43.4	3.8
VolBone (dm^3)	2.2	0.1	4.6	0.2	6.2	0.2	7.2	0.3
TotalVol (dm^3)	27.8	2.1	66.4	2.1	96.6	2.2	118.7	2.2
PLean (%)	66.1	2.8	61.7	4.3	55.1	2.6	53.4	2.5

[a]VolLean: volume between 0 Hounsfield units (HU) and 140 HU; VolFat: volume between −149 and –1 HU; VolBone: volume between 141 and 1400 HU; TotalVol: volume between −150 and 1400 HU; PLean: 100 × VolLean/TotalVol. [b]LD: Landrace; LW: Large White; PI: Pietrain; DU: Duroc.

Descriptive statistics of these loin and ham direct physical measurements are presented in Table 2.

Some physical measurements have been obtained to see whether their inclusion as predictors could reduce prediction error. From an image of the loin between the third and fourth last ribs (Figure 1a - without considering the fals rib), the following six direct physical measurements were obtained: i) maximum loin width (I); ii) loin area (G); iii) loin perimeter (H); iv) diagonal (maximum length) of the *longissimus thoracis* muscle (E); v) lateral subcutaneous fat thickness at the lateral extreme of the *longissimus thoracis* muscle and perpendicular to the skin (F); and vi) superior subcutaneous fat thickness at the centre of the dorsal part of the body and perpendicular to the skin (D). From an image of the ham (at the junction of the femur and pubis bones - Figure 1b), the following five direct physical measurements were obtained: i) width of the ham above the pubis bone (M); ii) area of the subcutaneous fat of the whole image (L); iii) lateral subcutaneous fat thickness at the same level as the width measurement (N); iv) subcutaneous fat thickness at the centre of the dorsal part of the body and perpendicular to the skin (K); and v) perimeter of the whole image of the ham (P). All lengths and areas were measured in millimetres and square millimetres, respectively.

Statistical analysis

The relationships between dependent variables (carcass and cuts composition) and independent variables (the CT-measured volume, ratio of volumes or physical measurements) were studied within genotypes, as preliminary analyses showed large differences between the studied genetic lines. Four different regression approaches, all performed with the REG procedure of the SAS software package (version 9.2; SAS Institute Inc., Cary, NC, USA), were studied. Because of the heteroscedasticity of variances related to the differences in slaughter weight, all the analyses were performed by weighting at each target weight the dependent variables by the inverse of the standard deviation of the residuals (weighted least squares approach). This practice allowed better estimation of the variables of interest within weight groups and adequate distribution of the residuals. The regression approaches studied were the following (see Table 3 for a detailed description of predictors):

- Linear regressions using CT volumes or CT ratios of volumes as predictors.
- Quadratic regressions using the previous CT volumes or CT ratios of volumes and their squared value as predictors.
- Allometric equations ($y = a \cdot x^b$ linearized as $\log y = \log a + b \cdot \log x$), in which CT predictors were chosen as for the previous regression models.
- Linear regression using CT volumes, CT ratios of volumes, and direct physical measurements recorded on loin and ham images as predictors. Predictors were selected using the stepwise procedure of SAS (selected criteria: $P<0.15$) and subjective criteria maximizing the coefficient of determination (R^2) and minimizing root mean square error (RMSE).

Table 2. Descriptive statistics (mean and standard deviation [s.d.]) of direct physical measurements (in mm or mm^2) taken from whole-animal CT images.[a]

	30 kg (*n* =15)		70 kg (*n* =15)		100 kg (*n* =12)		120 kg (*n* =18)	
	Mean	**s.d.**	**Mean**	**s.d.**	**Mean**	**s.d.**	**Mean**	**s.d.**
LD x LW								
Loin area	1307	58	3348	337	3932	481	4613	434
Loin perimeter	157	7	225	4	248	11	259	13
Loin width	140	3	181	2	195	8	209	10
Loin sup. subc. fat	7	1	16	1	30	3	34	5
Loin lat. subc. fat	7	1	13	3	22	8	24	4
Loin diagonal	75	2	98	1	102	6	110	5
Ham perimeter	255	10	245	6	275	11	305	10
Ham sup. subc. fat	5	1	8	3	17	4	24	6
Ham lat. subc. fat	5	1	11	2	18	3	27	5
Ham perimeter	750	26	925	32	1097	22	1226	55
Ham fat area	4037	771	9788	791	14539	4104	20993	3451
PI x (LD x LW)								
Loin area	1526	146	3669	375	5090	353	5158	693
Loin perimeter	161	9	234	10	270	8	266	17
Loin width	132	5	183	4	209	5	207	10
Loin sup. subc. fat	10	1	16	3	29	6	30	4
Loin lat. subc. fat	6	1	11	2	19	4	25	6
Loin diagonal	70	3	99	3	107	2	105	7
Ham perimeter	253	13	258	12	294	5	311	9
Ham sup. subc. fat	6	2	8	3	16	4	20	4
Ham lat. subc. fat	6	1	9	1	17	2	19	3
Ham perimeter	784	46	1025	39	1191	26	1258	51
Ham fat area	3709	767	8462	1141	12024	1643	16144	2646
DU x (LD x LW)								
Loin area	1527	86	3119	406	5026	273	5057	464
Loin perimeter	157	4	220	9	267	7	269	11
Loin width	132	1	175	8	208	6	214	7
Loin sup. subc. fat	9	1	16	2	29	3	35	4
Loin lat. subc. fat	6	2	13	3	18	3	25	6
Loin diagonal	71	2	92	5	108	3	109	5
Ham perimeter	252	9	242	6	282	13	299	10
Ham sup. subc. fat	6	2	9	1	14	1	23	5
Ham lat. subc. fat	7	2	10	2	18	2	20	3
Ham perimeter	742	73	992	18	1151	81	1217	75
Ham fat area	3735	372	8396	715	13286	1838	17334	1886

[a]Direct physical measurements were used as dependent variables (predictors) in the prediction equations. All lengths and areas are in millimetres and square millimetres, respectively.
LD: Landrace; LW: Large White; PI: Pietrain; DU: Duroc; sup.: superior; subc.: subcutaneous; lat.: lateral.

Table 3. Predictors used for each approach.

		Linear/Allometric[a]	Quadratic[a]	Combination[b]
Lean meat %		PLean	PLean, PLean2	Ham perimeter, ham superior subcutaneous fat, loin superior subcutaneous fat thickness, loin lateral subcutaneous fat thickness, diagonal muscle thickness, area
Main cuts				
	Lean	VolLean	VolLean, VolLean2	Ham width, loin width
	Fat	VolFat	VolFat, VolFat2	Loin superior subcutaneous fat, ham superior subcutaneous fat
	Bone	VolBone	VolBone, VolBone2	–
Ham				
	Weight	TotalVol	Total, Total2	Loin superior subcutaneous fat
	Lean	VolLean	VolLean, VolLean2	Loin superior subcutaneous fat
	Fat	VolFat	VolFat, VolFat2	Ham superior subcutaneous fat and fat area of the ham
	Bone	VolBone	VolBone, VolBone2	Ham lateral fat
Loin				
	Weight	TotalVol	Total, Total2	Loin superior subcutaneous fat
	Lean	VolLean	VolLean, VolLean2	Loin area, loin perimeter
	Fat	VolFat	VolFat, VolFat2	Ham superior subcutaneous fat, loin superior subcutaneous fat
	Bone	VolBone	VolBone, VolBone2	Ham perimeter, loin superior subcutaneous fat
Shoulder				
	Weight	TotalVol	Total, Total2	Loin superior subcutaneous fat
	Lean	VolLean	VolLean, VolLean2	Ham subcutaneous fat area
	Fat	VolFat	VolFat, VolFat2	Ham perimeter
	Bone	VolBone	VolBone, VolBone2	Ham superior subcutaneous fat, loin lateral fat
Belly				
	Weight	TotalVol	Total, Total2	Loin superior subcutaneous fat
	Lean	VolLean	VolLean, VolLean2	Loin area, PLean
	Fat	VolFat	VolFat, VolFat2	Ham lateral subcutaneous fat
	Bone	VolBone	VolBone, VolBone2	VolLean, loin superior subcutaneous fat
Filet		VolLean	VolLean, VolLean2	Loin superior subcutaneous fat

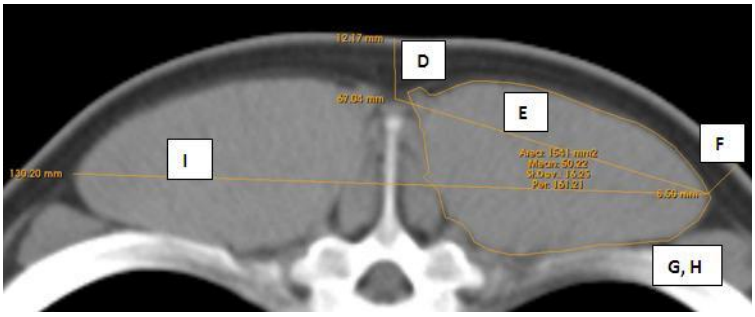
[a]VolLean: volume between 0 Hounsfield units (HU) and 140 HU; VolFat: volume between −149 and –1 HU; VolBone: volume between 141 and 1400 HU; TotalVol: volume between −150 and 1400 HU; PLean: 100 × VolLean/TotalVol. [b]Predictors were the volume or ratio used in the linear approach plus the variables in this column. These variables are not always the same for all the genotypes.

The use of prediction models with only direct physical image measurements was not considered, as previous results showed lower prediction accuracy compared with the use of volumes. Transformation of CT volumes to weight by means of voxel densities was also considered, but preliminary results also showed low prediction accuracy and it was decided to work directly with volumes.

Parameters used to quantify the predictive ability of the equations were the R^2 and the RMSE. Furthermore, the coefficient of variation (CV_c), that is, the percentage of RMSE with respect to the mean, was calculated to make errors comparable.

A cross-validation leave-one-out was used to determine the RMSE of prediction (RMSEPCV) by means of a SAS macro adapted from those presented by Caseur *et al.,* (2003). The CV_p computed as the percentage of RMSEPCV with respect to the mean, was calculated. Equations with the lowest CV_p for each trait and genotype were selected.

a)



b)

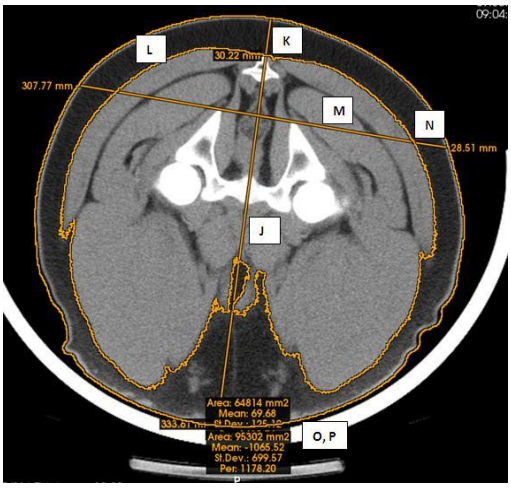


Figure 1. Physical direct measurements taken at the loin (a) and ham (b). (D: superior subcutaneous fat thickness; E: diagonal of the *longissimus thoracis* muscle; F:lateral subcutaneous fat thickness; G: loin area; H: loin perimeter; I: maximum loin width; K: subcutaneous fat thickness at the centre; L: area of the subcutaneous fat; M: width of the ham; N: lateral subcutaneous fat thickness; P: perimeter of the whole ham).

Results and discussion

The distribution of volumes associated with each HU value by genotype and target live weight is presented in Figure 2. As expected, the volume of live pigs increases as they grow older and heavier. Furthermore, from 70 kg live weight (Figure 2b), a fat peak start appearing (-80 to -120 HU) and grows as pigs gets heavier (Figures 2c and 2d) indicating that fat is deposited at late stages of life. This is corroborated by the fact that some works have shown that the allometric coefficient of fat tissue is higher than one indicating that fat is a late mature tissue (Kouba *et al.*, 1999; Landgraf *et al.*, 2006). It is possible to see differences in the shape of the curve depending on the genotype at each target weight, pointing out that tissue growth patterns differ among genotypes: LD x LW pigs are fatter, PI x (LD x LW) are leaner and DU x (LD x LW) are in between.

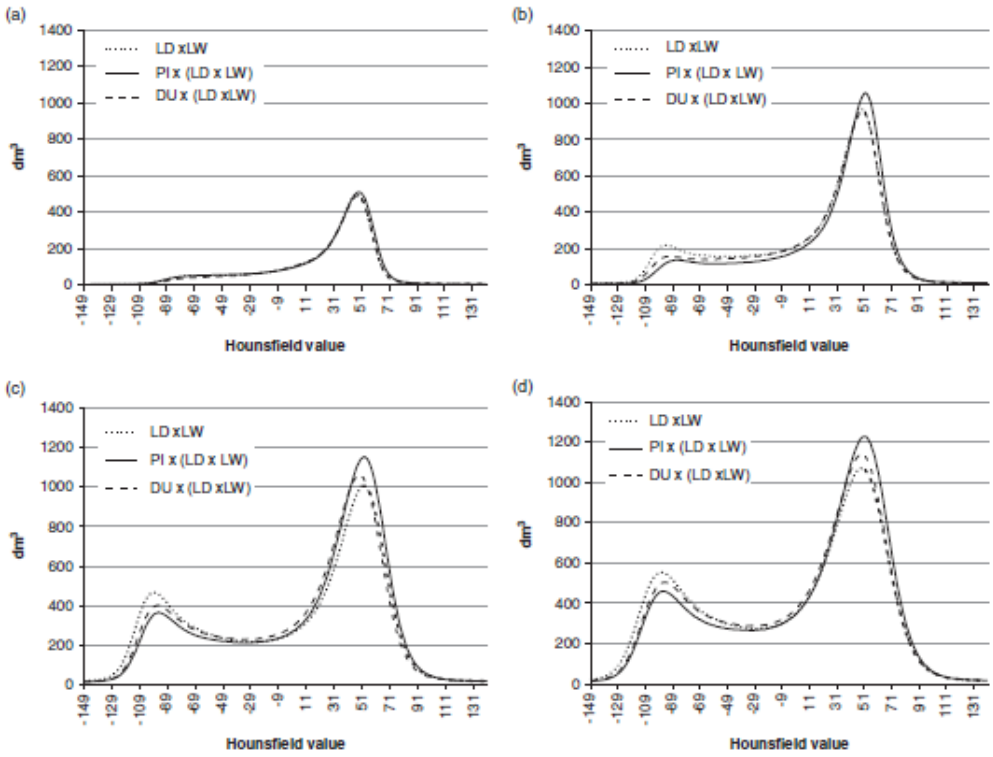


Figure 2. Average volumes associated with each Hounsfield value (in Hounsfield units [HU]) in the fat and lean area by genotype at target weights of (a) 30, (b) 70, (c) 100, and (d) 120 kg. Genotypes: LD×LW, Landrace × Large White; PI×(LD×LW), Pietrain × (Landrace × Large White); DU×(LD×LW), Duroc × (Landrace × Large White).

Fat and muscle thicknesses, perimeters, and areas obtained from CT images taken at specific anatomical positions in live pigs have been proven to be good predictors of carcass traits in young pigs (30 kg live weight) (Carabús *et al,.* 2011). Nevertheless, the use of images from the whole animal provides more complete information on its composition and allows more accurate determination of fat, lean, and bone volumes for the whole carcass. However the combination of both types of CT information improve prediction equations of some parameters such as lean meat %, loin weight and loin composition. The relationship between lean, fat, and bone of the carcass,

obtained by dissection of the four main cuts, and volumes associated with these tissues in CT images of whole live pigs (viscera included) of different genotypes and live weights is very strong ($r > 0.99$ for all the tissues and genotypes, Figure 3). It is strong although: (1) volumes are obtained from live pigs and dissection variables are obtained from cutting and dissection of half carcasses; (2) the live pig images also included white viscera and organs that do not belong in the carcass (some of them are closer to the muscle signal, some others are closer to the fat signal and some others closer to the air signal). The relative weight of white viscera and organs decreases or is kept constant with increasing animal weight, with the exception of flare fat (Font-i-Furnols *et al.,* 2012). Landgraf *et al.* (2006) also found a constant percentage of heart, spleen, and kidney, and a decrease in the percentage of lungs and liver during growth. In the present study, the lungs were almost completely removed from the analysis because of their low density (HU values lower than −140), and in agreement with Landgraf *et al.,* (2006) and Font-i-Furnols *et al.,* (2012), the proportion of the liver with respect to live body weight was low (2.3-2.9% at 30 kg and 1.4%-1.5% at 120 kg). As explained before, the weights of the lean, fat, and bone tissues of the main cuts are strongly related to the corresponding volumes obtained from the CT images of whole live pigs (Figure 3). Further research might be done to determine if scanning of live young piglet could be a good predictor of slaughter performances.

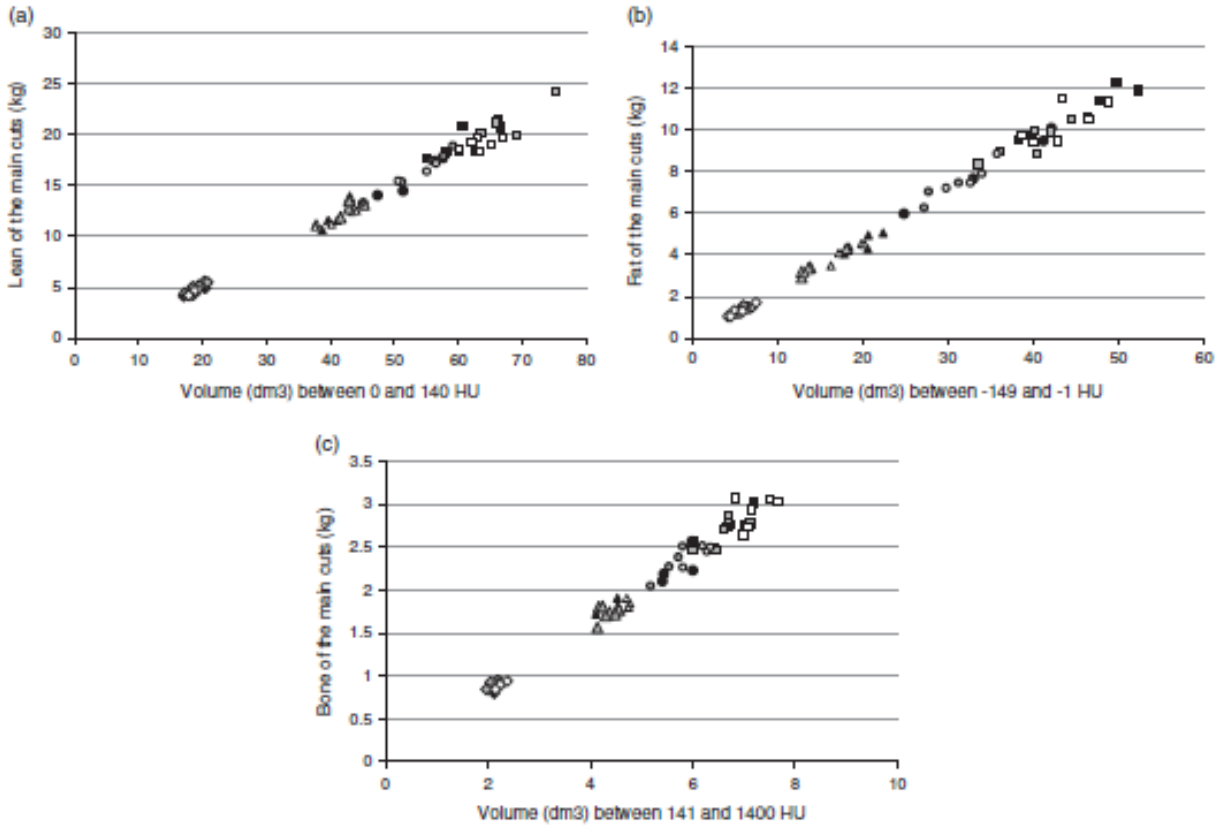


Figure 3. Relationship between the lean (a), fat (b), and bone (c) of the main cuts with the volume of different tissues obtained from the scan of live pigs of different genotypes and weights ($r > 0.99$ for each genotype). Genotypes: black symbols, Landrace × Large White; grey symbols, Pietrain × (Landrace × Large White); white symbols, Duroc × (Landrace × Large White). Target weights: ♦, 30 kg; ▲, 70 kg; ●, 100 kg; ■, 120 kg. HU: Hounsfield units.

The accuracy of the prediction in terms of relative RMSE (CV_c) and RMSEPCV (CV_p) of carcass composition and cut composition traits for each evaluated model is presented in Table 4 for LD x LW, in Table 5 for PI x (LD x LW) and in Table 6 for DU x (LD x LW). These predictions have been done for each genotype across the different weight categories. The large body weight range is responsible for the high R^2 values ($0.89 < R^2 < 0.95$) observed in all the prediction models. These R^2 values were somewhat lower when estimating lean meat percentage but were always higher than 0.86. In general, differences in CV_c between the quadratic and linear models are small, indicating that the inclusion of the quadratic term can seldom improve prediction accuracy. However when CV_p is considered, in general linear models produced lowest values in comparison with quadratic model, thus, they appear to be more robust. The allometric model yield the lowest CV_p values for some of the variables of interest, especially for PI x (LD x LW), although in some cases differences in comparison with the other models do not seem as large. Allometric model is useful for predicting tissue growth with respect to weight (Davies and Pryor, 1977; Kempster and Evans, 1979; Kouba and Bonneau, 2009), and also in some traits it can be the best choice for estimating tissue growth from tissue volume obtained by CT. Combining the information provided by tissue volumes and measurements (thicknesses, areas, or perimeters) improves the accuracy of some of the predictions, especially for LD x LW and DU x (LD x LW). This effect is very important in the estimation of lean meat percentage of the carcass. This importance makes sense, since in carcass classification, linear measurements of fat and muscle depth is well documented (Font i Furnols and Gispert, 2009; Engel *et al.*, 2012). Including physical measurements in the estimation of carcass fat content also reduced the error (CV_p between 3.89% and 6.70%). In a recent study, Lambe *et al.* (2013) showed correlation coefficients of 0.53, 0.14, and −0.28 between fat thicknesses measured in CT images and, respectively, fat, muscle, and bone weights obtained by dissection. Bone weights for the four main cuts have been estimated with similar accuracy in all the studied models.

Table 4. Coefficients of variation of calibration[a] and validation[b] (%) of different prediction models and coefficient of determination (R^2) of overall carcass lean meat and cut weights and tissue weights for Landrace × Large White pigs.

		Lineal			Quadratic			Allometric			Lineal + linear measurements		
	Mean	CV_c	CV_p		CV_c	CV_p		CV_c	CV_p		CV_c	CV_p	
Lean meat %	55.46	2.39	2.60		2.14	2.46		2.34	2.55		1.42	1.81	*
Main cuts[c] (g)													
Lean	12803	5.45	5.85		5.03	5.80		5.01	5.41	*	4.25	5.57	
Fat	6402	4.28	4.65		4.29	5.08		4.30	4.68		3.44	3.89	*
Bones	1934	4.42	4.77	*	4.40	4.99		4.41	4.77		4.42	4.77	
Ham (g)													
Weight	7642	5.40	5.80		5.24	5.90		5.28	5.66	*	5.27	5.92	
Lean	5097	5.58	6.08		5.00	5.86		5.10	5.54	*	5.03	5.58	
Fat	1921	6.73	7.35		6.76	8.31		6.81	7.45		5.42	5.97	*
Bones	623	5.59	5.96		5.53	6.36		5.64	5.99		5.08	5.65	*
Loin (g)													
Weight	5205	6.04	6.56		5.83	6.77		5.90	6.44		5.17	6.22	*
Lean	2780	6.65	7.06		6.66	7.51		7.80	8.33		5.40	6.85	*
Fat	1774	8.50	9.23		8.14	9.31		8.16	8.99		8.42	8.44	*
Bones	651	8.60	9.36		8.41	9.57		8.59	9.32		7.86	9.17	*
Shoulder (g)													
Weight	4340	8.84	9.48	*	8.75	9.63		8.84	9.48		8.85	10.29	
Lean	2716	8.06	8.63		7.64	8.90		7.84	8.38		7.87	8.36	*
Fat	1200	10.01	10.84		8.53	9.73	*	8.96	9.77		9.19	10.63	
Bones	425	5.57	5.90	*	5.49	6.09		5.63	5.99		5.03	6.62	
Belly (g)													
Weight	3503	9.27	10.08		8.67	9.84		8.76	9.53	*	9.30	11.18	
Lean	1760	10.49	11.32		9.84	11.02		9.99	10.79	*	8.91	11.84	
Fat	1507	10.43	11.53	*	10.46	12.24		10.86	11.90		9.35	11.57	
Bones	236	8.50	9.23		8.36	9.25		8.48	9.21		7.06	8.78	*
Tenderloin (g)	450	5.13	5.61	*	5.14	6.20		5.45	5.96		9.43	11.14	
R^2 **Lean%**		0.92			0.94			0.93					
R^{2d}		>0.94			>0.94			>0.94					

CV_c: 100*(Root mean square error-RMSE/Mean)

CV_p: 100*(RMSE of prediccion by cross-validation-RMSEPCV/Mean)

[c]: Ham, loin, shoulder, belly and tenderloin (tenderloin only for lean)

[d]: Rest of the variables

*: Equation with the lowest CV

Table 5. Coefficients of variation of calibration[a] and validation[b] (%) of different prediction models and coefficient of determination (R^2) of overall carcass lean meat and cut weights and tissue weights for Pietrain x (Landrace × Large White) pigs.

		Lineal			Quadratic			Allometric			Lineal + linear measurements		
	Mean	CV_c	CV_p		CV_c	CV_p		CV_c	CV_p		CV_c	CV_p	
Lean meat %	60.03	2.16	2.41		2.08	2.50		2.14	2.39		1.41	1.73	*
Main cuts[c] (g)													
Lean	14532	2.68	2.83		2.57	2.85		2.59	2.73	*	2.39	2.85	
Fat	5489	5.13	5.70		4.80	5.57		5.38	5.98		4.72	5.50	*
Bones	1922	4.52	4.91	*	4.49	5.34		4.57	4.95		4.52	4.91	
Ham (g)													
Weight	8212	4.27	4.66	*	4.06	4.70		4.48	4.89		4.15	4.69	
Lean	5964	4.48	4.86		4.48	5.10		4.56	4.96		4.14	4.63	*
Fat	1628	5.23	5.83		5.06	5.97		5.21	5.81	*	5.22	6.37	
Bones	620	4.21	4.51	*	4.17	4.93		4.28	4.58		4.05	4.70	
Loin (g)													
Weight	5362	4.33	4.73	*	4.26	4.95		4.38	4.80		4.25	5.32	
Lean	3232	4.96	5.41	*	4.84	5.67		4.97	5.40		3.11	3.91	
Fat	1485	10.39	11.43	*	10.29	11.88		10.38	11.50		7.85	11.59	
Bones	645	8.66	9.43	*	8.33	9.74		8.70	9.44		8.62	9.83	
Shoulder (g)													
Weight	4571	4.84	5.19		4.45	5.12	*	4.99	5.36		4.81	5.46	
Lean	3001	4.14	4.44		4.09	4.64		4.09	4.40	*	4.14	4.61	
Fat	1138	9.51	10.34		6.91	8.61	*	8.81	9.59		8.31	9.24	
Bones	431	7.19	7.60		6.91	7.97		7.17	7.57	*	6.55	8.31	
Belly (g)													
Weight	3311	8.47	9.14		8.11	9.29		8.21	8.88	*	7.96	8.94	
Lean	1848	9.85	10.61		9.46	10.67		9.64	10.40	*	9.67	12.10	
Fat	1238	9.40	10.49	*	9.04	10.85		9.67	10.78		9.07	10.60	
Bones	225	8.38	9.07		8.35	9.44		8.34	9.02	*	6.64	9.60	
Tenderloin (g)	487	6.67	7.17		6.55	7.38		6.57	7.01	*	10.44	11.86	
R^2 Lean%		0.87			0.88			0.88			0.95		
R^{2d}		>0.94			>0.94			>0.94			>0.95		

CV_c: 100*(Root mean square error-RMSE/Mean) CV_p: 100*(RMSE of prediccion by cross-validation-RMSEPCV/Mean) [c]: Ham, loin, shoulder, belly and tenderloin (tenderloin only for lean)
[d]: Rest of the variables *: Equation with the lowest CV_p

Table 6. Coefficients of variation of calibration[a] and validation[b] (%) of different prediction models and coefficient of determination (R^2) of overall carcass lean meat and cut weights and tissue weights for Duroc x (Landrace × Large White) pigs.

			Lineal			Quadratic			Allometric			Lineal + linear measurements	
		Mean	CV_c	CV_p		CV_c	CV_p		CV_c	CV_p		CV_c	CV_p
Lean meat %		56.59	2.61	2.93		2.54	2.93		2.59	2.91		1.53	2.02*
Main cuts[c] (g)													
	Lean	13053	3.14	3.37		3.04	3.51		3.92	4.16		2.79	3.28*
	Fat	5984	6.75	7.34		6.81	7.87		6.79	7.36		5.45	6.70*
	Bones	2040	4.82	5.08	*	4.69	5.11		4.87	5.13		4.82	5.08
Ham (g)													
	Weight	7461	3.78	4.03		3.43	4.03		3.99	4.25		3.44	3.97*
	Lean	5128	4.55	4.85		4.07	4.58	*	5.41	5.82		4.50	4.95
	Fat	1695	7.58	8.35		7.57	8.95		7.68	8.41		6.82	7.72*
	Bones	638	3.00	3.25	*	2.98	3.39		3.06	3.33		2.99	3.51
Loin (g)													
	Weight	5344	8.99	9.60		8.34	9.57		8.33	8.98		5.78	6.65*
	Lean	2982	8.95	9.36		8.78	9.98		8.70	9.20		5.71	7.23*
	Fat	1689	16.44	17.29		16.35	18.42		15.84	16.59	*	9.18	17.74
	Bones	673	9.90	10.70		9.56	10.70		10.00	10.78		7.32	8.57
Shoulder (g)													
	Weight	4445	4.14	4.48	*	4.11	4.62		4.23	4.58		4.10	4.65*
	Lean	2738	5.61	6.00		5.61	6.30		5.72	6.15		4.61	5.19
	Fat	1237	7.20	7.86		7.03	7.90		6.92	7.49		6.05	6.95*
	Bones	470	7.74	8.35	*	7.74	8.68		7.75	8.37		6.53	8.64*
Belly (g)													
	Weight	3387	6.04	6.58	*	5.78	6.73		6.90	7.52		5.84	6.85
	Lean	1766	5.48	5.93		4.84	5.66	*	6.53	7.09		5.33	6.42
	Fat	1362	10.67	11.64		9.73	11.24	*	11.13	12.17		10.47	11.68
	Bones	259	7.51	8.14	*	7.50	8.71		7.51	8.14		6.93	9.23
Tenderloin (g)		440	10.21	10.69		10.25	11.25		10.32	10.85		7.49	8.08*
***R^2* Lean%**			0.86			0.87			0.86			0.95	
R^{2d}			>0.94			>0.95			>0.94			>0.95	

CV_c: 100*(Root mean square error-RMSE/Mean)

CV_p: 100*(RMSE of prediccion by cross-validation-RMSEPCV/Mean)

[c]: Ham, loin, shoulder, belly and tenderloin (tenderloin only for lean)

[d]: Rest of the variables

*: Equation with the lowest CV_p

Regarding ham weight, the lowest CV_p was obtained with the allometric model for LDxLW genetic line (RMSEP = 432 g), with the lineal model for the PIx(LDxLW) genetic line (RMSEPCV = 382g) and with the lineal model plus measurements for the DUx(LDxLW) genetic line (RMSEPCV = 296 g). Linear, allometric and linear models using physical measurements obtained the lowest CV_p for ham lean, fat, and bone contents. The CV_p of the different ham tissues and ham weight were similar. However, in almost all cases, these errors were slightly higher than those obtained when estimating the tissue composition of the four cuts together. This difference makes sense, because these estimates were obtained from whole-animal images, which are closer to the composition of the four main cuts than to that of only the ham. Nevertheless, different ham tissue weights are highly correlated with the tissue volumes of the whole body of the live pig ($r \geq 0.99$ for the weight and all the tissues for each genotype; Figure 4). However, the errors for loin weight (CV_p between 4.73% and 6.65%) were lower than those observed for fat (CP_p: 8.44% to 16.59%), and bone (CP_p: 8.57% to 9.43%) tissues. In general CV_p was higher for loin than those observed for ham parameters. This difference indicates that whole-body composition presents a higher correlation with ham composition than with loin composition. It also shows that ham composition is a good predictor of whole-body volumes.

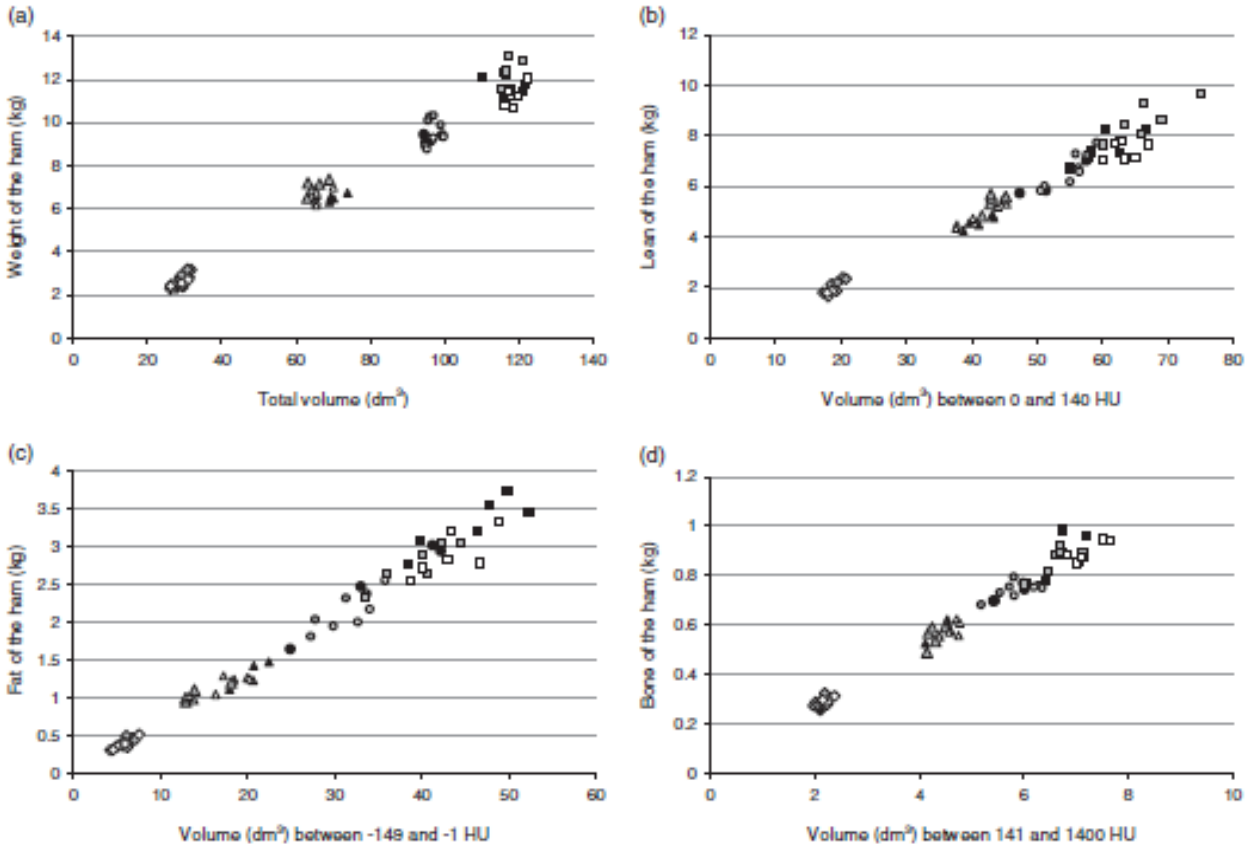


Figure 4. Relationship between (a) the weight (kg), (b) the lean (kg), (c) the fat (kg) and (d) the bone (kg) of the ham with the total, lean, fat and bone volume respectively, obtained from the scan of live pigs of different genotypes and weights ($r > 0.989$ for each genotype). Genotypes: black symbols, Landrace × Large White; grey symbols, Pietrain × (Landrace × Large White); white symbols, Duroc × (Landrace × Large White). Target weights: ♦, 30 kg; ▲, 70 kg; ●, 100 kg; ■, 120 kg. HU: Hounsfield units.

It has been reported that cutting error is greater in the separation of the shoulder from the carcass than in the separation of the ham (Nissen *et al.*, 2006). This can probably explain higher CV_p in the shoulder parameters compared with the ham ones. Thus, the obtained CV_p values were between 4.48% and 9.48% (RMSE between 184 and 384 g) for shoulder weight, between 4.40% and 8.36% for lean weight, between 6.95% and 9.73% for fat weight, and between 5.90% and 8.35 % for bone weight.

The belly was the cut for which weight and composition were predicted the worst from whole-pig CT images, although the relative errors were not considerably higher than those for the shoulder. According to Nissen *et al.* (2006), the belly produces a high dissection error because of the thin layers of fat and muscle, which are difficult to separate by knife. Additionally, these thin layers may also be the reason for the large number of voxels with partial volume effects, which makes it difficult to assign a given tissue type. There are some differences in the relationship between the lean volume and the weight of the lean of the different cuts. In accordance with the prediction results, this relationship is less precise in the belly than in the other cuts ($r > 0.98$-0.99 in the loin and shoulder and $r \geq 0.97$-0.99 in the belly, depending on the genotype; Supplementary Figure S2 to Supplementary Figure S4).

Tenderloin weight error was quite different across the genetic lines. These differences are probably due to the fact that the proportion of fillet in the whole pig body is very small, and consequently, its correlation with whole-body tissue composition is low.

Due to the observed differences in tissue growth patterns, prediction equations were obtained by genotype between 30 and 120 kg body weight, and it is worthwhile to see if they fit within weight group. Using the models that yielded the lowest error within genotypes (Tables 4, 5 and 6), prediction equations by weight group was drawn and their respective accuracy was assessed (Table 7 - selected prediction equations are presented in Supplementary Table S2). Lean meat percentage is estimated well for all the slaughter weights, although the accuracy is lower for the lightest carcasses. CT resolution in 30 kg animals probably is better than in heavier pigs, because of lower displayed field of view applied and lower thickness of the image, thus, this difference in accuracy is probably mainly due to difficulties in applying the European cutting procedures (Walstra and Merkus, 1995) and separating the tissues, in particular fat, in 30 kg carcasses. In fact, for the four main cuts, fat tissue shows the highest relative error, with values ranging from 6.42% in the shoulder to 13.97% in the loin. It is also important to note that loin bone and belly bone predictions had lower accuracy in terms of R^2 that was not significant ($P > 0.05$). Loin and belly fat estimates for the 70 kg animals also had a low accuracy, with CV values around 12%. However, in terms of R^2, the lowest accuracy was for loin bone and belly lean weight ($R^2 < 0.16$). At the 100 kg target weight, models predicting loin and belly weights did not explain a significant portion of the observed variances. At the 120 kg target slaughter weight, loin weight and bone were predicted much better than at the other target weights, while loin fat was predicted with worst accuracy than at 100 kg. Lambe *et al.* (2013) also found higher R^2 values between dissected and CT-predicted fat, muscle, and bone of the carcass side with increasing live weight (60, 85, and 115 kg). Moreover, all the belly parameters estimated in the present study also had higher or

similar accuracy at the 120 kg target weight than at the others. This can be explained with the fact that heavier carcasses are easier to cut and dissect, although that does not seem to be the case with the shoulder. In fact, only the models predicting shoulder weights at the 120 kg target slaughter weight did not explain a significant portion of the observed variation, probably because, as reported by Nissen *et al.* (2006), cutting error is the highest for this cut.

Table 7. Coefficient of variation (CV)[a] and coefficient of determination (R^2)[b] calculated within weight groups using prediction equations yielding the lower prediction error within genotypes and across weight groups.

		30 kg	70 kg	100 kg	120 kg
		CV(%) / R^2	CV(%) / R^2	CV(%) / R^2	CV(%) / R^2
Lean meat %		1.52 / 0.64	1.31 / 0.95	1.40 / 0.97	1.55 / 0.94
Main cuts[c]					
	Lean	2.97 / 0.91	3.32 / 0.81	2.19 / 0.97	2.20 / 0.87
	Fat	6.72 / 0.79	4.30 / 0.94	3.50 / 0.95	3.98 / 0.88
	Bone	2.76 / 0.68	4.39 / 0.29	3.94 / 0.71	4.56 / 0.58
Ham					
	Weight	4.56 / 0.83	3.53 / 0.61	2.42 / 0.81	4.63 / 0.36
	Lean	4.88 / 0.85	3.01 / 0.90	2.94 / 0.94	4.75 / 0.79
	Fat	9.44 / 0.60	5.32 / 0.88	4.55 / 0.94	5.10 / 0.84
	Bone	3.25 / 0.69	4.63 / 0.50	2.33 / 0.80	4.29 / 0.66
Loin					
	Weight	5.63 / 0.76	5.43 / 0.65	5.27 / *0.29*	3.98 / 0.58
	Lean	6.44 / 0.67	5.81 / 0.76	3.75 / 0.92	4.98 / 0.74
	Fat	13.97 / 0.58	12.87 / 0.83	7.04 / 0.92	10.67 / 0.54
	Bone	7.93 / *0.06*	8.08 / *0.01*	8.69 / 0.34	6.45 / 0.48
Shoulder					
	Weight	3.25 / 0.85	3.62 / 0.51	5.84 / 0.36	6.04 / *0.03*
	Lean	3.34 / 0.85	4.05 / 0.74	3.48 / 0.93	6.23 / 0.60
	Fat	6.42 / 0.76	6.31 / 0.78	6.40 / 0.66	6.91 / 0.48
	Bone	4.68 / 0.78	5.36 / 0.38	5.03 / 0.69	7.58 / 0.41
Belly					
	Weight	7.37 / 0.58	8.26 / *0.31*	8.01 / *0.03*	6.16 / *0.20*
	Lean	7.65 / 0.56	8.05 / *0.15*	7.69 / *0.67*	7.71 / *0.46*
	Fat	13.62 / 0.55	11.53 / *0.78*	9.90 / *0.66*	7.38 / *0.67*
	Bone	6.81 / 0.26	6.35 / *0.44*	9.07 / *0.63*	6.54 / *0.58*
Tenderloin		5.73 / 0.51	4.14 / 0.69	6.57 / 0.71	7.84 / 0.41

[a] 100*root mean square error/mean; [b]R^2 values in italics are not significant ($P > 0.05$) [c] Ham, loin, shoulder, belly and tenderloin (tenderloin only lean).

Conclusions

There is a very good relationship between cross-sectional CT images obtained in live growing female pigs of different genotypes (including viscera) and carcass and main cuts composition. For

this reason, measurements taken on CT images of whole-animal *in vivo* allow accurate estimation of carcass lean meat percentage as well as the weight and tissue composition of cuts in pigs from 30 to 120 kg body weight, using empirical regression equations. The prediction accuracy varied across genotypes, variables of interest, and body weights. Linear models using CT tissue volumes as predictors, allometric models or linear models using CT tissue volumes and physical measurements at specific anatomical positions of the animal body, were in general more robust than quadratic models. However, further work is needed to allow the accurate prediction of pig cut weights and composition using reconstructed 3D pig CT images from which the whole animal body is virtually cut and dissected, thus mimicking dissection by the butcher, in an attempt to render prediction accuracy independent of pig genetic traits and body weight. Also more work is needed to build growth models that would allow relate live young piglet CT images with carcass composition at slaughter.

Acknowledgements

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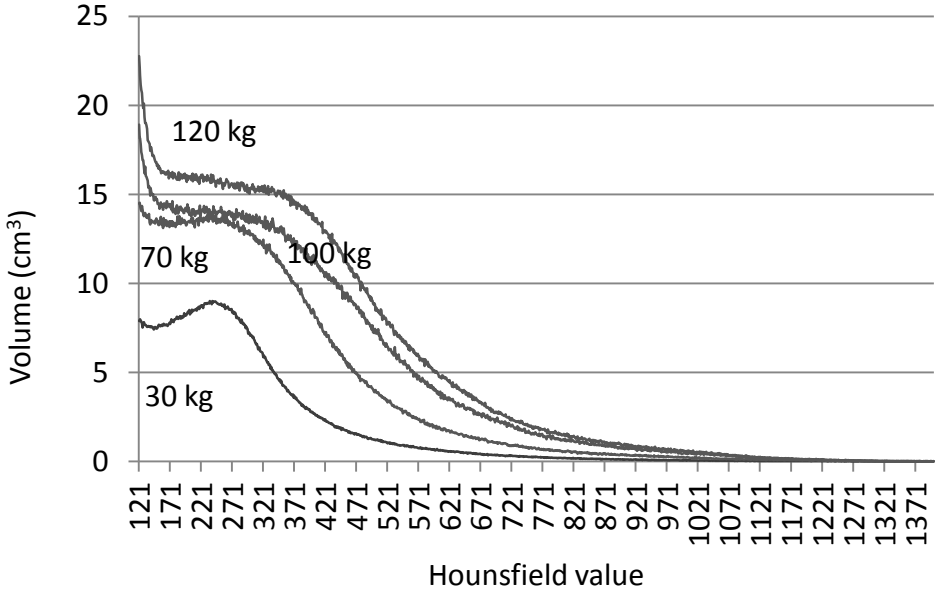
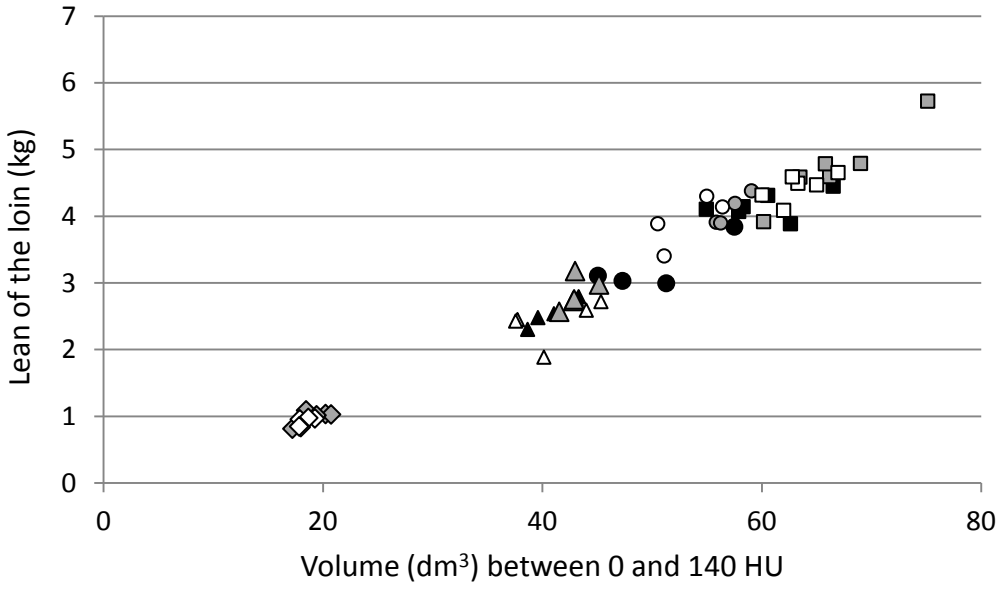
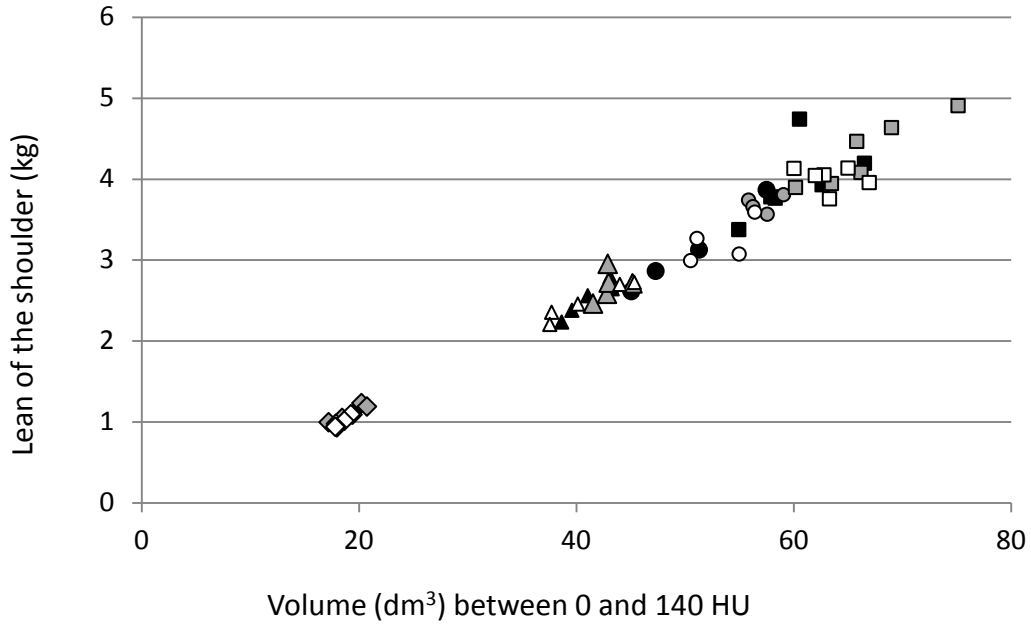
Suplementary information



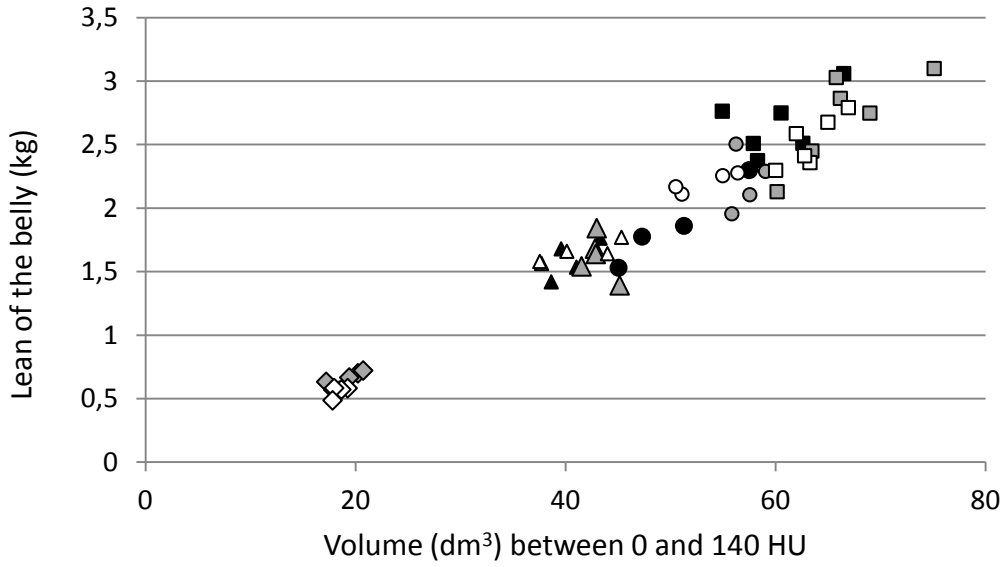
Supplementary Figure S1. Average volumes associated with each Hounsfield value (in Hounsfield units [HU]) in the bone area by target weight.



Supplementary Figure S2. Relationship between lean of the loin with the volume of lean tissue obtained from the scan of live pigs of different genotypes and weights (r > 0.982 for each genotype). Genotypes: black symbols, Landrace × Large White; grey symbols, Pietrain × (Landrace × Large White); white symbols, Duroc × (Landrace × Large White). Target weights: ♦, 30 kg; ▲, 70 kg; ●, 100 kg; ■, 120 kg. HU: Hounsfield units.



Supplementary Figure S3. Relationship between lean of the shoulder with the volume of lean tissue obtained from the scan of live pigs of different genotypes and weights (r > 0.982 for each genotype). Genotypes: black symbols, Landrace × Large White; grey symbols, Pietrain × (Landrace × Large White); white symbols, Duroc × (Landrace × Large White). Target weights: ♦, 30 kg; ▲, 70 kg; ●, 100 kg; ■, 120 kg. HU: Hounsfield units.



Supplementary Figure S4. Relationship between lean of the belly with the volume of lean tissue obtained from the scan of live pigs of different genotypes and weights (r ≥ 0.975 for each genotype). Genotypes: black symbols, Landrace × Large White; grey symbols, Pietrain × (Landrace × Large White); white symbols, Duroc × (Landrace × Large White). Target weights: ♦, 30 kg; ▲, 70 kg; ●, 100 kg; ■, 120 kg. HU: Hounsfield units.

Supplementary Table S1. Descriptive statistics (mean and standard deviation [s.d.]) of dissection variables.[a]

	30 kg (*n* = 15)		70 kg (*n* = 15)		100 kg (*n* = 12)		120 kg (*n* = 18)	
Variable	**Mean**	**s.d.**	**Mean**	**s.d.**	**Mean**	**s.d.**	**Mean**	**s.d.**
Lean %	60.7	1.6	60.5	3.6	54.8	4.4	53.7	3.4
Main cuts (g)								
Lean	4725	469	12 244	982	16 344	1769	19 839	1689
Fat	1321	185	3976	678	7819	1217	10 233	1112
Bone	884	44	1775	87	2340	175	2776	197
Ham (g)								
Weight	2654	300	6704	361	9519	527	11 761	663
Lean	1954	251	4955	476	650	735	7895	800
Fat	409	62	1177	158	2277	423	2988	371
Bone	292	17	572	37	739	33	878	64
Loin (g)								
Weight	1509	153	4164	363	6831	439	8397	518
Lean	933	103	2639	302	3796	497	4486	422
Fat	285	55	957	225	2243	474	2969	478
Bone	291	23	568	40	793	88	943	87
Shoulder (g)								
Weight	1592	132	3886	194	5428	399	6656	393
Lean	1053	91	2579	212	3365	410	4124	383
Fat	348	47	900	112	1532	155	1911	182
Bone	191	16	407	28	531	50	621	63
Belly (g)								
Weight	1011	119	2824	288	4159	340	5365	373
Lean	621	74	1653	136	2115	271	2665	276
Fat	280	47	943	236	1767	267	2365	301
Bone	110	9	228	19	277	40	335	34
Tenderloin (g)	164	13	418	31	565	67	668	66

[a]Dissection variables were used as independent variables (variables of interest) in the prediction equations.

Supplementary Table S2. Prediction equations selected.

Parameter	Genotype	Equation[a]
Lean %	LDxLW	33.3313+0.42723*Plean+(0.00119*LoinArea)+ (0.37608*LoinSubcutLateralFat)
	PIx(LDxLW)	24.6702+0.57191*Plean+(0.00081*LoinArea)+ (-0.24929*HamSubcutFat)
	DUx(LDxLW)	9.9202+0.59199*Plean+(0.00986*HamPerimeter)+ (-0.32093*LoinSubcutSupFat)+ (0.09318*DiagonalMuscleThickness)
Main cuts		
Lean	LDxLW	10**(2.128 + 253.172 *LogVolLean)
	PIx(LDxLW)	10**(2.25 + 1.14 *LogVolLean)
	DUx(LDxLW)	10**(-5037.41 + (275.949 * VolLean) + (24.8485 *amp_11_12)+(4.7186 *HamWidth))
Fat	LDxLW	-244.274 + 219.279 * VolFat +(46.9117 *HamSubcutFat)
	PIx(LDxLW)	-174.075 + 228.695 * VolFat +(34.7227 *HamSubcutFat)
	DUx(LDxLW)	-560.92 + 168.495 * VolFat +(100.71 *LoinSubcutSupFat)
Bone	LDxLW	-14.092 + 407.302 * VolBone
	PIx(LDxLW)	60.37 + 399.174 * VolBone
	DUx(LDxLW)	5.258 + 396.785 * VolBone
Ham		
Weight	LDxLW	10**(1.8373 + 1.075 *LogTotalVol)
	PIx(LDxLW)	-184.567 + 107.551 * TotalVol
	DUx(LDxLW)	-106.473 + 113.426 *TotalVol+(-58.79 *LoinSubcutSupFat)
Lean	LDxLW	-437.357 + 127.15 * VolLean +(19.775 *LoinSubcutSupFat)
	PIx(LDxLW)	10**(1.7569 + 1.1874 *LogVolLean)
	DUx(LDxLW)	-101.259 + 60.1792 * VolFat +(27.3005 *HamSubcutFat)
Fat	LDxLW	-952.16 + 159.064 * VolLean+(-0.44383 * VolLean* VolLean)
	PIx(LDxLW)	10**(1.8714 + 0.9863 *LogVolFat)
	DUx(LDxLW)	-70.054 + 46.5679 * VolFat +(0.05383 *HamFatArea)
Bone	LDxLW	0.3559 + 138.65 * VolBone+(-2.90522 *HamLateralFat)
	PIx(LDxLW)	30.3274 + 126.873 * VolBone
	DUx(LDxLW)	28.2768 + 119.213 * VolBone
Loin		
Weight	LDxLW	-680.02 + 61.1775 *TotalVol+(48.252*LoinSubcutSupFat)
	PIx(LDxLW)	-685.91 + 77.4938 * TotalVol
	DUx(LDxLW)	-808.03 + 38.4436 *TotalVol+(138.505*LoinSubcutSupFat)
Lean	LDxLW	63.15159 + 58.51575 * VolLean +(0.41809 *LoinArea) +(-5.42972 *LoinPerimeter)
	PIx(LDxLW)	-543.185 **+** 80.6152 * VolLean
	DUx(LDxLW)	801.3505 + 50.31777 * VolLean +(0.75025 *LoinArea) +(-12.3532 *LoinPerimeter)
Fat	LDxLW	-217.079 + 65.6474 * VolFat +(14.4885 *HamSubcutFat)
	PIx(LDxLW)	-167.014 + 71.4287 * VolFat

Parameter	Genotype	Equation[a]
	DUx(LDxLW)	10**(1.5788 + 1.1654 *LogVolFat)
Bone	LDxLW	-239.988 + 98.108 * VolBone+(0.41807 *HamPerimeter)
	PIx(LDxLW)	1.0276 + 138.424 * VolBone
	DUx(LDxLW)	15.955 + 75.566 * VolBone+(12.1084 *LoinSubcutSupFat)
Shoulder		
Weight	LDxLW	3.065 + 55.0624 * TotalVol
	PIx(LDxLW)	-329.783 + 70.721 * TotalVol +(-0.085215 * TotalVol * TotalVol)
	DUx(LDxLW)	-26.047 + 57.1905 * TotalVol
Lean	LDxLW	-302.048 + 76.2117 * VolLean +(-0.02464 *HamFatArea)
	PIx(LDxLW)	10**(1.6498 + 1.0907 *LogVolLean)
	DUx(LDxLW)	-167.279 + 56.4373 * VolLean +(0.03782 *HamFatArea)
Fat	LDxLW	47.93 + 51.668 * VolFat+(-0.26241* VolFat* VolFat)
	PIx(LDxLW)	-32.641 + 65.7754 * VolFat+(-0.47326* VolFat* VolFat)
	DUx(LDxLW)	67.45 + 52.5053 * VolFat+(-0.17932* VolFat* VolFat)
Bone	LDxLW	-11.3075 + 90.761 * VolBone
	PIx(LDxLW)	10**(1.976 + 0.9876 *LogVolBone)
	DUx(LDxLW)	-16.8623 + 95.27 * VolBone
Belly		
Weight	LDxLW	10**(1.2885 + 1.183 * LogTotalVol)
	PIx(LDxLW)	1.3559 + 1.1392 * LogTotalVol
	DUx(LDxLW)	-381.842 + 47.9655 * TotalVol
Lean	LDxLW	41.564 + 29.387 * VolLean+(0.16671 * VolLean* VolLean)
	PIx(LDxLW)	10**(1.3743 + 1.1278 *LogVolLean)
	DUx(LDxLW)	-485.445 + 61.5811 * VolLean+(-0.21133 * VolLean* VolLean)
Fat	LDxLW	-47.309 + 57.199 * VolFat
	PIx(LDxLW)	-37.346 + 55.5948 * VolFat
	DUx(LDxLW)	-111.898 + 67.8666 * VolFat+(-0.27937 * VolFat* VolFat)
Bone	LDxLW	16.5834 + 4.21416 * VolLean+(7.2243 * VolBone)+ (0.2292 *LoinSubcutSupFat)
	PIx(LDxLW)	10**(1.7457 + 0.9099 *LogVolBone)
	DUx(LDxLW)	-1.5791 + 51.1388 * VolBone
Tenderloin	LDxLW	-48.2966 + 11.5466 * VolLean
	PIx(LDxLW)	10**(0.7363 + 1.1611 *LogVolLean)
	DUx(LDxLW)	-62.121 + 12.3949 * VolLean+(-0.0248 * VolLean* VolLean)

[a]VolLean: volume between 0 Hounsfield units (HU) and 140 HU; VolFat: volume between −149 and –1 HU; VolBone: volume between 141 and 1400 HU; TotalVol: volume between −150 and 1400 HU; PLean: 100 × VolLean/TotalVol.
The other variables of the equations are explained in Figure 3 of the manuscript.

Chapter 5

Results II

The content of this chapter is published in the Livestock Science journal (2015) 170: 181-192.

In vivo computed tomography evaluation of the composition of the carcass and various cuts of growing pigs of three commercial crossbreeds

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This chapter deals with:

- Visual selection and image analysis
- Phenotypic differences of animals of three genetic types
- Allometric growth

Introduction

The evolution of the body composition of live animals during their growth period, taking into account different genetic types, provides valuable information. It is generally assumed that variations in body composition must play a large role in the growth of the pigs. As a result, more information about the background of genetic variation and, especially, its role on body composition is required for growing pigs (Luiting *et al.,* 1995). It is well known that at slaughter, pigs with different genetics have different carcass characteristics (Gispert *et al.,* 2007). Duroc sires are used to increase the intramuscular fat to obtain high-quality meat, which is prized in the manufacturing of dry-cured hams (Font-i-Furnols *et al.,* 2012). Pietrain sires are known for their lean potential deposition (Mas *et al.,* 2012), and finally, Landrace and Large White are used as a synthetic line because of their quick development. However, very few studies have shown: (1) if differences exist in commercial crossbreeds at early weights (Carabús *et al.,* 2011), (2) at which weights these differences appear, (3) how fat or lean body compositions are related to each weight and (4) how fast the tissues are deposited. One of the best ways to study the body composition of live pigs is using computed tomography (CT) (Gjerlaug-Enger *et al.,* 2012) because it is a non-invasive technology and it allows the study of the body composition of live animals during growth, avoiding serial slaughters. CT images are represented by a large number of X-ray attenuation values and show the various densities of the body tissues that have been scanned. Attenuation or CT values are expressed in Hounsfield units (HU). Knowing these different densities makes it possible to visualise and quantify lean mass, bone, fat and air (Picouet *et al.,* 2010). A detailed description of the CT techniques is given by Allen and Leymaster (1985). The aims of the present study were: (1) to evaluate variations in the body composition of three genetic types at the live weights of 30, 70, 100 and 120 kg by analysing live pigs with CT and (2) to determine the allometric growth of the main body parts in relation to their weight and their lean, fat and bone contents, depending on the genetic type.

Material and Methods

Animals and experimental design

A total of 45 gilts were studied in this experiment at different target body weights (TBW): 30, 70, 100 and 120 kg. Pigs were from three different genetic types (GEN): a) a high quality line, with intramuscular and visible fat: Duroc x (Landrace x Large White) (DU), b) a lean and conformed line: Pietrain x (Landrace x Large White) (PI) and c) an industrialised line, very efficient in terms of growth and with a high and fast growth rate: Landrace x Large White (LA). There are no parental relation within the breeds Landrace and Large White from different companies. All of the piglets were derived from the farms of different breeding companies. Piglets arrived at the facilities of IRTA-Monells (Girona, Spain) at 28 days of age, and they were fed *ad libitum.* Their diet had an energy content of 2670.3 kcal/kg and 18.7 % crude protein until they reach an average of 12 kg. From 12 to 25 kg, they were fed with a commercial starter diet with an energy content of 2570 kcal/kg and 17.6 % crude protein. During the last period, all of the pigs were weighed weekly and fed *ad libitum* with a commercial diet with an energy content of 2350.0 kcal/kg and 17.0 % crude protein. The experimental period started at a weight of 29.95±2.00 kg and continued to a final live weight of 123.05±3.47 kg. The distribution of the animals over GEN and TBW is presented in Table 1.

Table 1. Experimental design and animal distribution over genetic type (GEN) and target body weight (TBW).

TBW (kg)	GEN	n	Mean scanned weight (kg)
30	LA	15	30.0±2.1
	PI	15	30.2±2.3
	DU	15	29.6±1.6
70	LA	15	70.0±2.3
	PI	15	69.9±2.3
	DU	15	69.1±1.9
100	LA	15	103.1±3.5
	PI	15	101.8±2.7
	DU	15	101.3±3.0
120	LA	15	122.9±2.9
	PI	15	122.0±3.5
	DU	15	124.2±4.0

LA = Landrace x Large White, PI = Pietrain x (Landrace x Large White) and DU = Duroc x (Landrace x Large White)

CT scanning

Animals were scanned with a CT General Electric HiSpeed Zx/I, located in IRTA-Monells, and the instrumental settings were: 140 kV, 145 mA, matrix 512x512, axial, 7 mm thick (30 kg TBW) and 10 mm thick (70, 100 and 120 kg TBW). A specific cradle (PVC, Ø 0.30 m, length: 1.2 m for 30 kg pigs and Ø 0.46 m, length: 1.8 m for 70, 100 and 120 kg pigs) was used to keep the pigs during scanning (Figure 1). Pigs were scanned *in vivo*, fasted for a minimum of eight hours and weighed before scanning. To minimise disturbances in the CT images due to movements, intramuscular sedation with azaperon (0.1 mg/kg BW) and ketamine (0.2 mg/kg BW) and intravenous sedation with propofol (0.22 mg/kg BW) were applied. Intravenous sedation was only used at 100 and 120 kg TBW. No animals died during the experiment. The CT measurements were performed at the four weights: 30, 70, 100 and 120 kg TBW. After the scanning, the animals were returned to the IRTA experimental farm until their last scan at 120 kg TBW, at which time the experiment was completed. All the methodology used was approved by the ethical committee of IRTA.

Figure 1. Evaluation of live pigs with the computed tomography machine.

Image analysis for the phenotypic measurements

Phenotypic measurements were manually obtained in a reduced set of images. CT image analysis was carried out by the software VisualPork, developed by the Universitat de Girona (Catalonia, Spain) and the IRTA (Boada *et al.,* 2009; Bardera *et al.,* 2012). The parameters were established from the following six different tomograms. The anatomical location of the tomograms and the parameters evaluated for each one are presented in Table 2.

Table 2. Anatomical location of the parameters evaluated from each one.

Tomogram	Localisation	Parameters analysed
Shoulder (Figure 2)	Cross section -SS- (Pork.org, 2005)	· Subcutaneous fat **---** The subcutaneous fat thickness in the middle of the vertebral column and perpendicular to the skin (A) · Area **---** The area (mm^2) of the whole shoulder (B) · Perimeter **---** The perimeter (mm) of the shoulder (C)
Loin (4 tomograms) (Figure 3)	Between: · 6^{th}-7^{th} rib · 11^{th}-12^{th} rib · 14^{th}-15^{th} rib · 3^{rd}-4^{th} lumbar vertebrae	· Subcutaneous fat **---** Subcutaneous fat thickness (mm) in the middle of the vertebral column and perpendicular to the skin (D) · Width **---** Maximum width (mm) of the right loin (E) · Lateral fat **---** Lateral fat thickness (mm) of right loin eye perpendicular to the skin, at the bottom of the width (E) and in the right side of the loin (F) · Area **---** Right loin eye area (mm^2) (G) · Perimeter **---** Right loin perimeter (mm) (H) · Maximum length **---** Maximum length of the two loins (mm) (I)
Ham (Figure 4)	Cross section -N- (Pork.org, 2005)	· Height **---** Maximum vertical height of the ham (J) · Subcutaneous Fat **---** Subcutaneous fat thickness (mm) at the top of the ham and perpendicular to the skin (K) · Fat area **---** Area of the ham's subcutaneous fat (mm^2) (L) · Width **---** Ham's width (mm) above the bones (M) · Lat. Fat --- Lateral fat thickness (mm) at the previous level (N) · Area **---** Area of the whole ham (mm^2) (O) · Perimeter **---** Perimeter (mm) of the whole ham (P)

Image analysis for the carcass and the composition of the main body parts

The total lean, fat and bone content of the entire body and of the main parts was determined from all of the images by the use of the predictive equations reported by Font i Furnols *et al.,* (2014) Some of the parameters evaluated from the tomograms (Figure 2, 3 and 4) were used for the predictions as well as the volume of the fat, lean mass and the bones, obtained by the sum of the voxels with values between (-140 and 0, 1 and 150, and 151 and 1400). The parameters of the carcass and the composition of the main parts determined and studied are presented in Table 3.

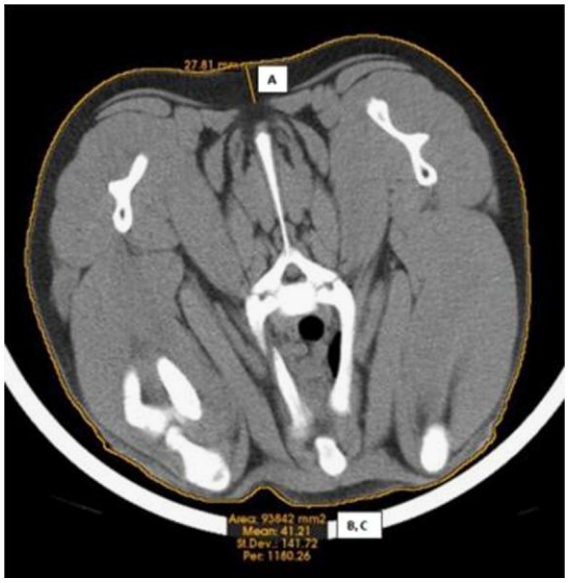

Figure 2. Anatomical measures obtained from the tomogram of the shoulder.

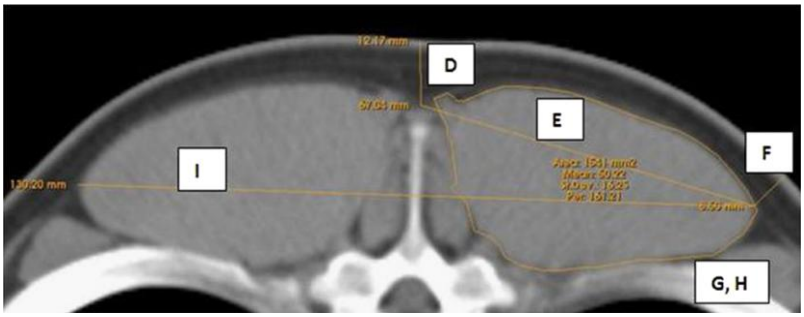

Figure 3. Anatomical measures obtained from the different tomograms of the loin.

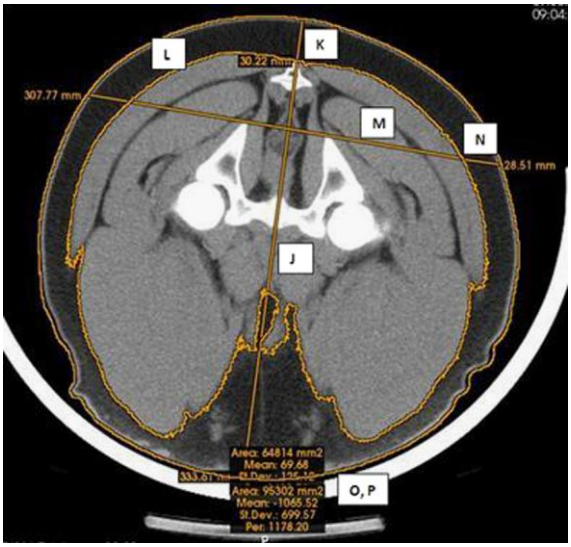

Figure 4. Anatomical measures obtained from the tomogram of the ham.

Allometric growth

Allometric growth was obtained for all of the variables described in Table 3 in relation to the live weight, except for the LMP089. The allometric growth was also determined for the lean mass, fat and bones of each cut in relation to its weight. The allometric function is:

$Y = aX^b$.

For calculation, the equations were linearised as follows:

$log\,Y = log\,a + b * log\,X$,

where *Y* is the weight of the tissue, and *X* is the live weight or the weight of the cut, depending of the variable analysed; *a* is an intercept and *b* is the allometric growth coefficient that describes the relationship between the two body constituents. A unity of the allometric growth is assumed if $b = 1$; then, *Y* grows at the same rate as *X*; if $b > 1$, *Y* grows faster than *X*, and the opposite is true if $b < 1$.

Statistical analysis

Statistical analysis was performed using SAS software (SAS Institute Inc, Cary, NC, USA, 2001). A mixed procedure with repeated measures was used to determine whether significant differences between treatments existed. The model included GEN, TBW and their interaction as the fixed effects. The type of the covariance matrix used in the model was selected for each parameter analysed as those that presented the lowest value of the Akaike's information criterion (AIC) or the corrected Akaike's information criterion AICC (AICC). Tukey's test was used to compare the least-squared mean values at the 0.05 significance level.

Table 3. Pieces and parameters obtained from the CT images for each pig by the prediction equations.

Pieces predicted	**Parameters predicted**	
Carcass	Lean%	Lean meat percentage (EU simplified dissection)
Ham, loin, shoulder, belly and tenderloin	Lean5p	Weight of the lean of the 5 pieces (g)
Ham, loin, shoulder and belly	Fat4p	Weight of the subcutaneous and intermuscular fat of the 4 pieces (g)
	Bone4p	Weight of the bones of the 4 pieces (g)
Shoulder	Weight	Weight of the shoulder (g)
	Lean	Weight of shoulder lean mass (g)
	Fat	Weight of shoulder's subcutaneous and intermuscular fat (g)
	Bone	Weight of shoulder bones (g)
Loin	Weight	Weight of the loin (g)
	Lean	Weight of loin lean mass (g)
	Fat	Weight of loin subcutaneous and intermuscular fat (g)
	Bone	Weight of loin bones (g)
Ham	Weight	Weight of the ham (g)
	Lean	Weight of ham lean mass (g)
	Fat	Weight of ham subcutaneous and intermuscular fat (g)
	Bone	Weight of ham bones (g)
Belly	Weight	Weight of the belly (g)
	Lean	Weight of belly lean mass (g)
	Fat	Weight of belly subcutaneous and intermuscular fat (g)
	Bone	Weight of belly bones (g)
Tenderloin		Weight of the tenderloin (g)

Results

Phenotypic measurements obtained by CT

The least-squares means and the significant effect of the phenotypic measurements obtained from the CT images are presented in Table 4 for the loin and in Table 5 for the ham and the shoulder. As expected, the TBW effect was significant ($P<0.001$) in all of the phenotypic measurements, and the GEN effect was significant in only some of them. Nevertheless, for most of the parameters, the effect of the GEN and the TBW presented a significant ($P<0.05$) interaction, indicating that the differences among the GEN are not constant at all the TBW values, but are TBW dependent.

Loin. No significant (P>0.05) differences for the GEN effect or for its interaction with TBW were reported for the majority of the parameters analysed at the 6^{th}-7^{th} and the 11^{th}-12^{th} cranial ribs level (Table 4). This suggests that the differences for the loin among the GEN during growth are more evident in the caudal area than in the cranial area. However, the 14^{th}-15^{th} cranial rib presented a significant GEN effect for the width of the loin and a significant interaction GENxTBW for the remainder of the parameters. The PI presented the widest loin (P<0.05), the DU showed the thinnest one, and the LA was intermediate. The subcutaneous fat presented significant differences at 30 kg TBW, and PI showed greater fat thickness than LA (P<0.05); however, no differences were found at the heavier weights. The lateral fat at 100 kg was thicker (P<0.05) in the LA pigs than in the PI, and the DU pigs had an intermediate thickness. At the other TBWs, no differences in the lateral fat thickness were found. The loin area was higher (P<0.05) in PI than in LA and DU at all weights, but this difference was more important at higher weights. The loin perimeter did not reveal significant differences among crossbreeds at the earliest weight, but these differences became significant at 70 kg and were clearly consolidated at 100 kg and 120 kg where PI registered the highest perimeter (P<0.05). Three parameters, the lateral fat, the area and the perimeter of the loin, evaluated between the third and the fourth lumbar vertebrae, presented a significant interaction, GENxTBW. There were no differences in the lateral fat between crossbreeds at 30 kg, although, in all the other target weights, LA presented more lateral fat (P<0.05) than PI and DU. In addition to the loin area, the loin perimeter presented a significant interaction, GENxTBW, which was observable at all weights but was consolidated at 100 and 120 kg TBW.

Ham and shoulder. A significant (P<0.05) GEN effect was found for the width and the area of the ham, which was independent of the TBW. PI was generally wider and presented a larger area for the ham compared with LA (P<0.05), which also presented higher values than DU (P<0.05). Moreover, a significant (P<0.05) interaction effect, GENxTBW, was found for the perimeter, the height, the superior and the lateral subcutaneous fat and the fatty area of the ham (Table 5). At 30 kg, PI presented greater (P<0.05) perimeter values than LA and DU, between which no difference was discernible. At 70 kg, PI and DU exhibited similar behaviour, showing a larger (P<0.05) ham perimeter than that of LA. At 100 kg, PI again exhibited a larger perimeter than LA, however, at this weight, DU was intermediate and did not differ (P>0.05) from PI and LA. Finally, at 120 kg, PI showed a larger (P<0.05) ham perimeter than DU, and LA was intermediate. The ham height exhibited a significant interaction GENxTBW. At 30 kg, the values observed in PI were higher (P<0.05) than in LA, and DU had intermediate values. At 120 kg, LA had a higher ham value than DU, and PI was intermediate. Growth of lateral fat tissue tended (P=0.0502) to be higher in the LA genotype, especially at high weights. The differences (P<0.05) in the ham subcutaneous fat were only visible at 70 kg and 100 kg. At 70 kg, LA had a greater amount of fat area than DU (P<0.05), and PI was intermediate. Despite this, at 100 kg, LA still had the fattest ham but differed significantly from PI, which had the lowest value, with DU being intermediate. At the heaviest weight, the fat area from the LA genotype was greater, but the differences were not significant. No significant interaction (GENxTBW) was observed in the shoulder zone. The perimeter and the area revealed significant differences between GENs. PI presented the biggest area and LA the

smallest one (P<0.05), and that of DU was intermediate. Similar results were reported for the perimeter; however, in this case, PI and DU had the largest values, followed by LA (P<0.05).

Composition of the carcass and main pieces obtained by CT

The least-squares means and differences obtained for the compositions of the carcass and main piece are shown in Table 6. The TBW effect was significantly different (P<0.001) in all of the parameters, and the interaction between GEN and TBW also presented significant differences. PI showed the highest lean meat percentage (LMP) and the highest weight of lean content in the entire body (P<0.05).The weight of the main pieces showed a significant interaction GENxTBW in most cases. PI presented the highest weights for the ham and the shoulder in almost all of the TBWs. At 30 kg, LA and PI did not differ (P>0.05) in belly weight and showed higher values than for DU. At 70 kg, insignificant differences were visible at 100 kg, LA presented heavier bellies than DU, which was heavier than PI; however, at 120 kg, LA had a heavier belly than the other two (P<0.05). LA and PI had greater tenderloin weights (P<0.05), especially at the heavier weights. The pieces that showed significant interaction (GENxTBW) for the lean parameter were the ham and the belly. PI had the highest lean content in the ham (P<0.05). For the belly, the differences between GEN were only significant at lighter weights, with LA and PI the leanest bellies at 30 kg and LA and DU the leanest bellies at 70 kg. The fat content showed a significant interaction GENxTBW effect for the ham, the loin, the shoulder, and the belly (P<0.05). The bone weight showed a significant interaction GENxTBW effect for all of the cuts analysed. At 120 kg, the bone weight of the entire body showed a significant difference, 300 grams, between the genotype with the heaviest bones, DU, and the genotype with the lightest bones, PI. The same result was observed for the weight of the belly bones, for which DU had greater values than LA (P<0.05) and PI (P<0.05). The situation changed for the weight of the loin and the ham bones because even DU had a larger amount of bones than PI (P<0.05), and LA did not differ from DU (P>0.05).

Allometric growth obtained by CT

The results of the weights of the main pieces and the lean mass, fat and bone content in relation to the live weight are represented in Table 7, and the results for the lean, fat and bone content in relation to the weight of the main pieces weight as a whole are presented in Table 8.

Pigs from the LA crossbreeds grew faster than those from the DU and PI crossbreeds (from 30 to 120 kg LA required 94 days, whereas DU and PI required 102 and 103 days, respectively). The allometric coefficients of growth (b) calculated for lean tissue were close to unity, lower than 1 in the majority of the cuts. This indicates a slower development of bones in relation to the live weight (Table 7) and to the weight of the main pieces as a whole (Table 8). For the fat, the b-coefficient was always higher than 1, indicating faster development of this tissue (Table 7 and 8). Significant differences (P<0.05) in the growth coefficients between crossbreeds were found for the ham, loin, belly and tenderloin weight in relation to the live weight (Table 7). LA revealed faster development of the ham (P<0.05) than PI and DU, which had similar values. The weights of the loin, belly and tenderloin were similar, consistent with the fact that the LA and PI crossbreeds showed faster development of these pieces than the DU crossbreeds.

The growth of lean mass, fat and bones in relation to the weight of each piece is shown in Table 8. From the results, it can be observed that for the lean mass, the growth of the ham presented significant differences between the crossbreeds. Lean deposition in the PI genotype was faster than in DU, LA was intermediate ($P>0.05$). The growth of fat in the loin and in the shoulder showed differences ($P<0.05$) among the crossbreeds and revealed the same conduct in relation to the live weight and to the weight of the cuts. LA and PI deposited loin fat faster than DU ($P<0.05$); however, this changed for the shoulder fat because DU had a higher coefficient of growth than PI ($P<0.05$), and LA was intermediate ($P>0.05$). The bone growth of the belly revealed that DU is the crossbreed with the quickest development ($P<0.05$) of the bones in relation to the live weight and to the belly weight.

Table 4. Least-square means of the parameters evaluated from CT images (n=45) of the loin, depending on the crossbreed (GEN) and the target body weight (TBW)

	30 kg				70 kg				100 kg				120 kg				P-Value	
Parameters	**LA**	**PI**	**DU**	**se**	**LA**	**PI**	**DU**	**se**	**LA**	**PI**	**DU**	**se**	**LA**	**PI**	**DU**	**se**	**GEN**	**GENxTBW**
6th- 7th																		
Sub. Fat	8	9	10	0.6	17	19	20	0.9	26^{ab}	25^{b}	29^{a}	1.2	31	30	33	1.4	0.123	0.012
Width	67	65	65	1.0	88	86	88	1.3	99	96	95	1.5	103	100	101	1.6	0.347	0.077
Lat. Fat	8	8	8	0.5	15	14	16	0.8	23	21	22	1.0	28	26	26	1.2	0.462	0.058
Max. Length	101	105	102	1.9	135	138	139	2.1	154	154	153	2.4	157	163	164	2.4	0.369	0.067
Area	1080	1095	1150	38.4	2003	2061	2196	59.6	2552	2636	2741	79.0	2758	2915	3046	84.8	0.057	0.532
Perimeter	122	123	126	2.4	166	168	171	2.4	186	188	192	3.0	193	198	202	2.9	0.108	0.886
11th- 12th																		
Sub. Fat	7	9	10	0.6	16	17	19	0.9	26	26	29	1.1	31	31	34	1.2	0.061	0.422
Width	73	70	70	0.9	98	91	94	1.1	108	103	103	1.4	113	108	109	1.5	0.001	0.059
Lat. Fat	7	6	6	0.4	13	13	12	0.7	21	20	20	1.1	24	25	25	1.4	0.929	0.795
Max. Length	138	132	132	1.8	182	178	179	2.0	207	201	201	2.2	214	212	211	2.6	0.082	0.304
Area	1437	1613	1518	58.6	3209	3523	3387	90.7	4233	4691	4500	113.8	4595	5160	4953	124.5	0.007	0.496
Perimeter	160	160	158	2.8	223	222	224	2.8	252	256	254	3.2	260	268	268	3.4	0.685	0.351
14th- 15th																		
Sub. Fat	6^{b}	8^{a}	7^{ab}	0.4	16	17	18	0.7	24	23	24	0.9	28	27	28	0.9	0.586	0.003
Width	76	76	73	0.8	98	98	96	0.8	109	111	107	1.0	115	115	113	1.0	0.027	0.550
Lat. Fat	6	6	5	0.3	13	12	13	0.5	22^{a}	19^{b}	21^{ab}	0.9	27	23	24	1.1	0.085	0.001
Max. Length	142	142	138	1.4	188	191	187	1.4	213^{ab}	217^{a}	209^{b}	1.5	224	226	221	1.7	0.014	0.023
Area	1473^{b}	1650^{a}	1475^{b}	52.7	3289^{b}	3887^{a}	3462^{b}	85.0	4199^{b}	5080^{a}	4434^{b}	104.0	4739^{b}	5497^{a}	4930^{b}	122.0	<.0001	<.0001
Perimeter	168	170	164	2.2	232^{b}	242^{a}	235^{ab}	2.4	258^{b}	275^{a}	262^{b}	2.6	273^{b}	286^{a}	276^{b}	2.9	0.001	0.017
3rd - 4th																		
Sub. Fat	9	11	11	0.5	25	26	27	1.1	35	35	36	1.3	40	41	41	1.4	0.620	0.899
Width	79	80	75	1.1	109	113	108	1.3	122	129	122	1.2	129	134	128	1.5	0.001	0.139
Lat. Fat	8	8	8	0.5	20^{a}	17^{b}	18^{ab}	0.7	28^{a}	23^{b}	23^{b}	1.0	33^{a}	27^{b}	27^{b}	1.3	0.002	0.003
Max. Length	142	145	138	1.9	191	199	192	1.6	217	221	213	2.3	225	230	226	2.5	0.005	0.139
Area	1844^{b}	2153^{a}	1809^{b}	60.1	3786^{b}	4591^{a}	4135^{b}	102.8	4914^{b}	5940^{a}	5097^{b}	127.0	5448^{b}	6593^{a}	5694^{b}	150.8	<.0001	0.0002
Perimeter	183^{ab}	191^{a}	180^{b}	2.8	247^{b}	276^{a}	265^{a}	4.8	290^{b}	316^{a}	294^{b}	3.5	303^{b}	331^{a}	312^{b}	3.9	<.0001	0.015

[+] Means sharing a common character in their superscripts are not significantly different (P<0.05); The TBW effect was significant (P<0.001) for all of the parameters; se = standard error; LA = Landrace x Large White, PI= Pietrain x (Landrace x Large White) and DU= Duroc x (Landrace x Large White). All measures are in mm, with the exception of the area which is in mm^2

Table 5. Least-square means of the parameters evaluated from CT images (n=45) of the shoulder and the ham, depending on the crossbreed (GEN) and the target body weight (TBW).

	30 kg				70 kg				100 kg				120 kg				P-Value	
Parameters	**LA**	**PI**	**DU**	**se**	**LA**	**PI**	**DU**	**se**	**LA**	**PI**	**DU**	**se**	**LA**	**PI**	**DU**	**se**	**GEN**	**GENxTBW**
Ham																		
Sub. Fat	6	6	5	0.4	10	10	11	0.7	17	16	16	1.1	23	20	21	1.2	0.650	0.027
Height	193^{b}	201^{a}	195^{ab}	2.4	261	258	256	2.4	304	302	301	2.7	334^{a}	325^{ab}	321^{b}	2.8	0.166	0.004
Width	260	259	244	3.6	244	256	240	2.1	285	291	277	2.6	303	311	296	2.5	<.0001	0.164
Lat. Fat	7	7	6	0.4	12	11	11	0.5	20	17	17	0.9	24	20	20	1.0	0.016	0.050
Area	38789	41389	37530	928.0	61097	64258	58977	767.1	81195	83823	77884	834.1	93113	94933	87976	916.6	<.0001	0.305
Fat area	3747	3783	3850	166.2	9576^{a}	8835^{ab}	8417^{b}	333.1	14967^{a}	12439^{b}	13697^{ab}	607.6	19172	16605	16944	781.1	0.064	0.010
Perimeter	753^{b}	831^{a}	737^{b}	17.7	944^{b}	1030^{a}	991^{a}	11.4	1120^{b}	1180^{a}	1138^{ab}	12.9	1237^{ab}	1263^{a}	1213^{b}	13.3	<.0001	0.030
Shoulder																		
Sub. Fat	12	13	14	0.5	21	21	22	0.7	28	27	29	1.0	32	31	33	1.1	0.258	0.630
Area	40709	41258	40350	692.5	70296	72337	71666	687.5	91038	93147	91848	833.7	100565	103829	104546	913.4	0.028	0.087
Perimeter	775	778	776	7.1	1022	1040	1035	7.8	1149	1166	1172	6.0	1211	1229	1234	5.6	0.017	0.684

[+] Means sharing a common character in their superscripts are not significantly different (P<0.05); The TBW effect was significant (P<0.001) for all of the parameters; se = standard error; LA = Landrace x Large White, PI= Pietrain x (Landrace x Large White) and DU= Duroc x (Landrace x Large White). All measures are in mm, with the exception of the area which is in mm^{2}

Table 6. Least-square means of the carcass and cuts composition, depending on the crossbreed (GEN) and the target body weight (TBW).

	30 kg				70 kg				100 kg				120 kg				P-Value	
Parameters (g)	**LA**	**PI**	**DU**	**se**	**LA**	**PI**	**DU**	**se**	**LA**	**PI**	**DU**	**se**	**LA**	**PI**	**DU**	**se**	**GEN**	**GENxTBW**
Carcass																		
Lean %	61	62	60	0.4	58	61	58	0.6	54	58	55	0.8	52	56	53	0.9	0.001	0.099
Lean5p	4553^{b}	5126^{a}	4467^{b}	156.6	11905^{b}	12827^{a}	11781^{b}	199.7	17138^{ab}	18014^{a}	16448^{b}	287.3	19467^{b}	20828^{a}	18988^{b}	358.4	0.001	0.081
Fat4p	1295	1369	1292	71.9	4238	4162	4356	131.9	8073	7348	7828	264.6	10634	9724	9990	333.5	0.364	0.024
Bone4p	872	888	898	14.0	1804^{ab}	1731^{b}	1850^{a}	22.5	2445^{ab}	2316^{b}	2529^{a}	37.0	2753^{b}	2601^{c}	2905^{a}	40.9	<.0001	<.0001
Ham																		
Weight	2546^{b}	2828^{a}	2488^{b}	54.7	6329^{b}	7231^{a}	6440^{b}	57.8	9704^{b}	10350^{a}	9407^{c}	70.6	11737^{b}	12153^{a}	11067^{c}	92.9	<.0001	<.0001
Lean	1881^{b}	2149^{a}	1825^{b}	42.7	4667^{b}	5315^{a}	4787^{b}	76.2	6697^{b}	7351^{a}	6450^{b}	117.2	7809^{b}	8473^{a}	7302^{b}	149.6	<.0001	<.0001
Fat	405	412	381	18.0	1270	1268	1200	37.4	2430	2180	2182	79.9	3210^{a}	2820^{b}	2820^{b}	97.7	0.014	0.005
Bone	281	295	297	4.7	586	564	584	7.2	781	749	784	12.1	870^{ab}	838^{b}	892^{a}	12.8	0.043	0.001
Loin																		
Weight	1420	1519	1589	68.6	4243	4516	4447	83.5	6692	6864	6978	112.9	8067	8328	8383	132.9	0.094	0.437
Lean	865	996	936	25.7	2608	2839	2650	47.6	3715	4058	3819	73.1	4281	4740	4497	92.2	0.001	0.147
Fat	246	276	273	35.6	1073^{b}	1086^{b}	1327^{a}	55.9	2234	2028	2345	96.8	3073	2734	2947	116.2	0.121	<.0001
Bone	288	294	302	7.1	595^{ab}	564^{b}	607^{a}	9.3	821^{ab}	778^{b}	845^{a}	14.1	942^{a}	888^{b}	970^{a}	16.3	0.003	<.0001
Shoulder																		
Weight	1561	1616	1534	32.0	3778^{b}	4045^{a}	3842^{b}	32.6	5495^{c}	5756^{a}	5622^{b}	36.5	6432^{b}	6741^{a}	6640^{a}	50.3	<.0001	0.001
Lean	1050	1101	1017	21.3	2504	2676	2449	39.4	3565	3695	3455	62.6	4147	4258	4029	81.9	0.009	0.190
Fat	338	333	337	12.9	906	968	933	21.1	1505	1529	1583	37.6	1829	1840	1969	43.7	0.215	0.003
Bone	184	197	191	4.6	402^{b}	390^{b}	439^{a}	6.3	540^{b}	526^{b}	590^{a}	10.3	602^{b}	592^{b}	670^{a}	10.2	<.0001	<.0001
Belly																		
Weight	1036^{a}	1013^{a}	926^{b}	22.5	2830	2856	2891	31.3	4491^{a}	4250^{b}	4376^{ab}	39.3	5513^{a}	5105^{b}	5211^{b}	50.9	<.0001	<.0001
Lean	622^{ab}	657^{a}	576^{b}	19.2	1698^{a}	1593^{b}	1671^{ab}	29.6	2325	2273	2260	44.4	2609	2673	2553	55.2	0.538	<.0001
Fat	330^{a}	270^{b}	248^{b}	15.4	1027	968	926	29.2	1918^{a}	1686^{b}	1758^{ab}	60.1	2506^{a}	2174^{b}	2303^{ab}	76.3	0.010	0.022
Bone	113	107	110	2.1	226^{b}	209^{c}	241^{a}	3.3	298^{b}	269^{c}	323^{a}	5.1	334^{b}	296^{c}	367^{a}	5.8	<.0001	<.0001
Tenderloin	168	165	158	3.8	427^{a}	424^{ab}	401^{b}	6.7	587^{a}	600^{a}	544^{b}	10.0	668^{a}	700^{a}	620^{b}	12.7	0.0003	0.001

[+] Means sharing a common character in their superscripts are not significantly different (P<0.05). The TBW effect was significant (P<0.001) for all of the parameters; se = standard error; LA = Landrace x Large White, PI = Pietrain x (Landrace x Large White) and DU = Duroc x (Landrace x Large White); Lean%=0.89 x [lean of (ham, loin, belly and shoulder and tenderloin)/weight of (ham loin belly shoulder and tenderloin)] x100; Lean5p: lean of ham, shoulder, loin, belly and tenderloin; Fat4p and Bone4p: fat and bone of ham, shoulder, loin and belly.

Table 7. Allometric growth of the main pieces weight and the lean mass, the fat and the bones content in relation to the live weight[+].

Parameters		a				b			
(g)		LA	PI	DU	P-Value	LA	PI	DU	P-Value
Carcass									
	Lean5p	196.39	218.27	222.40	0.306	0.97	0.95	0.93	0.172
	Fat4p	5.85^{b}	8.71^{ab}	11.79^{a}	0.001	1.59^{a}	1.48^{b}	1.42^{b}	0.001
	Bone4p	60.66^{b}	68.45^{a}	60.11^{b}	0.006	0.80^{a}	0.76^{b}	0.81^{a}	0.0004
Ham									
	Weight	63.11^{b}	101.31^{a}	93.24^{a}	<.0001	1.09^{a}	1.00^{b}	1.00^{b}	<.0001
	Lean	76.31^{b}	103.38^{a}	116.11^{a}	0.0001	0.97^{a}	0.92^{a}	0.87^{b}	<.0001
	Fat	1.76^{b}	3.12^{a}	2.82^{a}	0.003	1.59^{a}	1.43^{b}	1.45^{b}	0.0003
	Bone	21.72^{b}	24.34^{a}	24.22^{a}	0.019	0.77^{a}	0.74^{b}	0.75^{ab}	0.014
Loin									
	Weight	27.77^{b}	32.27^{ab}	42.19^{a}	0.004	1.19^{a}	1.16^{ab}	1.12^{b}	0.017
	Lean	32.83	34.31	35.88	0.519	1.02	1.03	1.01	0.492
	Fat	0.76^{b}	1.14^{b}	4.22^{a}	<.0001	1.76^{a}	1.65^{a}	1.44^{b}	<.0001
	Bone	17.38	20.24	20.16	0.051	0.83^{a}	0.79^{b}	0.81^{ab}	0.007
Shoulder									
	Weight	58.41	61.2	56.89	0.220	0.98	0.98	0.99	0.400
	Lean	60.87^{a}	53.79^{ab}	47.72^{b}	0.007	0.88^{b}	0.91^{ab}	0.92^{a}	0.022
	Fat	5.48	6.49	4.68	0.053	1.22^{ab}	1.19^{b}	1.27^{a}	0.014
	Bone	13	14.39	13.63	0.381	0.80^{ab}	0.78^{b}	0.82^{a}	0.029
Belly									
	Weight	18.87^{b}	20.01^{b}	25.87^{a}	<.0001	1.18^{a}	1.16^{a}	1.11^{b}	<.0001
	Lean	24.27^{b}	25.26^{b}	35.01^{a}	0.003	0.99^{a}	0.98^{a}	0.90^{b}	0.003
	Fat	1.81	2.18	1.41	0.147	1.53	1.47	1.56	0.107
	Bone	9.29^{ab}	10.38^{a}	7.97^{b}	0.001	0.75^{b}	0.70^{c}	0.80^{a}	<.0001
Tenderloin		8.65^{a}	6.46^{b}	9.64^{a}	<.0001	0.91^{a}	0.98^{a}	0.87^{b}	<.0001

[+] Means sharing a common character in their superscripts are not significantly different (P<0.05); se = standard error; a = scaling exponent (which is equal to the slope of the line when plotted on logarithmic coordinates); b = allometric growth coefficient; LA = Landrace x Large White, PI = Pietrain x (Landrace x Large White) and DU = Duroc x (Landrace x Large White); Lean5p: lean of ham, shoulder, loin, belly and tenderloin; Fat4p and Bone4p: fat and bone of ham, shoulder, loin and belly.

Table 8. Allometric growth of the lean, fat and bones content in relation to the weight of the main pieces[+].

Parameters	a				b			
(g)	LA	PI	DU	P-Value	LA	PI	DU	P-Value
Ham								
Lean	2.09	1.62	2.42	0.088	0.89^{ab}	0.92^{a}	0.87^{b}	0.041
Fat	0.005	0.003	0.003	0.47	1.45	1.48	1.5	0.465
Bone	1.20^{a}	0.93^{b}	0.89^{b}	0.018	0.71	0.73	0.74	0.053
Loin								
Lean	2.11	1.73	1.66	0.366	0.86	0.88	0.90	0.169
Fat	0.004^{b}	0.01^{b}	0.03^{a}	<.0001	1.53^{a}	1.47^{a}	1.28^{b}	<.0001
Bone	1.96^{ab}	2.25^{a}	1.54^{b}	0.008	0.69^{ab}	0.67^{b}	0.72^{a}	0.001
Shoulder								
Lean	1.81a	1.26^{ab}	1.15^{b}	0.021	0.89	0.93	0.93	0.106
Fat	0.03	0.04	0.03	0.143	1.26^{ab}	1.23^{b}	1.29^{a}	0.032
Bone	0.51	0.63	0.55	0.348	0.82	0.78	0.82	0.038
Belly								
Lean	2.27	2.09	2.80	0.142	0.83	0.84	0.80	0.096
Fat	0.04^{ab}	0.06^{a}	0.01^{b}	0.009	1.29^{b}	1.26^{b}	1.47^{a}	<.0001
Bone	1.50^{a}	1.70^{a}	0.93^{b}	<.0001	0.63^{b}	0.61^{b}	0.70^{a}	<.0001

[+] Means sharing a common character in their superscripts are not significantly different (P<0.05); se = standard error; a = scaling exponent (which is equal to the slope of the line when plotted on logarithmic coordinates); b = allometric growth coefficient; LA = Landrace x Large White, PI = Pietrain x (Landrace x Large White) and DU = Duroc x (Landrace x Large White).

Discussion

Evaluating the muscle and fat parameters and their development in live pigs is a common practice that is very useful for the breeding industry. Several body characteristics have been used to assess these measures. The use of new technologies such as CT or magnetic resonance imaging (MRI) have allowed more accurate quantification and make it possible to perform as many measures as are needed with accuracy and with no time restriction. However, visual analysis methods require the technical ability of the person who controls the equipment and also the ability of the technician that analyses the images.

Backfat and the loin thickness are generally used to estimate the relative amount of muscle and body fat; therefore, many studies have been carried out using carcass measurements or visual image analysis to quantify these parameters (Font i Furnols and Gispert, 2009). Wiseman *et al.,* (2007) and Edwards *et al.,* (2003) reported that Duroc-sired progeny and low-lean progeny exhibited higher subcutaneous fat (P<0.05) at all weights, contrary to our results at the 11th-12th level, where no significant interaction GENxTBW (P=0.422) or GEN effect (P=0.061) were found. These differences could be explained by four possibilities. First, the crossbreeds used in the experiments were not the same; the crossbreeds used by Wiseman *et al.,* (2007) were [(Yorkshire x Landrace) x Hampshire] for the low-lean line and [(Large White x Landrace) x Newsham] for the

high-lean line, whereas Edwards *et al.,* (2003) used [(Yorkshire x (Yorkshire x Landrace)) x Pietrain] and [(Yorkshire x (Yorkshire x Landrace)) x Duroc]. The second aspect to take into account is that the Duroc genotype has a huge variability, and its characteristics depend on the breeding company. The significant variability between the Duroc crossbreeds has been shown by Cilla *et al.,* (2006). The third factor is the feed characteristics. The diet composition differed between the works. Moreover, in the present trial, the same feed characteristic was considered for the three crossbreeds, which caused the animals not to express their full potential. And fourth, Edwards *et al.,* (2003) and Wiseman *et al.,* (2007) performed this measurement in the 10^{th} cranial rib, whereas, in the present study, it was measured between the 11^{th} and the 12^{th} cranial ribs. Differences between the crossbreeds were reported for the width of the loin and the loin area. For the width, LA had the widest loin ($P<0.05$), and DU and PI had smaller values and did not differ from each other ($P>0.05$). The loin area revealed differences ($P=0.007$), for which PI presented a larger area than LA, and DU was intermediate and not significantly ($P>0.05$) different from the other two. These results are in agreement with the findings by Kušec, *et al.,* (2004), who measured the loin eye area by a geometric procedure and did not observe significant differences between PI and DU at 100 kg. However, this is in contrast to the results from Ellis *et al.,* (1996), who reported that Duroc-sired progeny had a smaller loin area than Pietrain-sired and a commercial European breed (39, 40 and 40.7 cm^2, respectively), and the results from Edwards *et al.,* (2003), who presented similar results with the Pietrain and Duroc breeds (50.2 vs 53.2 cm^2). The subcutaneous fat thickness in the 3^{rd}-4^{th} lumbar vertebrae presented insignificant effects, for both the interaction GENxTBW and for the GEN. These differ from the results reported by Kanis *et al.,* (1990), in which Duroc pigs had more backfat than Pietrain at 60 kg (10.5 and 8.7 mm, respectively) at 100 kg (17.5 and 12.3 mm, respectively) and at 140 kg (24.4 and 17.4 mm, respectively). At the same level, PI showed larger areas ($P<0.05$) than LA and DU. These results support the findings of García-Macías *et al.,* (1996), which reported that, in light carcasses (72.8 kg) and in heavier carcasses (100.1 kg), the Pietrain crossbreed presented a greater loin area ($P<0.05$) than the Duroc crossbred and the Large White x Landrace crossbred, which were similar to each other (40.51, 36.77 and 37.09 cm^2, respectively).

The value of the pig carcass is determined, primarily, by the lean content (Gispert *et al.,* 2007). The total lean, fat and bone content increased ($P<0.05$) with TBW. The PI genotype had a higher lean proportion and lean content and thus, a lower fat content than those of DU and LA, which agrees with previous research (Gispert *et al.,* 2007). Quiniou *et al.,* (1996) reported that, at a carcass weight of approximately 84 kg, Pietrain x Large White castrated males had three percentage units more lean mass than Large White castrates, which corresponds with the results reported here for PI and LA (61 % and 58 % at 70 kg, respectively, and 58 % and 54 % at 100 kg, respectively). The only differences are that the results reported in the present study are from gilts and from live animals, instead of from castrated males and carcasses. The genotype did not affect the total fat, which agrees with Armero *et al.,* (1999), who compared the Duroc and Large White lines. However, Ellis *et al.,* (1996) and Gispert *et al.,* (2007) reported that Duroc pigs were fatter than Pietrain pigs. These discrepancies among the results of various researchers could be due to the variability in the Duroc population. The Duroc lines used in the present trial allowed better

productive performance and produced meatier carcasses than previously reported for other Duroc lines.

Differences between the crossbreeds were detected for the weights of the main pieces. PI had heavier hams and tenderloins than DU and the lightest belly, with values that are similar to those reported by Gispert *et al.,* (2007). However, in contrast to our results, Gispert *et al.,* (2007) found that Duroc had fatter loins than Pietrain, whereas these differences did not exist in the present trial. This could be explained by the use of pure genetic lines (Gispert *et al.,* 2007) instead of commercial crossbreeds. The allometric coefficients (b-values) relating the growth of the total lean tissue content to the body weight and to the weights of the main pieces were close to unity. This allometric growth of the lean mass was also reported in other studies. For example, Mohrmann, *et al.,* (2006) found b-values of 1.026 of the total lean content, 0.974 of the lean content of the shoulder and 0.951 of the lean content of the ham relative to the body weight. The results for the growth of lean tissue in the shoulder are in agreement with the results of Fisher *et al.,* (2003), who studied the allometric growth of various tissues of three crossbreeds (Pietrain, Landrace and Meishan) and found values less than one.

The relative growth coefficient for fat (subcutaneous + intermuscular) was the lowest in PI and DU and was higher for LA, implying that this tissue matured at a relatively low weight for PI and DU and at a high weight for LA. PI and DU did not differ in the fat growth coefficient, but DU was much fatter than the other two crossbreeds. The allometric coefficient of growth for the fat relative to the weight of the main pieces was lower in the belly and the shoulder than in the ham and the loin, which agrees with the results of Kouba and Bonneau (2009). However, these authors differentiated between subcutaneous and intermuscular fat, whereas, in the present trial, the fat content was computed as overall fat. A major contribution to the understanding of this area was made by Baulain (1997) who used Landrace pigs at different live weights and used magnetic resonance imaging (MRI) to determine the growth of lean and fat tissue. Additionally, Gu *et al.,* (1992) reported results for the growth of five genetic lines and a summary of the growth coefficients for the carcass component traits in the literature. These works were based on MRI and serial slaughtering, whereas the present work is performed by CT, and because the industrialised pig genotypes have changed over time, the data from this study represents results from completely different genotypes than were studied 16 and 21 years ago, respectively.

Conclusions

The results of the measurements collected reflect clear differences in the body composition between crossbreeds, particularly when pigs are close to the commercial weight. However, certain significant differences also appeared at the earliest weight of 30 kg BW, which reflects the real importance of genetic traits. Additionally, it can be concluded that the genotype and the live weight are major factors that affect the relative growth coefficients. The fat growth rate relative to the live weight and to the weight of the main pieces was faster than the lean mass and the bone growth rates. Additionally, the growth rates for DU of fat from the main pieces was higher than the those of the other breeds; therefore, for the low-lean crossbreeds, it would be

appropriate to use an specific diet with a high energy content at heavier weights to economise their feed. As the results presented high levels of fat in all the genotypes, it would be appropriate to use specific diets for each genotype, according to their weight and nutritional requirements, to maximise efficiency. Although PI had more lean content at all weights, there were no differences for the lean growth deposition of the entire body among the crossbreeds. Nevertheless, differences between crossbreeds were visible in the main pieces. These variations reflect that different crossbreeds are suitable for different markets, with low-lean crossbreeds, such as the Pietrain x (Landrace x Large White) analysed in the present study, being adequate for fresh meat production, and high-lean crossbreeds, such as Duroc x (Landrace x Large White) analysed as well, being better suited for the ham industry. Moreover, the results of this study suggest that CT and visual image analysis have a high potential for use as a tool to validate and test populations across different breeds or genetic lines. Moreover, with the use of predictive equations, CT can be notably useful for the meat industry because the carcass quality parameters can be known at early weights of the live animals. If an animal does not reach a specific value for a certain weight, it can be changed into another farming group and directed toward a different market. As a result, the use of this information can provide economic benefits for all of the stakeholders involved in the meat chain.

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Chapter 6

Results III

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Predicting fat, lean and the weights of primal cuts for growing pigs of different genotypes and sexes using computed tomography

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This chapter deals with:

- Predicting models using CT and potential on farm predictors
- Use of the same equation, independently of the genetic type or sexual condition

Introduction

Fat and muscle thickness at different levels of the ribs and HCW have traditionally been used to developed equations to predict pork carcass composition (Engel *et al.,* 2012; Font-i-Furnols and Gispert, 2009; Forrest *et al.,* 1989). However, alternative methods such as image analysis are becoming popular, especially because predictions can be done *in vivo*. Total body scans using dual energy X-ray absorptiometry (**DEXA**) can be used to measure composition of anaesthetized pigs (Mitchell *et al.,* 1996). Total body scans of pigs generated by magnetic resonance imaging (**MRI**) or by x-ray computer tomography (**CT**) are also highly correlated with the total body composition of pigs (Mitchell *et al.,* 2001). These non-invasive technologies enable the study of the body composition of live animals during growth, avoiding the need for serial slaughters (Gjerlaug-Enger *et al.,* 2011). Nevertheless, slaughters are still needed to establish the relationships between CT data and dissection to obtain prediction equations for body composition. However, once the equations are validated, serial slaughter can be replaced by *in vivo* estimates. Font-i-Furnols *et al.,*(2014) analyzed serial slaughter data (30 to 120 kg) from gilts of different genotypes and obtained separate prediction equations for body composition of each genotype based on CT images. Ideally, a single prediction equation would be applicable to pigs of different genotypes and sexes, without the necessity of having separate equations for each group. However, no single prediction equation has been developed for pigs of different genotypes and sexual conditions including immunocastrated males.

The aim of the present study was to develop regression equations to predict the amounts of fat, lean, weights of the primal cuts and composition of ham of pigs from 30 to 120 kg live weight regardless of genotype and sex. Two different sets of possible regression equations were analyzed, using: 1) CT predictors and 2) potential on-farm predictors.

Materials and methods

Animals and experimental design

Two data sets were used in this study (Tables 1 and 2). The first set (Exp. 1; Font-i-Furnols *et al.,*(2014)) included 90 gilts of three different genotypes (**GEN**): 30 (Duroc x (Landrace x Large White)), 30 (Pietrain x (Landrace x Large White)) and 30 (Landrace x Large White) gilts. There were with no parental relationships within the breeds as Landrace and Large White pigs came from different companies. The second set (Exp. 2) included 92 (Pietrain x (Landrace x Duroc)) pigs, all of them from the same company, and of different sexual conditions (**SEX**): 24 each of females (**FE**), entire males (**EM**), castrated males (**CM**) and 20 immunocastrated males (**IM**). Improvac® (Zoetis, Spain) was injected at 12 and 18 wk of age. All the pigs were fed a commercial diet on an *ad libitum* basis, weighed weekly and CT scanned at 30, 70, 100 and 120 kg target body weight (**TBW**). After each scan, subsets of five pigs of each GEN and four of each SEX were transported to the experimental abattoir, stunned with CO_2, slaughtered following standard commercial procedures and dissected. After chilling for 24 h to 48 h, carcasses were cut and dissected.

Table 1. Number and BW of pigs of each genotype and target BW at CT-scanning (Exp. 1)

Target BW[1], kg	Genotype[2]	*n*	Mean BW, kg
30	LA	20	29.99
	PI	20	30.52
	DU	20	29.37
	Pooled SD		*2.08*
70	LA	20	70.30
	PI	20	69.33
	DU	20	69.67
	Pooled SD		*2.49*
100	LA	20	102.03
	PI	20	101.20
	DU	20	101.75
	Pooled SD		*3.09*
120	LA	15	122.93
	PI	15	122.00
	DU	15	122.70
	Pooled SD		*3.90*

[1]5 pigs of each genotype were slaughtered after every CT-scan
[2]Genotypes: LA = Landrace x Large White, PI = Pietrain x (Landrace x Large White), DU = Duroc x (Landrace x Large White)

Computed tomography

Animals were fully scanned with a General Electric HiSpeed Zx/I tomograph, located in IRTA-Monells (Catalonia, Spain), and the instrumental settings were: 140 kV, 145 mA, matrix 512x512, axial, 7 mm thick (30 kg TBW) and 10 mm thick (70, 100 and 120 kg TBW). A custom-built half-tube cradle (PVC, Ø 0.30 m, length: 1.2 m for 30 kg pigs and Ø 0.46 m, length: 1.8 m for 70, 100 and 120 kg pigs) was used to hold the pigs in the prone position during scanning. Pigs had free access to water but not solid feed for a minimum of 8 h before weighing and scanning. Pigs were sedated i.m. with azaperon (0.1 mg/kg BW), ketamine (0.2 mg/kg BW) and propofol (0.22 mg/kg BW, i.v. in the ear) to minimize disturbances in the CT images due to movement. Intravenous sedation was only used at 100 and 120 kg TBW. Only one animal died during the procedure, during Exp. 2, and was not replaced. After scanning, the animals were returned to the IRTA experimental farm until their last scan, at which time the experiment was concluded. All procedures were approved by the ethics committee of IRTA.

Table 2. Number and BW of pigs of each sexual condition and target BW at CT-scanning (Exp. 2)

Target BW[1], kg	Sexual condition[2]	*n*	Mean BW, kg
30	FE	16	31.49
	EM	15	32.07
	IM	12	31.21
	CM	16	31.68
	Pooled SD		*1.18*
70	FE	16	71.16
	EM	15	72.30
	IM	16	71.28
	CM	16	71.66
	Pooled SD		*1.92*
100	FE	16	102.28
	EM	15	100.75
	IM	16	101.72
	CM	16	100.75
	Pooled SD		*2.89*
120	FE	12	121.42
	EM	11	120.18
	IM	12	120.27
	CM	12	120.58
	Pooled SD		*2.37*

[1]4 pigs of each sex (except IM at 30 kg) were slaughtered after CT-scanning
[2]Sexual conditions: FE = Female, EM = Entire male, IM = Immunocastrated male, CM = Castrated male

Slaughter and dissection

For Exp.1, five animals of each GEN were slaughtered at 30, 70 and 100 kg TBW and 15 animals at 120 kg TBW. Carcasses were kept refrigerated at 2ºC for 24 to 48 h until dissected. The left side of each carcass was prepared and cut following the European Union reference method (Walstra and Merkus, 1995). Thereafter, four primal cuts plus tenderloin were weighed and manually dissected. Lean, s.c. fat including the skin, intermuscular fat, and bone were separated with a knife by trained technicians, and the weights of all these tissues were recorded to obtain the total amounts of fat, lean and bone in the primal cuts, considering the tenderloin weight as lean. For Exp. 2, four animals of three 3 SEX (FE, EM and CM) at 30 kg TBW, four animals of each SEX (FE, EM, CM and IM) at 70 and 100 kg TBW and 12 animals of each SEX (FE, EM, CM and IM) at 120 kg TBW were slaughtered. Due to lack of skilled labor, the dissection included only the weights of the tissues of the four primal cuts, s.c. fat including the skin of the 4 primal cuts and dissection of the ham (s.c. fat including the skin, intermuscular fat, lean and bone). So, for Exp. 2 the total amounts of fat and lean needed to be estimated.

Image analysis - CT predictors

Acquisition of volume. The entire body of the pig was scanned to obtain the total number of voxels. Density measurements based on the Hounsfield scale (in Hounsfield units [**HU**]) were obtained from CT images using the VisualPork software package, which was developed for that purpose by the University of Girona and the IRTA (Bardera *et al.,* 2012; Boada *et al.,* 2009). The cradle was removed from all the images, but the viscera remained. The frequencies of voxels between −1,000 and +1,400 HU were converted into volumes (**vol**) following the methodology of Font-i-Furnols *et al.,*(2014). In brief, Hounsfield vol distributions were studied further to determine the limits for fat, muscle, and bone tissues. The HU value of 0 was selected as the separation between muscle and fat. Thus, the partial vol estimated between −149 and −1, between 0 and 140, and between 141 and 1,400 HU were associated with fat, muscle and bone vol, respectively, and were used as independent variables in the regression analysis. Volumes between −1,000 and −150 HU, which belong mainly to the less dense parts of the viscera, were considered only in calculating the total vol.

Acquisition of phenotypic measurements. Although the entire body of the pig was scanned, CT phenotypic measurements were manually obtained in a reduced set of images. The measurements were determined from six different tomograms. The anatomical location of the tomograms and the parameters evaluated for each one are presented in Table 3 and in Figure 1.

Table 3. Anatomical location of the measurements taken from each tomogram.

Tomogram	Location	Measurements	Abbreviation
Shoulder (Fig. 1a)	Cross section -SS- (Pork.org, 2005)	Subcutaneous fat thickness in the middle of the vertebral column and perpendicular to the skin (A)	Sh_sub_fat
		Area (mm^2) of the whole shoulder (B)	Sh_area
		Perimeter (mm) of the shoulder (C)	Sh_per
Loin (Fig. 1c)	Between: 6th-7th last rib 11th-12th last rib 14th-15th last rib 3rd-4th lumbar vertebrae	Subcutaneous fat thickness (mm) in the middle of the vertebral column and perpendicular to the skin (D)	Sub_fat_6_7, 11_12, 14_15, 3_4VL
		Maximum width (mm) of the right loin (E)	Width_6_7, 11_12, 14_15, 3_4VL
		Lateral fat thickness (mm) of right loin eye perpendicular to the skin, at the bottom and in the right side of the loin (F)	Lat_fat_6_7, 11_12, 14_15, 3_4VL
		Right loin eye area (mm^2) (G)	Area_6_7, 11_12, 14_15, 3_4VL
		Right loin perimeter (mm) (H)	Per_6_7, 11_12, 14_15, 3_4VL
		Maximum length of the 2 loins (mm) (I)	Max_l_6_7, 11_12, 14_15, 3_4VL
Ham (Fig. 1b)	Cross section -N- (Pork.org, 2005)	Maximum vertical height of the ham (J)	H_height
		Subcutaneous fat thickness (mm) at the top of the ham and perpendicular to the skin (K)	H_sub_fat
		Area of the ham's subcutaneous fat (mm^2) (L)	H_fat_area
		Ham's width (mm) above the bones (M)	H_width
		Lateral fat thickness (mm) at the previous level (N)	H_lat_fat
		Area of the ham (mm^2) (O)	H_area
		Perimeter --- Perimeter (mm) of the whole ham (P)	H_perimeter

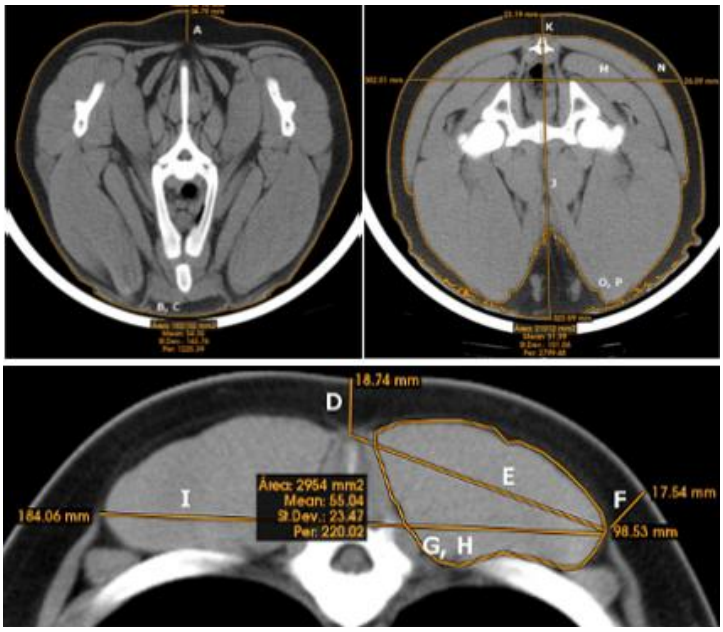

Figure 1. Anatomical measures obtained from the tomogram of the shoulder (a), ham (b) and loin (c).

Potential on-farm predictors

Potential on-farm predictors were obtained by CT in this study, but could be obtained without the necessity of the device, for example by use of ultrasound. These were selected based on their ease of on-farm measurement with widely available equipment. The potential on-farm parameters evaluated, as well as the device proposed to obtain them, are presented in Table 4.

Components predicted

Equations, using CT and potential on-farm predictors, were derived to predict the total amounts of fat (s.c. and intermuscular fat of the four primal cuts) and lean (lean of the four primal cuts + tenderloin), as well as the weights of shoulder, belly, loin and its s.c. fat and ham and its lean and bone. For the fat and the lean tissue it was necessary to realize a previous estimation for Exp. 2 (animals of different SEX), because those values were not directly obtained from the dissections.

Table 4. Potential on-farm predictors of weights and compositions of primal cuts in pigs.

Tomogram	Potential on-farm predictors	Equipment suggested
Shoulder (Fig. 1a)	Subcutaneous fat thickness in the middle of the vertebral column and perpendicular to the skin (A)	Ultrasound
Loin (Fig. 1c)	Subcutaneous fat thickness (mm) in the middle of the vertebral column and perpendicular to the skin (D)	Ultrasound
	Maximum width (mm) of the right loin (E)	Ultrasound
	Lateral fat thickness (mm) of right loin eye perpendicular to the skin, at the bottom and in the right side of the loin (F)	Ultrasound
	Right loin eye area (mm^2) (G)	Ultrasound
	Right loin perimeter (mm) (H)	Ultrasound
Ham (Fig. 1b)	Subcutaneous fat thickness (mm) at the top of the ham and perpendicular to the skin (K)	Ultrasound
	Lateral fat thickness (mm) at the previous level (N)	Ultrasound
	Perimeter (mm) of the whole ham (P)	Tape measure

Statistical analyses

Statistical analyses were performed using SAS software (SAS Institute Inc, Cary, NC, USA, 2001). The REG procedure was used to determine the best predictors for the regression equations. The models included the values from dissection as the dependent variables, and CT and potential on-farm predictors as independent variables for animals of different GEN or SEX. Then, the GLM procedure was used to detect differences in regression parameters among GEN or SEX. The model included GEN or SEX as a class and the predictors obtained from the REG procedure. Even if the GEN or SEX effect was significant, the equations selected were those that presented lower variance than the variance within GEN or SEX and TBW. The accuracy and precision of each equation were evaluated from the R^2 and the Root Mean Square Error (**RMSE**). Moreover, to investigate lack of fit of equations for both data sets, without distinction of GEN or SEX, the Mean Square Error of Prediction (**MSEP**) was decomposed into mean bias, slope bias and random error. Ideally, most of the error should reside in the random component of MSEP (Tedeschi, 2006). If the proportion of random error for any of the groups was lower than 0.70, another regression was

performed using different predictors. Furthermore, when necessary to standardize the variance, the dependent and independent variables were transformed into natural logarithms.

Results and discussion

The prediction equations using CT and potential on-farm predictors are presented in Tables 5 and 6, respectively, as well as the R^2, RMSE and proportions of random error for GEN and SEX. In general, the correlations from CT predictors were slightly greater than the correlations for potential on-farm predictors when comparing the amounts of fat, lean, the weights of the main primal cuts and the composition of the ham.

Fat. First of all, the total amount of dissected fat (s.c. + intermuscular) of the primal cuts needed to be estimated for Exp. 2 (animals of different SEX), because this value was not obtained directly from the dissections. The following regression equation was developed, using values from Exp. 1 (animals of different GEN) (R^2 = 0.995, MSEP = 0.138 kg):

*Total amount of dissected fat = (s.c. fat of ham + s.c. fat of loin + s.c. fat of shoulder) * 1.588*

This equation showed a non-significant (P > 0.05) GEN effect and was applied to the second set of animals of different SEX. The results obtained were considered as the total amount of dissected fat of the 4 main cuts of the half carcass. Coefficient of determination and proportions of random error in GEN and SEX effects were greater than 95% for equations using either CT or potential on-farm predictors. However, the best equation was obtained using a CT predictor (vol of fat), which presented the lowest RMSE and greatest R^2 (Fig. 2 and 3). Although the literature about the accuracy of predicting the amount fat in live pigs of different GEN and SEX using CT is limited, this particular issue has been extensively studied over the years using other devices and predictors. The present equation shows a greater accuracy than those reported by Higbie *et al.,*(2002), who reported poorer predictions of fat using different carcass measurements ($0.74 \leq R^2 \leq 0.96$ and 0.48 kg ≤ RMSE ≤ 1.30 kg). The equations proposed by Font-i-Furnols *et al.,*(2014) are more precise (0.09 kg ≤ RMSE ≤ 0.26 kg), however predictions are limited to the specific genotypes and sexual condition used in that study (same as Exp. 1 here). By contrast, the present equation may be used in different GEN and SEX. The selected equation would be most useful in a laboratory situation, especially for those organizations with access to a CT device. However, for practical situations the results presented using potential on-farm predictors (BW, s.c. fat of the shoulder and lateral fat of the ham) revealed a R^2 = 0.982 and RMSE = 0.496 kg and a great level of accuracy (> 0.90) for different GEN and SEX, similar to Higbie *et al.,*(2002).

Table 5. Regression equations using CT predictors.

Dependent variable	Predictor[1]	Equation type	Intercept	Slope	P-value	R^2	RMSE[2]	Proportion of random error associated with	
								Genotype	Sexual condition
Fat in 4 primal cuts[3]	Vol of fat	Linear	-0.051	0.238	<0.0001	0.994	0.293	0.998	0.946
Lean in 4 primal cuts + tenderloin	Vol of lean Fat-free mass[4]	Linear	-1.316	0.189 0.134	0.008 0.036	0.993	0.486	1.000	0.891
Carcass wt	BW Per_14_15	Linear	-9.712	0.769 0.053	<0.0001 <0.0001	0.998	1.233	1.000	0.802
Wt of 4 primal cuts	BW Area_14_15	Linear	-1.934	0.245 0.0007	<0.0001 <0.0001	0.997	0.547	1.000	0.992
Ham wt	BW Vol of lean	Linear	-0.647	0.064 0.071	<0.0001 <0.0001	0.988	0.390	1.000	0.978
Ham fat	BW Vol of lean H_fat_area	Linear	-0.225	0.044 -0.048 0.00004	<0.0001 <0.0001 0.001	0.978	0.160	1.000	0.885
Ham lean	H_area Vol of lean Vol of bone	Linear	-0.916	0.00003 0.145 -0.503	<0.0001 <0.0001 <0.0001	0.980	0.340	0.995	0.753

	Vol of bone	Linear	-0.132	0.089	<0.0001	0.991	0.023	0.998	0.761
	Sub_fat_6_7			0.003	0.004				
	Lat_fat_11_12			-0.005	<0.0001				
Ham bone	Area_11_12			-0.00007	<0.0001				
	Lat_fat_3_4VL			0.002	0.020				
	Area_3_4VL			0.00006	<0.0001				
	H_height			0.001	0.0001				
	BW	Linear	-1.094	0.066	<0.0001	0.990	0.203	1.000	0.763
	Lat_fat_11_12			-0.021	0.016				
Shoulder wt	Lat_fat_Ham			-0.035	0.002				
	Vol of bone			-0.205	0.013				
	Sh_per			0.002	0.007				
	BW	Linear	-2.650	0.068	< 0.0001	0.990	0.265	1.000	0.836
	H_fat_area			-0.0001	0.001				
Loin wt	H_width			0.005	0.032				
	Sh_per			-0.003	0.0003				
	Sub_fat_6_7			0.054	< 0.0001				
	Diag_14_15			0.042	0.001				
	Sh_per	Linear	0.467	-0.003	< 0.0001	0.991	0.104	1.000	0.803
	Total vol			0.021	<.0001				
	H_height			-0.005	0.002				
Loin fat	Sub_fat_11_12			0.020	0.001				
	Sub_fat_14_15			0.029	0.001				
	Per_14_15			-0.013	<.0001				
	Lat_fat_11_12			0.043	<.0001				
	Area_14_15			0.0002	0.0004				

	Area_3_4VL			-0.0002	0.0004				
	Max_l_6_7			0.004	0.020				
	Width_14_15			0.062	<.0001				
	Width_3_4VL			-0.012	0.019				
	H_lat_fat	Linear	-0.387	0.042	0.0012	0.977	0.266	1.000	0.890
Belly wt	Total vol			0.045	<0.0001				
	Lat_fat_11_12			-0.022	0.0431				

[1]For list of abbreviations, see descriptions in Table 3.
[2]RMSE, Root mean square error
[3]Primal cuts: ham, loin, shoulder and belly.
[4]Fat free mass = estimated carcass weight * (1- estimated fat weight/estimated 4 cuts weight)

Table 6. Regression equations using potential on-farm predictors.

Dependent variable	Predictor[1]	Equation type	Intercept	Slope	Linear coefficient	Exp[3]	P-value	R^2	RMSE[3]	Proportion of random error associated with	
										Genotype	Sexual condition
Fat in 4 primal cuts[4]	BW	Linear	-2.659	0.043			<0.0001	0.982	0.496	0.989	0.937
	H_lat_fat			0.207			<0.0001				
	Sh_sub_fat			0.095			<0.0001				
Lean in 4 primal cuts + tenderloin	BW	Linear	-0.058	0.055			<0.0001	0.992	0.514	1.000	0.942
	Estimation of ham lean without CT[5]			1.180			<0.0001				
	Sh_sub_fat			-0.060			0.017				
	Area_14_15			0.001			<0.0001				

Ham wt	BW	Linear	-2.043	0.058			<0.0001	0.993	0.322	0.997	0.780
	Area_14_15			0.0007			0.0002				
	H_area			0.00003			0.050				
	Area_11_12			-0.0004			0.035				
	H_per			0.002			0.004				
Ham fat	BW	Linear	-0.432	0.023			<0.0001	0.984	0.141	1.000	0.939
	Lat_fat_11_12			0.018			0.003				
	Lat_fat_3_4VL			0.013			0.009				
	Area_3_4VL			-0.0002			<0.0001				
	H_lat_fat			0.035			<0.0001				
Ham lean	BW	Linear	-2.764	0.023			<0.0001	0.981	0.345	0.999	0.780
	Sh_per			0.004			0.001				
	H_per			0.003			0.0007				
	Area_3_4VL			0.0007			<0.0001				
	Per_11_12			-0.018			0.0004				
	Sub_fat_6_7			-0.042			0.0003				
Ham bone	BW	Linear	0.099	0.007			<0.0001	0.979	0.037	0.994	0.898
	Lat_fat_11_12			-0.005			0.004				
	Area_11_12			-0.0001			<0.0001				
	Area_3_4VL			0.00005			<0.0001				
Shoulder	BW	Exponentia			-3.891	0.956	<0.0001	0.987	0.228	1.000	0.750

wt		l								
	Area_3_4VL				0.164	0.007				
	Lat_fat_ham				-0.076	0.025				
Loin wt	BW	Exponentia l		-6.595	0.837	<0.0001	0.988	0.297	0.990	0.809
	Sub_fat_6_7				0.160	0.0001				
	Width_14_1 5				0.877	0.0004				
Loin fat	BW	Exponentia l		5.895	1.630	<.0001	0.985	0.156	0.996	0.794
	Sh_per				-1.707	0.007				
	Sub_fat_11_ 12				0.499	<.0001				
	Per_14_15				-2.075	<.0001				
	Width_14_1 5				1.709	0.006				
	Lat_fat_6_7				0.350	0.001				
Belly wt	Area_14_15	Linear	-0.569	0.001		<0.0001	0.957	0.360	1.000	0.985
	H_lat_fat			0.119		<0.0001				

[1]For list of abbreviations, see descriptions in Table 3
[3]Exponential
[3]RMSE, Root mean square error
[4]Primal cuts: ham, loin, shoulder and belly
[5]Estimation presented in the same Table

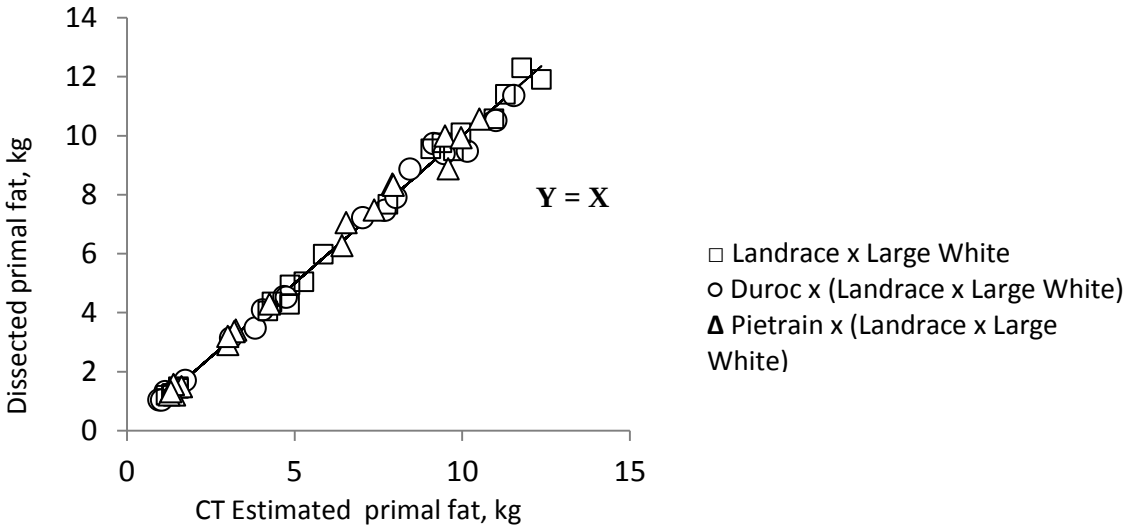

Figure 2. CT-prediction of primal fat for pigs of different genotypes (○, Duroc x (Landrace x Large White); □, Landrace x Large White; Δ, Pietrain x (Landrace x Large White)). Solid line is the line of identity.

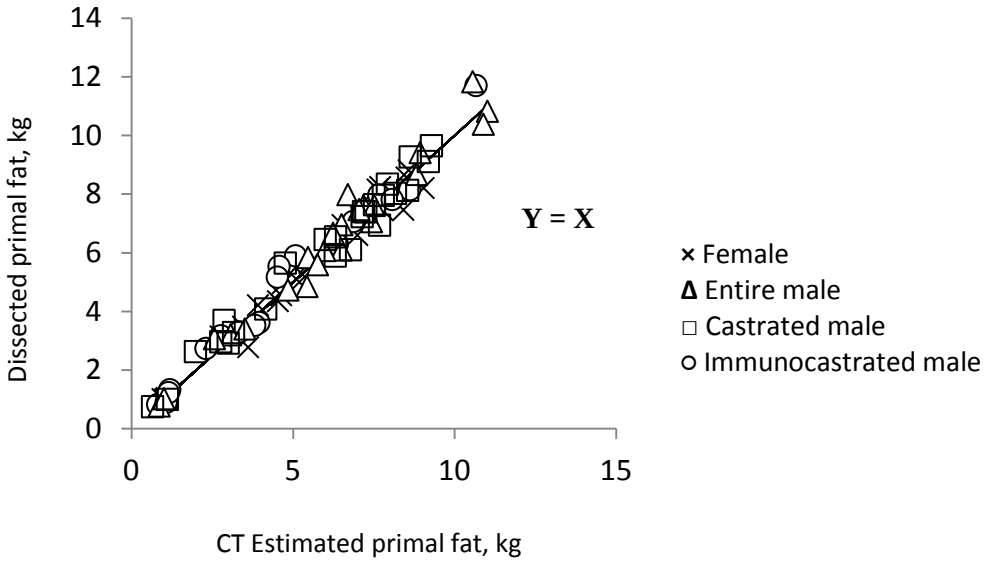

Figure 3. CT-prediction of primal fat for pigs of different sexual conditions (×, Females; Δ, Entire males; □, Castrated males; ○, Immunocastrated males). Solid line is the line of identity.

Lean. As for fat, the total amount of dissected lean had to be estimated for Exp. 2 (animals of different SEX), because this value was not directly obtained from the dissections. Therefore, the following regression equation was developed using dissected values from Exp. 1 (animals of different GEN) (R^2 = 0.999 and MSEP = 0.512 kg):

$$Total\ amount\ of\ dissected\ lean = 2.790 * lean\ of\ the\ ham^{0.824} + Shoulder\ weight^{0.435} + Ham\ weight^{-0.229}$$

This equation showed no GEN effect (P > 0.05) and was applied to the second set of animals of different SEX. The results obtained were considered as the total amount of lean of the 4 main cuts plus tenderloin of the half carcass.

Typically, the percentage of lean in the live pig is difficult to predict accurately. Although statistically significant (P < 0.001), the relationships between the CT predictors of the percentage of lean in the soft tissue and the lean from the dissections were weaker than observed for fat content and the RMSE was greater (0.486 and 0.514 kg for CT and on-farm predictors, respectively). One factor that might weaken this relationship is that the viscera largely fall within the lean tissue range of HU. The vol of lean and fat free mass (**FFM**) were the predictors used for the CT equation; FFM was estimated using the following equation:

*FFM = Predicted HCW * (1 – (predicted Fat weight / predicted 4 cuts weight))*

Fig. 4 and 5 illustrate the accuracies of the predictions, with high proportions of random error for different GEN and SEX (1.000 and 0.891, respectively).

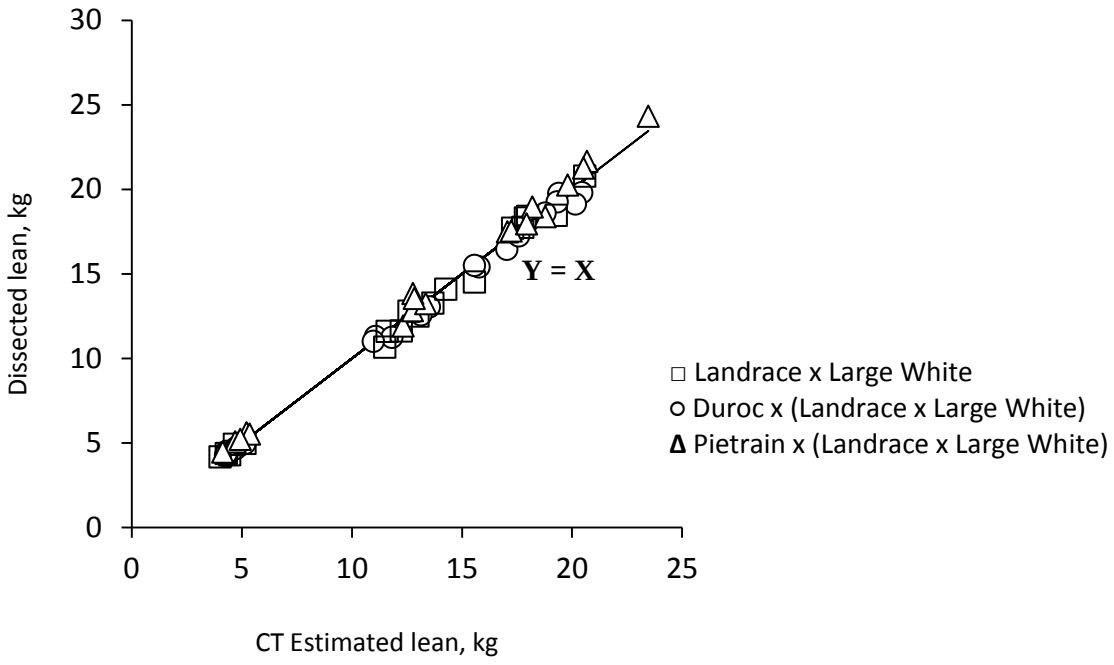

Figure 4. CT-prediction of lean for pigs of different genotypes (○, Duroc x (Landrace x Large White); □, Landrace x Large White; Δ, Pietrain x (Landrace x Large White)). Solid line is the line of identity.

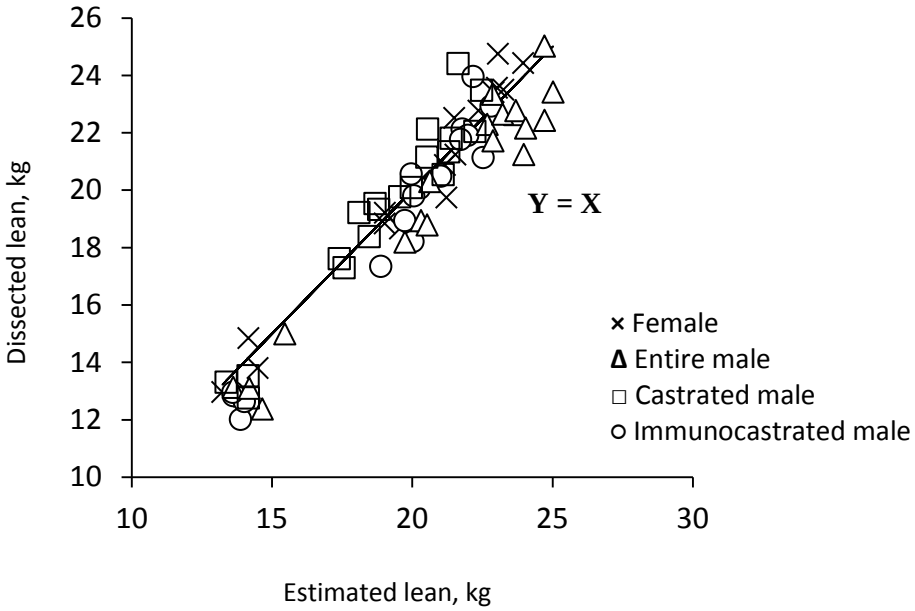

Figure 5. CT-prediction of lean for pigs of different sexual conditions (×, Females; Δ, Entire males; □, Castrated males; ○, Immunocastrated males). Solid line is the line of identity.

The prediction equation for the lean using potential on-farm predictors presented an R^2 of 0.992 with a proportion of random error of 1.000 for the GEN effect and 0.942 for the SEX effect. However, it also presented a high RMSE (0.514 kg) with a coefficient of variation of 3.929. These results make this equation useful for prediction of lean in animals of different GEN and different SEX. Gu *et al.,*(1992) reported that the prediction of whole carcass lean from ham lean alone would overestimate the carcass lean differences between genotypes. In the present study, the lean of the ham was used as a predictor in the previous regression to find the total amount of dissected lean for the Exp. 2 (SEX), but the equation also included the weights of the ham and the shoulder. Jia *et al.,*(2010) reported similar results for the prediction of the amount of lean from HCW, 10th rib backfat depth and 10th rib loin eye area with a coefficient of determination of 0.90. When their model included ham weight * ham percentage lean area and ham weight * ham percentage fat area, carcass lean was only slightly better predicted (R^2 = 0.91). Other studies in live pigs have reported similar results. Higbie *et al.,* (2002) presented a lean prediction equation for gilts using live weight and s.c. fat at the 10th rib (measured by ultrasound) as a predictors, with an R^2 of 0.620 and RMSE of 1.68 kg. Therefore, both equations for prediction of lean obtained in this study were considered adequate.

***Ham weight*.** The equation using potential on-farm predictors presented the lowest RMSE and the greatest R^2, however, the random error components for the GEN and SEX effects were greater using CT predictors, thus both equations were considered adequate. The CT equation used 2 predictors: BW and the vol of lean ($P < 0.0001$) whereas the equation using potential on-farm predictors included 5 predictors: BW, loin eye areas between the 14-15th and 11-12th ribs and the

area and perimeter of the ham. Notably, BW explained 98% of the variability in ham weight which is greater than that obtained by Daza *et al.,*(2010) and Ayuso *et al.,* (2013) with multiple regression equations for heavy Iberian pigs. It is important to note that Daza *et al.,*(2010) used carcass measurements and different techniques from those reported in the current study, whereas Ayuso *et al.,* (2013) and Daza *et al.,* (2006) used ultrasound to study the variables in live pigs. Font-i-Furnols *et al.,* (2014) analyzed different models to find the best ham weight prediction for each genotype, and reported that quadratic models had the lowest coefficient of variation with RMSE from 0.256 to 0.400 kg. Similar model performance is presented in this study (RMSE = 0.322 kg), but the equation is applicable to animals of different GEN and SEX.

Ham fat. The equation using potential on-farm predictors showed lower RMSE and greater coefficient of determination and proportions of random error for GEN and SEX effects than the equation obtained using CT predictors. Moreover, these particular on-farm predictors (lateral fat between the 11-12th ribs, loin area and lateral fat between the 3-4th lumbar vertebrae and lateral fat of the ham) can be obtained easily with an ultrasound device in all kinds of farming conditions.

Ham lean. Similar coefficient of determination and RMSE were found for equations for prediction of ham lean based on CT and potential on-farm predictors, but the proportion of random error for the SEX effect was greater using on-farm predictors. Six predictors from all over the pig's body were used: from the shoulder, from 4 different parts of the loin and from the ham.

Ham bone. The CT equation was best for predicting the amount of bone in the ham, using 8 different predictors, including the partial vol of lean and bone. A small RMSE (0.023 kg) was found, even though the proportion of random error for the SEX effect did not reach 90%.

Shoulder, loin, loin's fat and belly. The belly was poorly predicted from both whole-pig CT images and potential on-farm predictors (RMSE = 0.266 and 0.360 kg, respectively). According to Nissen *et al.,* (2006) the belly is characterized by a high dissection error because of the thin layers of fat and muscle, which are difficult to separate by knife. However, its prediction for different SEX presented high proportions of random error for both equations (0.890 vs. 0.985, for CT and on-farm predictors, respectively). The shoulder presented the lowest proportion of random error for different SEX of the 4 main cuts (0.763 and 0.750, using CT and on-farm predictors, respectively). However, the predictions of loin weight were good, with high coefficients of determination for both equations, an average RMSE of 0.265 kg and proportions of random error of 1.000 and 0.836 for GEN and SEX effects, respectively, using CT predictors. The fat of the loin also presented great coefficient of determination and great proportion of random error for GEN and SEX effect. In this case, loin fat included the s.c. fat of the loin. Initially, the amount of fat included both types of fat, the s.c. and the intermuscular fat, but it presented a low proportion of random error for the SEX effect (results not shown), as a result it would not be useful in any case. In addition, IM pigs had unique characteristics, differing from EM and FE, with very particular carcass and meat characteristics, especially regarding the loin (Gispert *et al.,* 2010) thus, a prediction equation for

the loin weight and its fat would be novel and very helpful. Consequently, with the aim of obtaining useful equations for animals of different SEX and GEN, an alternative prediction, taking into account the s.c. fat of the loin as the loin's fat, was suggested, analyzed and finally, selected.
Linear and nonlinear measurements obtained from CT images at specific anatomical positions in live pigs are good predictors of carcass characteristics in young pigs (Carabús *et al.,* 2014; Carabús *et al.,* 2011). However, the addition of vol obtained by scanning the whole animal can improve prediction equations compared to linear and nonlinear measurements. The present study showed that the predictions of fat, lean, ham weight, ham composition, shoulder and belly included tissue vol as predictors and in all cases except for ham weight and ham fat, the use of vol improved the accuracy of the predictions.

Conclusions

Variation in body and carcass composition affects profitability of the swine industry. Available tools for use on live animals, such as CT or ultrasound, can support management and breeding decisions. Prediction equations derived from CT or on-farm measurements can be useful for genetic improvement, feeding programs and management. Despite large phenotypic variations between pigs from different genotypes and sexual conditions, single equations were developed to predict amounts of fat, lean and primal cuts for all, including immunocastrated males. However, more research is required on the selection of images and prediction equations to improve accuracy and reduce costs.

Acknowledgements

The present study was supported by the Instituto Nacional de Investigaciones Agrarias –INIA (Evaluación *in vivo* del crecimiento alométrico de los tejidos muscular y adiposo de los cerdos según la genética y el sexo mediante tomografía computerizada. RTA2010-00014-00-00). INIA is also thanked for the scholarship to Anna Carabús. The authors wish to thank Albert Brun, Carles Francàs, Albert Rossell, Agustí Quintana, Albert Fontquerna, Carlos Millán y Alfons Varas for their invaluable technical assistance.

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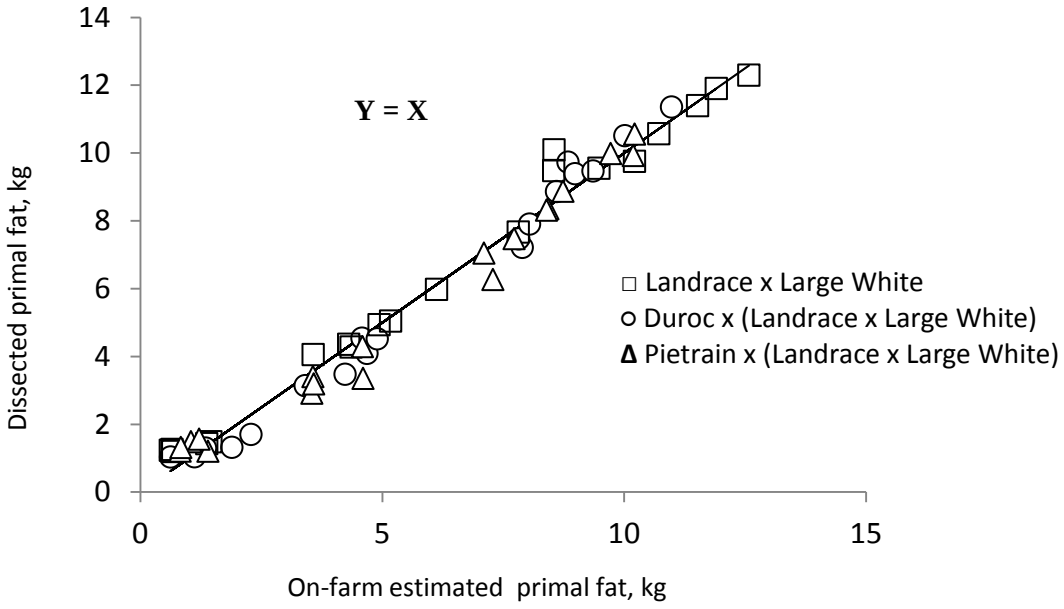
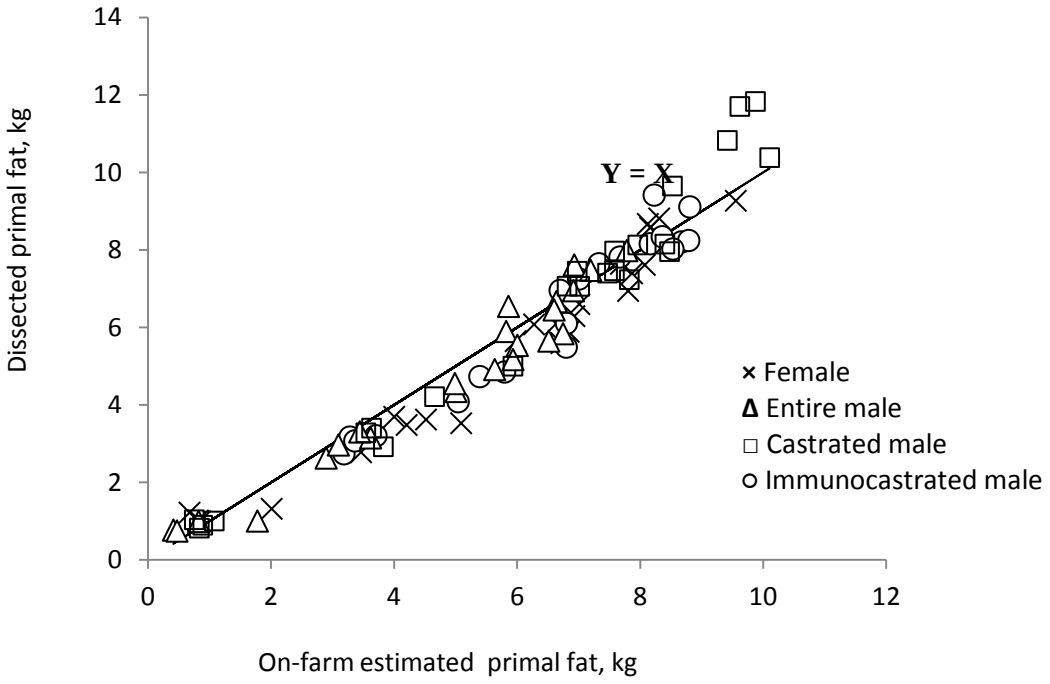
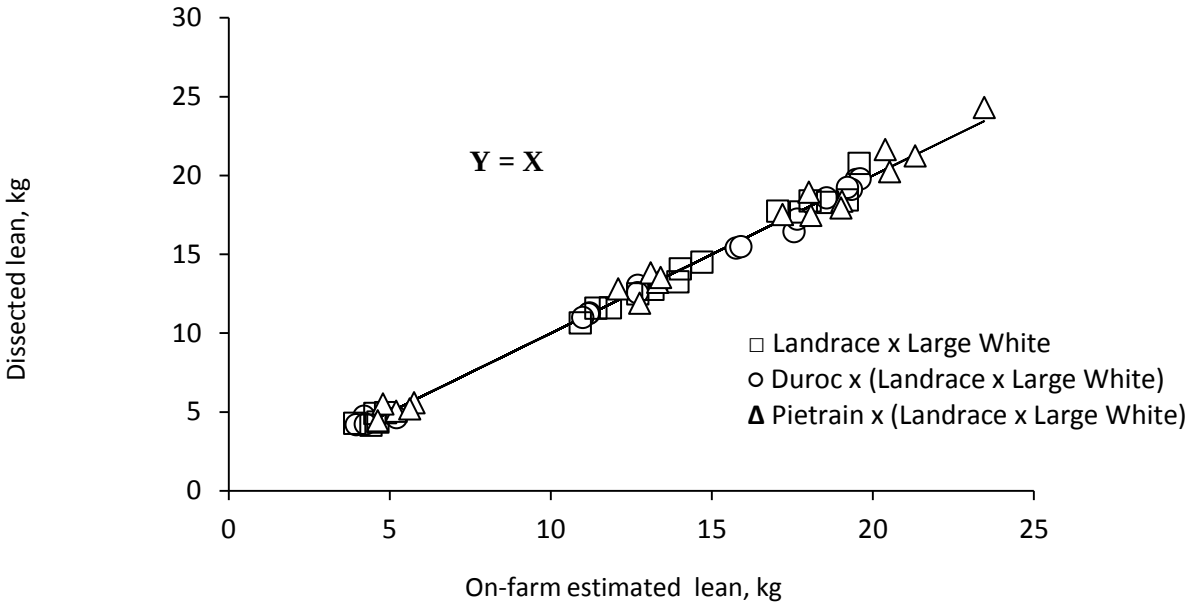
Suplementary Figures



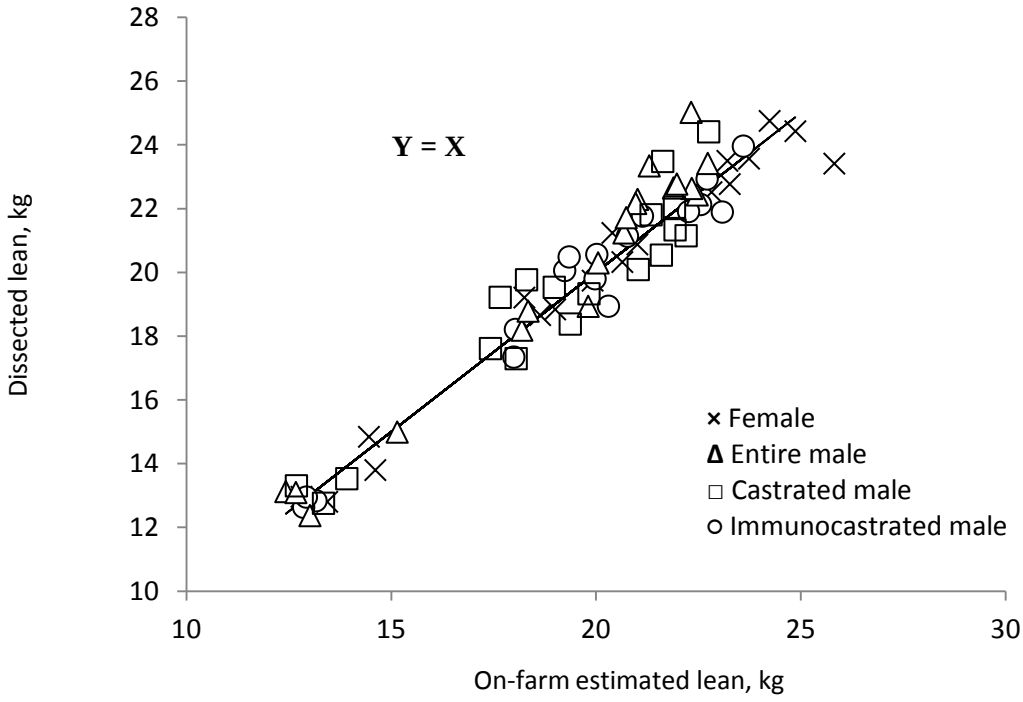
Suplementary Figure S1. On farm-prediction of fat for pigs of different genotypes (○, Duroc x (Landrace x Large White); □, Landrace x Large White; Δ, Pietrain x (Landrace x Large White)). Solid line is the line of identity.



Suplementary Figure S2. On-farm prediction of primal fat for pigs of different sexual conditions (×, Females; Δ, Entire males; □, Castrated males; ○, Immunocastrated males). Solid line is the line of identity.



Suplementary Figure S3. On farm-prediction of lean for pigs of different genotypes (○, Duroc x (Landrace x Large White); □, Landrace x Large White; Δ, Pietrain x (Landrace x Large White)). Solid line is the line of identity.



Suplementary Figure S4. On-farm prediction of lean for pigs of different sexual conditions (×, Females; Δ, Entire males; □, Castrated males; ○, Immunocastrated males). Solid line is the line of identity.

Chapter 7

Results IV

The content of this chapter is submitted in the Animal journal

Growth of total fat and lean and the primal cuts in relation to estimated mature weight in pigs of different sexual conditions, assessed using computed tomography

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This chapter deals with:

- How and how fast the pig body develops from birth to maturity
- Age-dependent growth capacity
- Composition of growth in female, entire male, castrated males and immunocastrated pigs
- Mathematical descriptions of growth characteristics

Introduction

Pig growth results from a multitude of biological processes. The age, genotype and sexual condition of an animal determines the maximum level at which these processes can occur, whereas environmental factors such as nutrition and health status determine the degree to which genetic potential is expressed. Growth functions have been extensively used to describe the size *versus* age relationship in pigs, and many functions are presented in the literature, including polynomials (Knap, 2000, Wellock *et al.,* 2004). Most of these functions are available for the description of growth such as Brody's, logistic, Gompertz, von Bertalanffy, and the four-parameter Richards function, which combines aspects of all the above growth functions into one. Schinckel *et al.* (2009) compared growth curves of different sexual conditions from light to heavy weights. However, very few studies have included the immunocastrated pig (Fàbrega *et al.,* 2010, Gispert *et al.,* 2010). To provide a complete picture of the impacts of immunocastration of pigs for retailers and consumers, and to understand whether this is a viable production practice, it is also necessary to know the growth performance and body composition of immunocastrated pigs relative to other sexual conditions over time. Computed tomography (**CT**) is a non-invasive technology that enables the study of the body composition of live animals during growth (Kolstad, 2001, Font-i-Furnols *et al.*, 2014). Moreover, with the use of validated equations it is possible to know the weights of different cuts or tissues at different live weights without the necessity of slaughter and dissection. This tool allows the study of growth performance and body composition at the same time. The aims of the present study were (1) to evaluate variation in the body composition of four sexual conditions at 30, 70, 100 and 120 kg of live weight; (2) to model the allometric growth of the total body fat and lean, the four main cuts and composition of the ham,

and (3) to estimate the mature body weight (**MBW**) of the four SEX and study the relationships between the growth models and the MBW.

Materials and methods

Animals and experimental design

Forty eight piglets were moved from a commercial farm with high health status to the weaning unit at IRTA-Monells at a mean age of 21 days. The piglets were crosses between Duroc x Landrace hybrid sows and recessive homozygous (nn) Pietrain boars, all of them from the same company, and of different **SEX**: 12 each of females (**FE**), males (**EM**), castrated males (**CM**) and immunocastrated males (**IM**). The immune-vaccine Improvac® (Zoetis, Spain), which contains 200 µg GnRH-protein conjugate/ml in an aqueous adjuvant system, was administered twice by technical staff in accordance with the manufacturer's instructions. Each pig in the IM group was injected 2 ml subcutaneously just behind and below the base of the ear, at 12 and 18 weeks of age. All the pigs were fed a commercial diet on an *ad libitum* basis (two-phase feeding program containing 10.24 and 10.08 MJ net energy/kg, 18.00% and 17.02% crude protein and 0.91% and 0.90% digestible lysine as-fed basis during the first and second phases, respectively), weighed weekly and CT scanned at 30, 70, 100 and 120 kg target body weight (**TBW**).

Computed tomography

Animals were fully scanned with a General Electric HiSpeed Zx/I tomograph, located in IRTA-Monells (Catalonia, Spain), and the instrumental settings were: 140 kV, 145 mA, matrix 512x512, axial, 7 mm thick (30 kg TBW) and 10 mm thick (70, 100 and 120 kg TBW). Custom-built half-tube cradles (PVC, Ø 0.30 m, length: 1.2 m for 30 kg pigs and Ø 0.46 m, length: 1.8 m for 70, 100 and 120 kg pigs) were used to hold pigs in the prone position during scanning. Pigs had free access to water but not feed for a minimum of 8 h before weighing and scanning. Animals were sedated and anaesthetised intramuscularly with azaperon (0.1 mg/kg BW), ketamine (0.2 mg/kg BW) and propofol (0.22 mg/kg BW, intravenously in the ear) to minimize disturbances in the CT images due to movement. Intravenous sedation was only used at 100 and 120 kg TBW. One animal from the EM group died during the procedure, and was not replaced. After scanning, the animals were returned to the IRTA experimental farm until their last scan, at which time the experiment was concluded. All procedures were approved by the ethics committee of IRTA.

Image analysis

Image analysis was split into linear, area and volume measurements and were carried out using the VisualPork software, developed by the Universitat de Girona and IRTA (Boada *et al.*, 2009, Bardera *et al.*, 2012). Measurements similar to the ones used by Carabús *et al.* (2014) were obtained manually from different tomograms (Table 1), and are graphically visualized in Fig 1.

Table 1. Anatomical location of the measurements taken from each tomogram.

Tomogram	Location	Measurements
Shoulder (Fig. 1.1)	Cross section -SS- (Pork.org, 2005)	Subcutaneous fat thickness in the middle of the vertebral column and perpendicular to the skin (A) Area (mm^2) of the whole shoulder (B)
Loin (Fig. 1.2)	Between: 6^{th}-7^{th} rib 11^{th}-12^{th} rib 14^{th}-15^{th} rib 3^{rd}-4^{th} lumbar vertebrae	Subcutaneous fat thickness (mm) in the middle of the vertebral column and perpendicular to the skin (C) Lateral fat thickness (mm) of right loin eye perpendicular to the skin and in the right side of the loin (D) Right loin eye area (mm^2) (E)
Ham (Fig. 1.3)	Cross section -N- (Pork.org, 2005)	Subcutaneous fat thickness (mm) at the top of the ham and perpendicular to the skin (F) Lateral fat thickness (mm) at the level above the bones (G) Area of the ham (mm^2) (H)

Volume measurements required the use of all scanning images for each animal. Volumes of fat, lean and bone were obtained as the sums of voxels with Hounsfield Unit (**HU**) values between -149 and 0, 1 and 150, and 151 and 1400, respectively (Font i Furnols *et al.,* 2014).

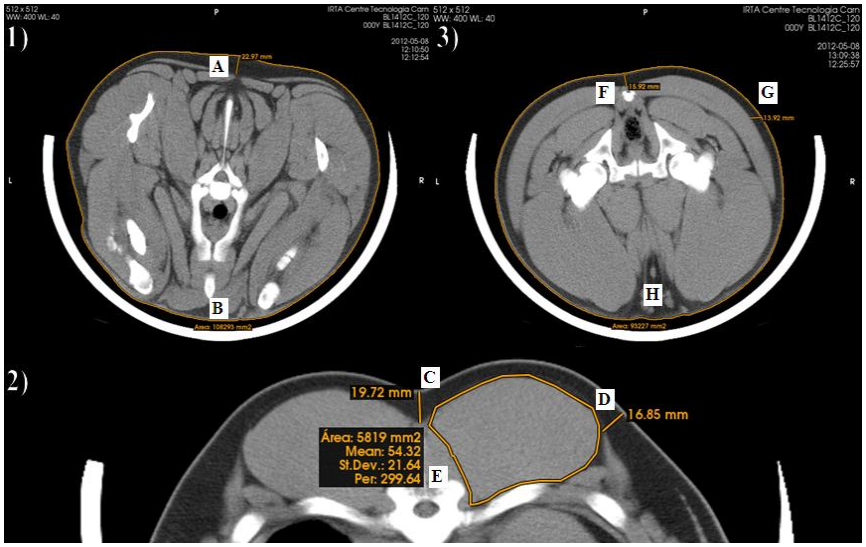

Figure 1. Anatomical measurements obtained by CT from the (1) shoulder, (2) different tomograms of the loin, and (3) ham.

Predictions and parameters modeled

Prediction equations developed by Carabús *et al.* (2015) were used to determine the growth of fat and lean of the four main cuts, the weights of shoulder, belly, loin and the fat of the loin as well as the weight of ham and its amount of fat, lean and bone. All modeled variables are presented in Table 2.

Table 2. Parameters modeled using CT predictors.

	Parameters modeled
Fat	Weight of the subcutaneous and intermuscular fat of the 4 main cuts* (kg)
Lean	Weight of the lean of the 4 cuts + tenderloin (kg)
Ham	Weight of the ham (kg)
H. Fat	Weight of ham subcutaneous and intermuscular fat (kg)
H. Lean	Weight of ham lean mass (kg)
H. Bone	Weight of ham bones (kg)
Shoulder	Weight of the shoulder (kg)
Loin	Weight of the loin (kg)
L. Fat	Weight of loin subcutaneous fat (kg)
Belly	Weight of the belly (kg)

*Shoulder, loin, belly and ham

Allometric growth

The allometric equation was chosen to model the growth of the selected variables. In 1891, Snell first fit it as follows, described in Gould (1971):

$Y = aX^b$.

For parameter estimation, the equation was linearised as follows:

$\log Y = \log a + b * \log X$,

where Y is the weight of the tissue, and X is the live weight or the weight of the cut, depending of the variable analysed; a is an intercept and b is the allometric growth coefficient that describes

the relationship between the two body constituents. A unity of the allometric growth is assumed if $b = 1$; then, Y grows at the same proportional rate as X; if $b > 1$, Y grows proportionately faster than X, and the opposite is true if $b < 1$. Snell's power function was extended by Huxley in the 1930s (Huxley, 1932) and 1950s (Huxley, 1950) to the wide range of phenomena that encompass differential or allometric growth. The interpretation of b as the ratio of specific growth rates of y/x has been accepted by all, but the meaning of the coefficient a has generated a large and inconclusive literature (Gould, 1971).

Estimation of mature body weight

The MBW of each group of pigs was obtained using the Gompertz equation (Gompertz, 1825):

$$Y(t) = a.\, e^{(-be)^{(kt)}},$$

where Y is the BW, t is the time period generally expressed in days or weeks (expressed in days in the present study), a is an asymptote equivalent to MBW, b sets the displacement along the x axis (time; translates the graph to the left or right), k sets the growth rate (y scaling) and e is Euler's number. The function is simple, sigmoidal in shape, and fits a range of growth data well (Kyriazakis *et al.*, 1991, Ferguson *et al.*, 1994). It adequately describes the more rapid growth in the early stages of life and the decline in growth in the later stages. The parameters are empirically derived, but may have biological meaning attributed to them, such that comparisons can be made between different animals of different SEX.

Statistical analysis

Statistical analyses was performed using SAS software (SAS Institute Inc, Cary, NC, USA, 2001). A mixed procedure including repeated measures was used to determine whether significant phenotypic differences existed among the four SEX. The model included SEX, TBW and their interaction as fixed effects. The covariance matrix type used in the model was selected for each variable, so as to present the lowest values of Akaike's information criterion (AIC) and the corrected Akaike's information criterion (AICC). Tukey's test was used to compare the least-squared mean values at the 0.05 significance level.

To determine the allometric coefficients for each SEX, a MIXED procedure was applied, including SEX as a fixed effect, the natural log of BW as the covariate within SEX, and the repeated subject was the animal (**ID**). Tukey's test was used to compare the least-square mean values at the 0.05 significance level.

A three stage procedure was adopted for the estimation of MBW. Initially, it was necessary to establish biological minimum and maximum values for the parameters a, b and k from the literature (Vincek *et al.,* 2012), forcing the MBW estimates to fall between these two values of a. Then the NLIN procedure was applied to fit the Gompertz equation, using ID as a repeated measure. Once an average MBW (parameter a) and consequently parameters b and k were obtained for each SEX, the average group b and k values were used to find the individual MBW for each animal. To study the relationships between the allometric models and the MBW a MIXED

procedure was used, using %MBW (100*BW/MBW) as a covariate. The selected variables were studied as a percentage of the total weight of the four main cuts and the BW was presented as a percentage of the MBW at scanning.

Results and discussion

Measurements obtained by CT

Volumes of fat, lean and bone, depending on SEX, TBW and the interaction between SEX and TBW effect, are presented in Table 3. For the conditions of the present experiment and the HU distribution used (Font-i-Furnols et al., 2014), there were significant SEX and TBW effects (P<0.001), however the only significant interaction was between the volumes of fat and lean. At the heaviest weight, IM and FE presented the same volume of fat and lean. Moreover, at the same weight, EM showed the most amount of volume of lean and CM the least one, while the opposite situation was found for the volume of fat. For bone the SEX effect revealed two clearly differentiated groups, with greater volumes (P<0.05) of bone in EM and IM compared to FE and CM.

Table 3. Volume of lean, fat and bone depending on the SEX and target body weight (TBW)*.

Volume (dm^3)	TBW	CM	FE	IM	EM	SEX	TBW	SEX*TBW
						P-value	P-value	P-value
Lean	30	21.48	20.92	21.66	22.6	<.0001	<.0001	<.0001
	70	43.503^{b}	44.72^{ab}	47.66^{a}	48.13^{a}			
	100	56.93^{c}	62.25^{b}	62.43^{ab}	65.71^{a}			
	120	65.73^{c}	71.41^{b}	69.43^{b}	75.98^{a}			
Fat	30	4.68	4.74	3.52	3.69	<.0001	<.0001	<.0001
	70	16.52^{a}	14.42^{ab}	11.75^{b}	12.49^{ab}			
	100	28.96^{a}	24.81^{ab}	23.65^{bc}	20.44^{c}			
	120	38.31^{a}	31.89^{b}	33.38^{b}	25.39^{c}			
Bone	30	2.36	4.55	5.85	6.72	<.0001	<.0001	0.467
	70	2.28	4.55	6.07	6.84			
	100	2.43	5.00	6.30	7.00			
	120	2.49	4.91	6.44	7.32			

* Means sharing a common character in their superscripts are not significantly different (P<0.05); CM = Castrated males, FE = Females, IM = Immunocastrated males and EM = Entire males; Lean = Volume of lean (dm^3) calculated using HU distribution between 1 and 150, Fat = Volume of fat (dm^3) calculated using HU distribution between -149 and 0, Bone = Volume of bone (dm^3) calculated using HU distribution between 151 and 1400.

The linear and area measurements obtained from the CT images are shown in Figure 2 for the different loin images and in Figure 3 for the ham and the shoulder. As expected, the TBW effect was significant (P<0.001) for all of the linear and area measurements (results not shown), and the SEX

effect was significant in some of them as well as the interaction SEX x TBW, indicating that the differences among the SEX are not constant at all the TBW values, but are TBW dependent.

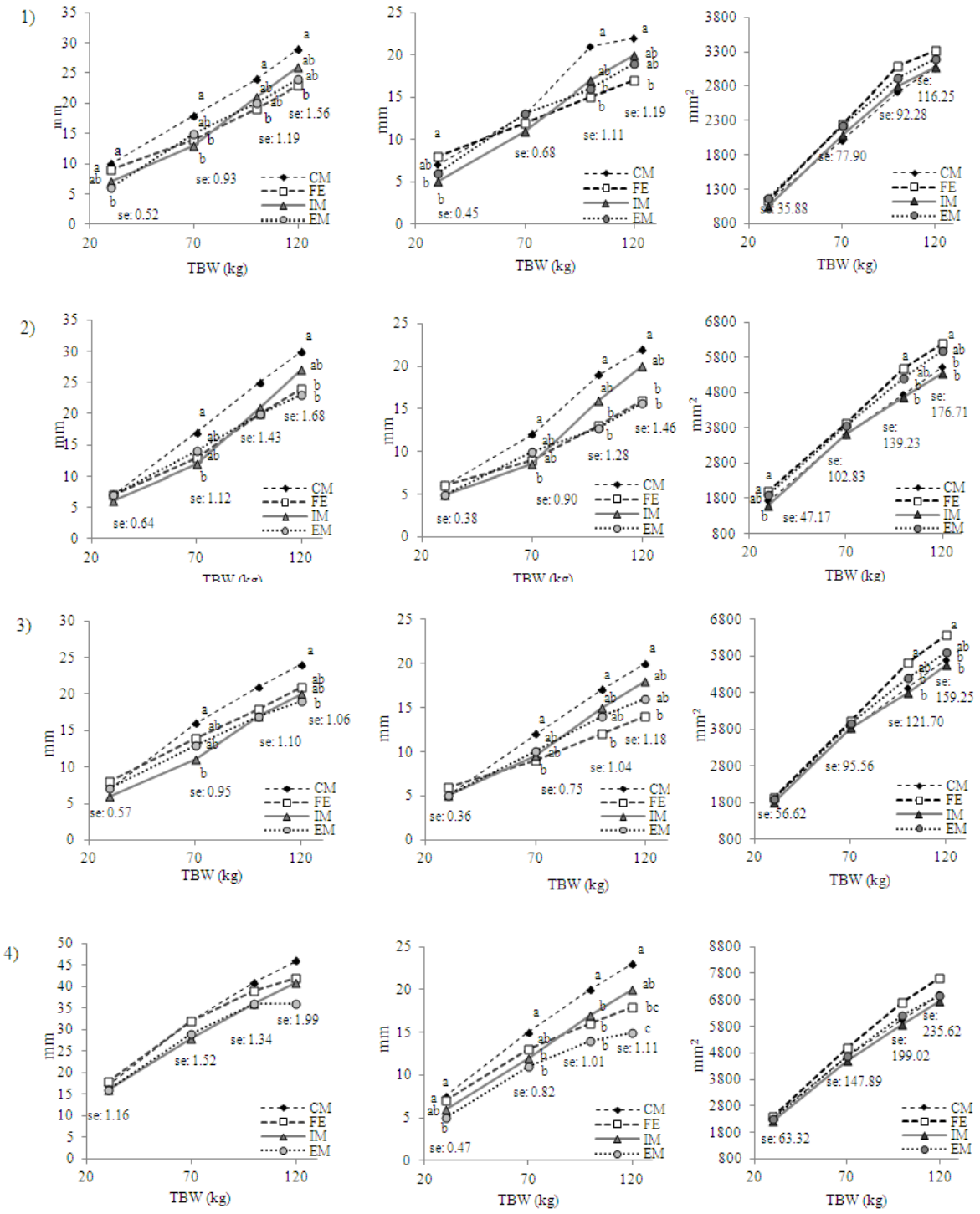

Figure 2. From left to right: vertical subcutaneous fat, lateral subcutaneous fat and area of the loin evaluated from CT images of the loin at the level (1) between 6th-7th, (2) between 11th-12th, (3) between 14th-15th and (4) between 3rd-4th lumbar vertebrae, depending on the SEX (CM: Castrated males, FE: Females, IM: Immunocastrated males and EM: Entire males) and target body weight (TBW). Different subscripts indicate significant differences (P<0.05) between SEX by TBW.

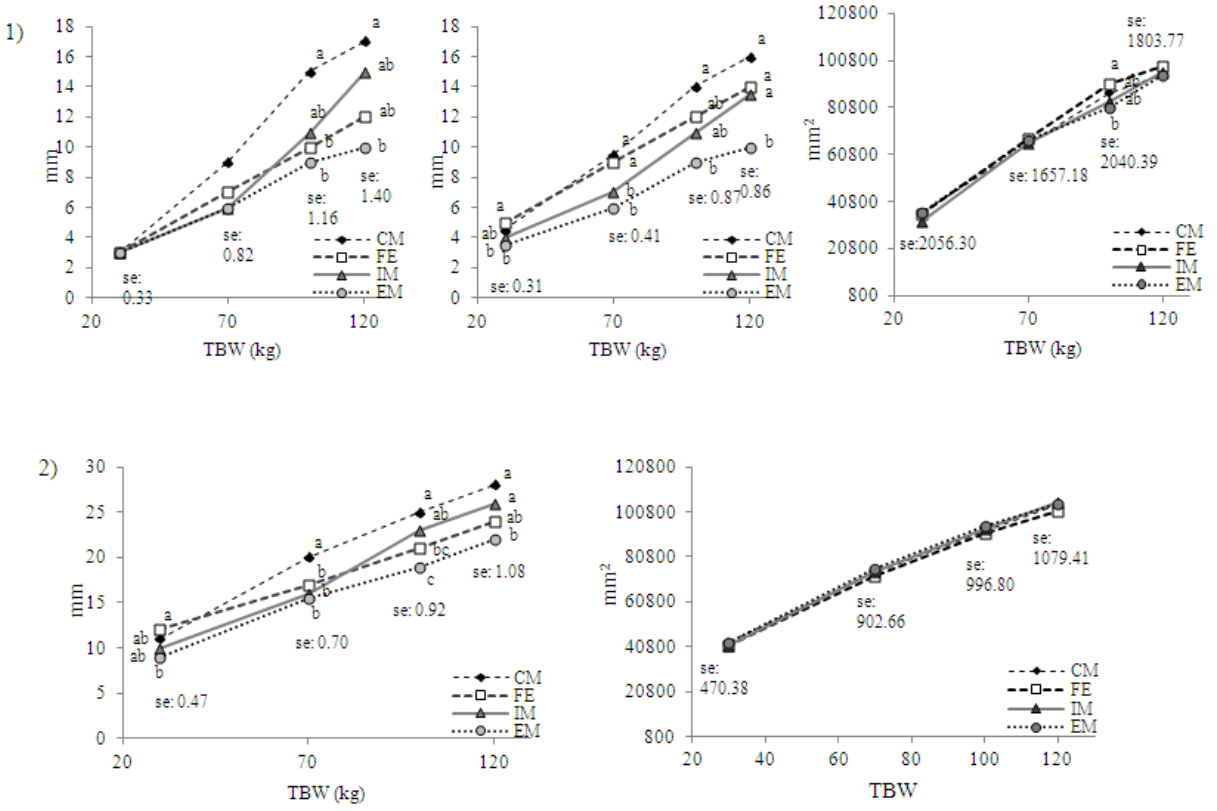

Figure 3. (1) From left to right: vertical subcutaneous fat, lateral subcutaneous fat and area of the ham and (2) vertical subcutaneous fat and area of the shoulder, evaluated from CT images and depending on the SEX (CM: Castrated males, FE: Females, IM: Immunocastrated males and EM: Entire males) and target body weight (TBW). Different subscripts within a row indicate significant differences (P<0.05) between SEX by TBW.

Loin. Significant (P<0.05) effects of SEX or its interaction with TBW existed for the majority of the variables analysed at the four anatomical parts of the loin. A significant SEX effect appeared at the 3rd-4th lumbar vertebrae (**LV**) for the vertical subcutaneous fat, where CM presented more fat than IM and EM, and FE were intermediate. However, at early weights (30 kg), vertical subcutaneous fat did not present significant differences at the 11th-12th, 14th-15th ribs, but this situation changed for the other points evaluated in the loin. Castrated males appeared to have thicker lateral and vertical subcutaneous fat all over the loin, compared to other SEX. At 70 kg, IM had not yet received the second immunocastration dose and they showed less fat than CM at the four locations of the loin, however, this situation varied at heavier weights (100 and 120 kg). For the lateral and vertical subcutaneous fat at the 6th-7th ribs, CM presented higher values (P<0.05) of fat than FE, with IM and EM being intermediate. A similar situation occurred for the lateral subcutaneous fat at the 14th-15th rib, however it changed at the 3rd-4th LV. At that point of the loin, at 100 kg TBW, CM had more lateral subcutaneous fat than FE, IM and EM but it evolved at 120 kg TBW. At the heaviest weight, CM showed more lateral subcutaneous fat than IM and EM. Females presented more fat than EM and the same amount as CM and IM, and the IM had the same behavior as the EM. Fàbrega *et al.,* (2010) reported that at final weights between 109 and 123 kg,

IM and CM presented more (P<0.05) subcutaneous fat than EM and FE. D'Souza and Mullan (2002) presented differences for the backfat at the P2 level (close to the 14^{th}-15^{th} rib), where IM > CM > FE (P<0.05). In the present study, CM were fatter (P<0.05) than EM at the last rib (14^{th}-15^{th}), while IM and FE were intermediate. The loin muscle area presented significant SEX x TBW interactions at the 11^{th}-12^{th} and 14^{th}-15^{th} ribs (P<0.05). In both cases, at 100 and 120 kg TBW, loin muscle areas were greatest (P<0.05) in FE than in CM and IM, and EM were intermediate (P>0.05). These results are in accordance with McLaren *et al. (1988)*, who compared the loin muscle area at the 10^{th} rib between gilts and barrows of the same genetic type. The loin muscle area at the 6^{th}-7^{th} ribs did not present significant SEX or SEX x TBW effects, however at the 3^{rd}-4^{th} LV FE had larger loin muscles than IM and CM and EM were intermediate.

Ham. Significant interactions between SEX and TBW effects were found for the area of the ham, as well as for its vertical and lateral subcutaneous fat (Figure 3). The lateral fat of the ham differed among SEX throughout the growth period, whereas differences for the area were visible only at 100 kg TBW. At 120 kg TBW, differences in ham area among sexes were not significant although the same tendency can be observed. At 30 kg, FE presented more lateral fat (P<0.05) than EM and IM, and CM were intermediate. At 70 kg, two differentiated groups were visible: CM and FE had more lateral fat than IM and EM (P<0.05). However, by 100 kg (after the second immunocastration dose), IM pigs increased lateral fat and presented thickness similar to CM and FE. At 120 kg, positions were clearly differentiated, with the lowest values (P<0.05) of lateral fat in EM compared with CM, FE and IM, which did not differ (P>0.05). At 120 kg, vertical subcutaneous fat presented less differentiation among SEX, with CM being fatter than EM (P<0.05) and FE and IM in between. This confirms and extends the findings of Latorre *et al.* (2003) that at 117 kg, CM presented higher amount (P<0.05) of subcutaneous fat than FE (19.5 *vs* 17.3 mm).
Shoulder. A significant SEX effect was found for the area of the shoulder, being greatest in EM and least in FE (Figure 3). A significant interaction between SEX and TBW was found for the vertical subcutaneous fat of the shoulder, which was greatest in CM and least in EM. Immunocastrated males also showed greater values (P<0.05) of subcutaneous fat than EM, but only at heavier weights (100 and 120 kg), probably due to the second vaccine.

Allometric growth

The allometric coefficients for the weights of the main pieces and the lean mass and fat content in relation to the live weight are represented in Table 4. Significant differences among SEX were found for the total amounts of fat and lean and for the fat and lean contents in the ham. The allometric growth coefficient (*b*) for total fat tissue was greater than 1, indicating a proportionately faster development of fat in relation to the live weight. Figure 4 illustrates total body fat deposition in relation to TBW, allowing visualisation of the more rapid deposition of fat in IM than in EM, probably due to the second vaccine (after 70 kg TBW). Castrated males were intermediate between IM and EM, as were EM between CM and FE (Table 4). A different situation was found for the deposition of the lean mass (Figure 5), with values close to unity, indicating a proportional growth rate similar to live weight. Lean tissue development was similar in FE and EM

(P>0.05), both faster than in CM and IM. It is also possible to see the change of tendency in IM curve after the second vaccine.

Table 4. Allometric growth of the main tissues* and cuts in relation to the live weight*.

Parameters (g)	a (g)					b				
	CM	FE	IM	EM	P-Value	CM	FE	IM	EM	P-Value
Fat	4.12^{b}	8.26^{a}	2.71^{b}	4.76^{b}	<.0001	1.63^{ab}	1.43^{c}	1.71^{a}	1.51^{bc}	<.0001
Lean	179.36^{a}	138.68^{b}	172.40^{a}	146.25^{b}	<.0001	1.00^{b}	1.07^{a}	1.02^{b}	1.07^{a}	<.0001
Ham										
Weight	76.98	69.68	75.66	71.43	0.600	1.05	1.08	1.06	1.08	0.607
Fat	1.11^{b}	1.95^{a}	0.73^{b}	1.08^{b}	<.0001	1.64^{ab}	1.47^{c}	1.71^{a}	1.56^{bc}	<.0001
Lean	59.56	46.26	48.56	47.73	0.043	1.04	1.11	1.13	1.11	0.061
Bone	20.32	18.35	20.37	18.89	0.435	0.78	0.81	0.78	0.80	0.372
Shoulder	59.68	56.59	58.74	55.99	0.843	0.99	1.02	1.00	1.01	0.368
Loin	13.02	12.03	9.04	11.58	0.247	1.40	1.42	1.47	1.42	0.351
Fat	2.61	1.96	1.15	1.92	0.763	2.05	1.62	2.13	1.88	0.241
Belly	16.78	19.04	16.76	18.07	0.089	1.19	1.17	1.19	1.17	0.100

*Defined in Table 2; **Different subscripts within a row and coefficients indicate significant differences (P<0.05); a = scaling exponent; b = allometric growth coefficient; CM = Castrated males, FE = Females, IM = Immunocastrated males and EM = Entire males

Although no significant differences among SEX were found for the allometric growth of the main cut weights, the values are worth noting. The ham and the shoulder weights presented similar results as the total lean, with *b*-coefficients close to unity, showing a parallel development of the cut/tissue with the live weight. By contrast, the loin cut presented higher values of the *b*-coefficient, more similar with the fat values, indicating faster and later development than the other cuts. The belly was intermediate, indicating that it grows faster than the ham and the shoulder and slower than the loin in relation to the live weight. The bones of the ham were the only tissue that presented *b*-coefficients lower than unity, indicating that this tissue grows earlier and slower than the others relative to live weight. These results are in accordance with Fisher *et al.,* (2003), who presented detailed results of the allometric coefficients (*a* and *b*) of fat (split into subcutaneous and intermuscular), skin, lean, bone and different cuts of swine.

Estimation of mature body weight and its relationship to the growth model

Parameters of growth functions calculated for the pigs of different SEX are shown in Table 5. Figure 6 presents the resulting growth curves for CM, FE, IM and EM.

Significant differences among SEX were found for the three parameters of the Gompertz function (*a, b* and *k*). Estimated mature weight (MBW, *a*) was greatest in IM, lowest in CM and FE, and intermediate in EM. However, Vincek *et al.,* (2012) estimated final weights of 233 kg for barrows and 180 kg for gilts, using a sigmoidal function. Literature values of the final live weights indicate

differences between breeds (Wellock *et al.*, 2004), sexual conditions and the prediction equations (Strathe *et al.,* 2009). Strathe *et al.* (2009) reported MBW of 406, 471 and 354 kg for barrows, boars, and gilts, respectively.

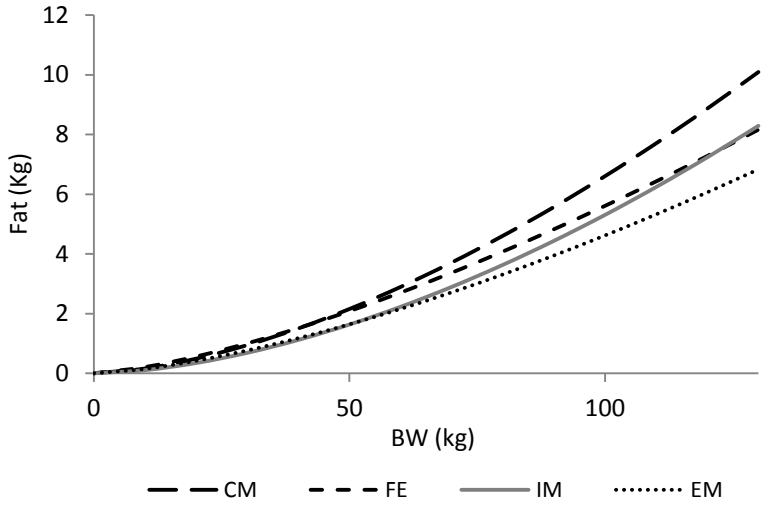

Figure 4. Allometric growth of the fat tissue of different sexes (CM: Castrated males, FE: Females, IM: Immunocastrated males and EM: Entire males) related to body weight (BW)

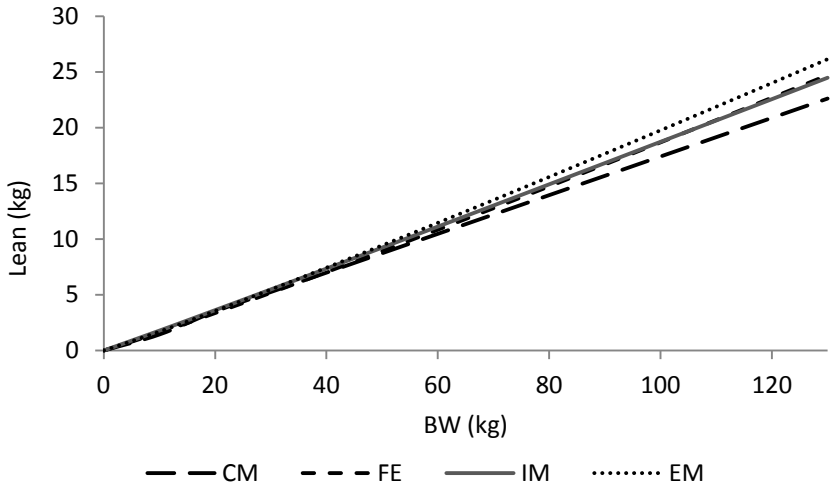

Figure 5. Allometric growth of the lean tissue of different sexes (CM: Castrated males, FE: Females, IM: Immunocastrated males and EM: Entire males) related to body weight (BW)

These estimates are much larger than the present results and the ones previously reported by Knap (2000), which was partly due to the duration of the experimental period. Strathe *et al.* (2009) caution that when growth data below 200 kg BW are analyzed by sigmoid growth functions, asymptotic values are unreliable. To our knowledge, the final weight (biological

maximum) of IM have not been reported, therefore we attempted to estimate this parameter. In this study, the Gompertz curve fit the data very well from 0 to 150 days for all SEX (Figure 6) but seemed to overestimate live weights after that point, especially for IM. One mathematical reason that could explain these results is the lack of observed weights above 120 kg, thus the earlier points of the curve acquire more importance for the fitting of the Gompertz curve. Real weights after 120 kg (170 days approximately) showed a low decrease of the slope and the very initial part of the asymptote for the EM, FE and CM, but this change was not visible for the IM. Furthermore, for the EM, FE and CM, this small decrease of the slope was shown by only two points of the graph (Figure 6.1). Therefore, it was impossible to determine the mature weight from these data with any degree of confidence.

Table 5. Parameters of the Gompertz function of the four sexes studied*

SEX	a	P-Value	b	P-Value	k	P-Value
CM	219.15^{b}		5.04^{a}		0.013^{a}	
FE	215.66^{b}	0.001	4.64^{b}	0.010	0.012^{ab}	0.001
IM	302.96^{a}		4.86^{ab}		0.010^{b}	
EM	247.07^{ab}		4.83^{ab}		0.011^{b}	

*Different subscripts within a column indicate significant differences (P<0.05); a = an asymptote with the biological meaning of the mature body weight, *b* sets the displacement along the *x* axis, *k* sets the growth rate (*y* scaling); CM = Castrated males, FE = Females, IM = Immunocastrated males and EM = Entire males

With regard to growth rate (*k* coefficient), CM had more rapid weight gain (P<0.05) than EM and IM over the entire growth period. However, IM presented a significant gradual increase of the slope after 130 days (80 kg approximately) (Figure 6.2). This change is more noticeable at 150 days (100 kg approximately), the moment that the IM reaches the FE growth rate. The second immunocastration vaccine was injected at 18 weeks (126 days); the growth rates for EM and IM were very similar from 0 to 130 days, and then the slopes diverged. These results suggest that the full effects of immunocastration are obtained only after the second injection of the vaccine. Jaros *et al.* (2005) suggested that the effect of the immunocastration is visible after the second injection and before reaching that point IM have the same behaviour as EM. As suggested by previous studies, pigs vaccinated with Improvac® may be regarded as entire males until the second vaccination (Dunshea *et al.*, 2001) which is consistent with results of the present study.

Allometric growth of fat and lean in the whole body and in the ham were significantly different among SEX. A statistical model, including the SEX and %MBW effect, was applied to determine if the allometric differences could be explained by differences in estimated MBW. However, significant SEX effects (P<0.05; results not shown) remained after MBW correction, indicating that the differences in allometric growth were not due to differences in MBW. Because the MBW estimates were suspect, we cannot draw firm conclusions regarding the role of MBW in allometric growth differences among SEX.

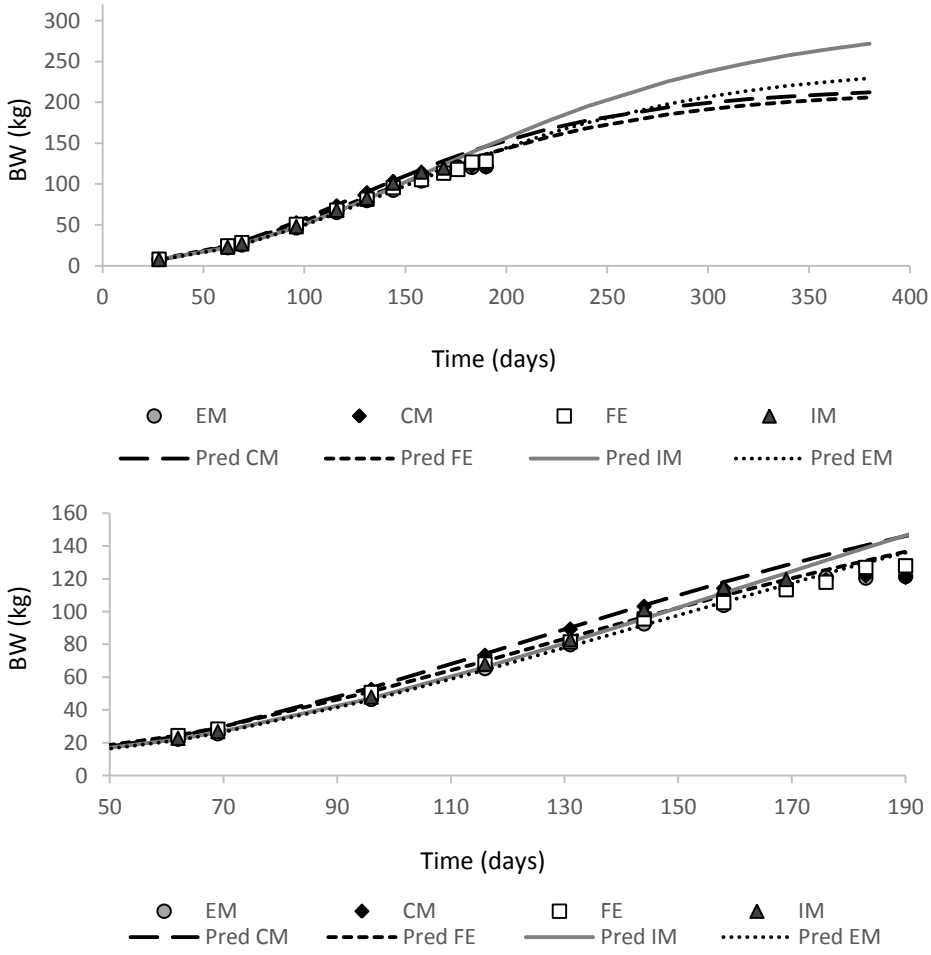

Figure 6. (1) Comparison of the body growth of different sexes (CM: Castrated males, FE: Females, IM: Immunocastrated males and EM: Entire males) by the Gompertz function from 0 to 350 kg and (2) from 50 to 190 kg.

General discussion

Improving production system efficiency in the swine industry requires knowledge of the growth performance and development of the main cuts and tissues of all animal categories. For swine, three main sexual conditions (FE, EM and CM) have been considered in the past. In some countries the use of IM is now becoming very common, thus necessitating studies of IM growth and body composition in relation to the other SEX. Results from this study reveal that there are significant phenotypic differences in the growth of fat and lean among SEX, with CM being fattest and EM being leanest. These differences were not related to estimated MBW, however MBW may have been overestimated, especially for IM. The predicted MBW for IM was also conditioned by the fact that this group of animals presented two clear behaviours, being similar to EM from birth to the second injection of the vaccine (average of 80 kg) and more comparable to CM from that point to the final weight. This change of conduct was reflected in an increase of the slope of the

Gompertz curve, resulting in higher values for MBW. Resolution of these differences will require analysis of growth curves with data at heavier weights, and could potentially yield valuable biological insights into growth of swine of different sexual conditions.

Conclusions

In general, we conclude that fat deposition was proportionately most rapid in IM and CM and least rapid in EM and FE, and lean deposition behaved inversely. Thus, IM and CM have a very similar performance regarding the speed of deposition of lean and fat, although IM behave as EM until the second vaccine administration. Nutrition companies segment pig growth into several (3, 4 or 5) periods and diets, but generally do not differentiate diets among sexual conditions. According to the results of this study, diets specific to the growth period and also sexual condition could improve growth and efficiency and minimize residues and cost of feeding. Furthermore, the use of non-invasive techniques, such as CT, can be useful for the livestock and meat industry because growth and carcass parameters can be studied *in vivo* without costly and laborious slaughter and dissection. However, more research at heavier weights is needed to accurately determine MBW and its relationship to allometric growth of cuts and tissues.

Acknowledgements

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Suplementary material

Suplementary Table 1. Least-square means of the carcass and cuts composition, depending on the sexual condition (SEX) and the target body weight (TBW).

Parameters (g)	30 kg					70 kg					100 kg					120 kg					P-Value	
	CM	EM	FE	IM	se	CM	EM	FE	IM	se	CM	EM	FE	IM	se	CM	EM	FE	IM	se	SEX	SEXxTBW
Carcass																						
4cuts	7,17	7,21	7,12	6,96	0,11	18,27	18,46	18,30	18,14	0,16	26,15	26,55	27,02	26,47	0,21	31,64	31,58	32,29	31,44	0,23	0.018	0.059
Lean5p	5,50^{ab}	5,77^{a}	5,40^{b}	5,53^{ab}	0,09	13,14^{b}	14,31^{a}	13,56^{b}	14,22^{b}	0,16	17,67^{c}	20,14^{a}	19,35^{b}	19,52^{b}	0,20	20,60^{c}	23,60^{a}	22,44^{b}	21,61^{bc}	0,28	<.0001	<.0001
Fat4p	1,03^{a}	0,84^{b}	1,08^{a}	0,77^{b}	0,04	3,75^{a}	2,87^{b}	3,36^{a}	2,67^{b}	0,10	6,64^{a}	4,72^{c}	5,77^{b}	5,41^{bc}	0,19	8,84^{a}	5,89^{c}	7,45^{b}	7,70^{b}	0,26	<.0001	<.0001
Ham																						
Weight	2,90^{ab}	2,99^{a}	2,86^{b}	2,88^{ab}	0,04	7,07^{b}	7,39^{a}	7,12^{b}	7,27^{ab}	0,06	9,87^{b}	10,52^{a}	10,34^{a}	10,31^{a}	0,08	11,74^{c}	12,42^{a}	12,21^{ab}	11,96^{bc}	0,09	<.0001	<.0001
Lean	2,09	2,15	2,03	1,96	0,06	5,11^{b}	5,55^{a}	5,31^{ab}	5,41^{ab}	0,08	7,01^{b}	7,84^{a}	7,69^{a}	7,58^{a}	0,10	8,11^{c}	9,20^{a}	8,93^{ab}	8,48^{bc}	0,12	<.0001	<.0001
Fat	0,28^{a}	0,24^{b}	0,29^{a}	0,22^{b}	0,01	1,10^{a}	0,91^{c}	1,00^{b}	0,88^{c}	0,02	1,87^{a}	1,42^{c}	1,65^{b}	1,63^{b}	0,04	2,42^{a}	1,79^{c}	2,10^{b}	2,18^{ab}	0,06	<.0001	<.0001
Bone	0,30	0,30	0,30	0,30	0,01	0,58	0,60	0,59	0,59	0,01	0,74	0,78	0,77	0,76	0,01	0,85	0,86	0,86	0,86	0,01	0,495	0,521
Loin																						
Weight	1,43	1,41	1,42	1,25	0,06	4,94	4,92	4,93	4,72	0,06	7,41	7,42	7,58	7,35	0,08	9,07	8,95	9,13	8,85	0,11	0,031	0,812
Fat	0,32	0,30	0,35	0,21	0,05	1,44^{a}	1,31^{ab}	1,25^{ab}	1,10^{b}	0,06	2,57^{a}	2,13^{b}	2,24^{b}	2,16^{b}	0,08	3,20^{a}	2,61^{b}	2,82^{ab}	2,85^{ab}	0,11	0,004	0,002
Shoulder	1,84	1,86	1,81	1,80	0,04	4,22	4,35	4,23	4,29	0,04	5,83	6,08	6,05	5,99	0,06	6,96	7,13	7,15	6,98	0,07	0,029	0,066
Belly	1,05^{ab}	1,05^{ab}	1,07^{a}	0,99^{b}	0,02	2,80^{ab}	2,77^{ab}	2,84^{a}	2,73^{b}	0,03	4,13^{ab}	4,07^{ab}	4,24^{a}	4,05^{b}	0,04	5,01^{a}	4,77^{b}	5,06^{a}	4,89^{ab}	0,05	<.0001	0,006

$^{+}$Different superscripts within a row and weight group indicate significant differences (P<0.05). The TBW effect was significant (P<0.001) for all of the parameters; se = standard error; LA = Landrace x Large White, PI = Pietrain x (Landrace x Large White) and DU = Duroc x (Landrace x Large White); Lean%=0.89 x [lean of (ham, loin, belly and shoulder and tenderloin)/weight of (ham loin belly shoulder and tenderloin)] x100; Lean5p: lean of ham, shoulder, loin, belly and tenderloin; Fat4p and Bone4p: fat and bone of ham, shoulder, loin and belly.

Chapter 8

Results V

The content of this chapter is submitted in the Agriculture Systems journal

Keys to select a prediction model for carcass composition from computed tomography images

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This chapter deals with:

- Comparison of prediction equations

Highlights

- Individual and global prediction equations have advantages and disadvantages.
- Error decomposition allows determining the random error and the goodness of fit.
- Individual prediction equations were more precise but more specific and less global.

Abstract

Linear, nonlinear and volume measurements obtained from computed tomography (CT) images of live pigs are good predictors of carcass characteristics. There are different ways to analyse the goodness of a prediction equation, including the decomposition of the predicted error and the biases and coefficient of determination. The present paper compares the goodness of fit of individual prediction equations within three different genotypes and the prediction obtained by a global equation for the different genotypes at the same time. Comparison is performed by means of the error decomposition, the standard deviation of the bias and the coefficient of model determination. The results showed a good mean square prediction error and a high error due to disturbances (random effects) for most of the predictions; however, the prediction of lean obtained by the global equation and applied to the specific genotypes presented a low error due to disturbances and a high error due to central tendency. Different results are obtained when comparing individual and global equations for the estimation of lean without the distinction of the genotype predicted. In general, the comparison shows that both equations are properly developed and useful; however, the utility is not the same for both of them.

Keywords: error decomposition, coefficient of model determination, computed tomography, pigs, body composition

1. Introduction

Mathematical prediction models are used to explain the behaviour of natural processes. They are useful for researchers, industries and policy makers to explain knowledge or discoveries acquired in scientific trials and/or to challenge old dogmas (Tedeschi, 2006). They are commonly used in livestock animals to assist companies in making decisions; thus, model usefulness must be assessed by its sustainability for a particular purpose. This means that adequate statistical analysis

is an indispensable step during the development, evaluation, and revision phases of a model. The swine and pork industry have used prediction models over the years to assess the growing rate of the animals (Kusec et al., 2007; Schinckel et al., 2008), as well as the mortality (Arango et al., 2006), prolificity (Pomar and Pomar, 2005), behaviour (Labroue et al., 1997), tissue development and deposition (Carabús et al., 2014) and carcass composition (Engel et al., 2012; Font i Furnols and Gispert, 2009; Forrest et al., 1989). When talking about livestock animals, there are different types of prediction models, such as linear regression, allometric, and quadratic (Font-i-Furnols et al., 2015), and a model's goodness depends on a mixture of different factors: R^2, coefficient of variation, root mean square error and, mainly, its utility. Moreover, there are a huge variety of predictors for several characteristics of live pigs. In swine, for example, predictors can be obtained for live animals on the farm by observing the animals or measuring them with devices, such as vision systems or ultrasounds (Doeschl-Wilson et al., 2005), in the laboratory using samples obtained *in vivo* during growth (Bosch et al., 2009) or, recently, using images obtained with the use of new technologies or devices, such as dual X-ray absorptiometry, magnetic resonance imaging (Kremer et al., 2013; Mitchell et al., 2002) and computed tomography (CT) (Kongsro, 2013; Carabús et al., 2014; 2015).

The aim of this paper was to compare and discuss the goodness of fit by genotype (GEN) and globally (all GEN together) of two methodologies for predicting the carcass composition of live pigs: (1) individual equations developed for each GEN obtained by Font-i-Furnols et al. (2015) and (2) global equations developed for the three GEN together obtained by Carabús et al. (2015). The prediction equations were obtained using the measurements of the pig body obtained from CT image analysis as predictors and the weight of the carcass pieces and tissues obtained by manual dissection as the reference values (observed or "true" values).

2. Material and methods

The present paper makes a comparison between the prediction equations obtained by Font-i-Furnols et al. (2015) and Carabús et al. (2015) using data from the same animals.

2.1. Animals and computed tomography scanning

In brief, the study included 90 gilts of 3 different GEN, 30 (Duroc x (Landrace x Large White)) (DU), 30 (Pietrain x (Landrace x Large White)) (PI) and 30 (Landrace x Large White) (LA), with no parental relation within the breeds Landrace and Large White from different companies. The entire bodies of the animals were CT scanned with a General Electric HiSpeed Zx/I tomographer at different target body weights (TBW): 30, 70, 100 and 120 kg. A total of 15 animals (five for each GEN) were scanned at 30, 70 and 100 kg and 45 animals (15 for each gen) were scanned at 120 kg. The instrumental settings of the CT were: 140 kV, 145 mA, matrix dimensions of 512x512, axial, 7 mm thick (30 kg TBW) and 10 mm thick (70, 100 and 120 kg TBW). A custom-built cradle (PVC, Ø 0.30 m, length of 1.2 m for the 30 kg pigs and Ø 0.46 m, length of 1.8 m for the 70, 100 and 120 kg pigs) was used to hold the pigs during scanning. Pigs had free access to water and were fastened

for a minimum of 8 h before weighing and scanning. Pigs were sedated to minimize disturbances in the CT images due to movement.

2.2. Dissections

After scanning, animals were slaughtered. The left half carcasses were kept refrigerated at 2ºC for 24 to 48 h until dissected. Each carcass was prepared and cut following the European Union reference method (Walstra and Merkus, 1995). Thereafter, four primal cuts plus tenderloin were weighed and manually dissected. Lean, subcutaneous fat, including the skin, intermuscular fat, and bone of most of the cuts were separated with a knife by trained technicians, and the weights of all of these tissues were recorded to obtain the total amount of different fat, lean and bone in the primal cuts, considering all of the tenderloin weight as lean. Only dissected carcasses were used for the development of prediction equations.

2.4. Computed tomography image analysis

The distribution of density volume based on the Hounsfield scale (in Hounsfield units [**HU**]) was obtained from CT images using the VisualPork software package, which was developed for that purpose by the University of Girona and the IRTA (Bardera et al., 2012; Boada et al., 2009). The partial volumes estimated between −149 and −1, between 0 and 140, and between 141 and 1,400 HU were associated with fat, muscle and bone volume, respectively, and were used as independent variables in the regression analysis. Volumes between −1,000 and −150 HU, which belong mainly to the less dense parts of the viscera, were considered only in calculating the total volume. Moreover, CT phenotypic measurements (thickness, lengths and areas) were manually obtained in a reduced set of images as detailed in Font-i-Furnols et al. (2015) and Carabús et al. (2015).

2.5. Variables of interest to be predicted

Equations, using CT predictors, were derived to predict the total amounts of fat (subcutaneous and intermuscular fat of the four primal cuts) and lean (lean of the four primal cuts + tenderloin), as well as the shoulder weight, the loin and its subcutaneous fat weights, the belly weight and the ham and its fat, lean and bone weights.

2.6. Prediction equations

The prediction equations were carried out following two different approaches:

One approach included an individual equation for each GEN and was developed by Font-i-Furnols et al. (2015). Four types of regressions equations for the same parameter estimation were obtained: (1) linear regressions using CT volumes or CT ratios of volumes as predictors, (2) quadratic regressions using the previous CT volumes or CT ratios of volumes and their squared value as predictors, (3) allometric equations ($y = ax^b$ linearized as $\log y = \log a + b \cdot \log x$), in which CT predictors were chosen as for the previous regression models and (4) linear regression using CT volumes, CT ratios of volumes and direct physical measurements recorded on loin and ham

images as predictors. Predictors were selected using the stepwise procedure of SAS (selected criteria: P <0.15) and subjective criteria maximizing the coefficient of determination (R^2) and minimizing root mean square error (RMSE). The criterion to choose the best prediction equation of this methodology was the lowest CV_p (100 × (RMSE of prediction by cross-validation /mean)). The selected prediction equation was the one used in the present work.

Carabús et al. (2015) presented the same equation for the three GEN to apply the equation on animals of different GEN and to a set of animals of different SEX (results not analysed in the present paper). For that, it was necessary to establish a criterion based on the accuracy and the decomposition of the mean square predicted error (MSPE). The accuracy and precision of each equation were evaluated by R^2 and the Root Mean Square Error (RMSE). Moreover, to investigate the lack of fit of the equations for both datasets, without the distinction of GEN or SEX, the MSEP was decomposed and compared. Ideally, most of the error should reside in the random component of MSEP (Tedeschi, 2006). If the proportion of random error for any of the groups was lower than 0.70, another regression was performed using different predictors. Furthermore, when necessary to standardize the variance, the dependent and independent variables were transformed into natural logarithms.

2.7. Statistical analysis

The criteria selected to compare both models for each parameter predicted were found by decomposing the error into (1) error due to central tendency (ECT), (2) error due to regression (ER) and (3) error due to disturbances or random effects (ED) (Gispert et al 2000, Tedeschi 2006). ECT indicates how the average of the predicted values deviates from the observed values average, ER measures the deviation of the regression coefficient of the slope from one and ED is the unexplained variance due to random effects or disturbances. A good prediction is expected to have a high ED error, considering that ECT and ER errors can be eliminated by linear corrections of the predictions (Theil, 1961). The decomposition was carried out as follows:

$$\text{MSE= ECT + ET + ED}$$

$$ECT = (\bar{\hat{Y}} - \bar{Y})^2$$

$$ER = (S_P - r \times S_O)^2$$

$$ED = (1 - r^2) \times S_O^2$$

where $\bar{\hat{Y}}$ is the mean of the predicted values, $\bar{Y}$ the mean of the observed values, S_P the standard deviation of the predicted values, S_O the standard deviation of the observed values, and r the coefficient of correlation between the predicted and observed values. ECT, ER and ED are expressed in proportion, thus their sum is one.

The decomposition of the prediction errors obtained using the equations developed by Font-i-Furnols et al. (2015) and Carabús et al. (2015) were analysed by first considering the prediction and observed values of all of the GEN at the same time globally and then considering them by

each GEN individually. The bias between the dissection and the predictions of Font-i-Furnols et al. (2015) and Carabus et al. (2015) was analysed, and the standard deviation was obtained as a measure of imprecision, also considering both all three GEN together and each GEN separately. Moreover, the coefficient of model determination (CD), which is the ratio of the total variance of the observed data to the square of the difference between the predicted and the mean of the observed data, was calculated for both predictions using the data of the three GEN together and for each GEN separately. It is calculated as follows (Tedeschi, 2006):

$$CD = \frac{\sum_{i=1}^{n}(Y_i - \bar{Y})^2}{\sum_{i=1}^{n}\left(\hat{Y}_i - \bar{Y}\right)^2}$$

where Y_i is the observed *i*th value, $\bar{Y}$ is the mean of the observed values and $\hat{Y}_i$ is the predicted *i*th value. The CD statistic represents the proportion of the total variance of the observed values explained by the predicted values (Loague and Green, 1991).

Results and discussion

The decomposition of the error in both methodologies, when predictions of all of the animals (three GEN) were considered together, is presented in Table 1. Both methodologies showed high ED (> 95% in all of the cases), indicating that the prediction is correct. All of the estimated parameters presented a similar MSPE between both equations and also a high proportion of random error; however, the global equations developed by Carabús et al. 2015 did present better results for the ED, exhibiting values higher than >0.99 in 10 of the 11 predicted parameters. Only the estimation of the weight of the four main cuts was lower.

This high ED is most likely because this was the criterion for selecting the prediction equation in that paper. This means that these equations are useful for the entire population of DU, LA and PI studied in Carabús et al. (2015) and Font-i-Furnols et al. (2015). Moreover, the genotypes used are the typical ones used for commercial conditions in Spain, thus these equations could also be useful for a large number of animals. The coefficient of model determination and the standard deviation of the bias for both approaches when all of the GEN were considered together are presented in Table 2. The highest imprecision (standard deviation of the bias) was for the weight of the four main cuts in both approaches. The CD values close to one indicate a good prediction, while CD values lower than 1 indicate overprediction of the model and CD values higher than 1 indicate underprediction of the model.

Table 1: Decomposition of the mean square prediction error (MSPE) considering all the genotypes together in error due to central tendency (ECT), error due to regression (ER) and error due to disturbances (ED) depending on the prediction approach.

Estimated parameter (kg)	Individual equations approach				Global equation approach			
	Font-i-Furnols *et al*. (2015)				Carabús *et al.* (2015)			
	MSPE	ECT	ER	ED	MSPE	ECT	ER	ED
Lean[a]	0.382	0.000	0.001	0.999	0.410	0.000	0.001	0.999
Fat[b]	0.148	0.002	0.017	0.981	0.156	0.000	0.001	0.999
4 cuts[c]	1.077	0.000	0.001	0.999	1.204	0.024	0.018	0.958
Ham	0.138	0.000	0.003	0.997	0.147	0.000	0.00	1.000
Ham fat	0.027	0.007	0.029	0.964	0.024	0.000	0.00	1.000
Ham lean	0.095	0.018	0.013	0.969	0.110	0.000	0.00	1.000
Ham bone	0.001	0.007	0.012	0.981	0.0005	0.0004	0.0005	0.999
Loin	0.083	0.000	0.002	0.998	0.089	0.000	0.000	1.000
Loin fat	0.031	0.012	0.011	0.978	0.028	0.000	0.001	0.999
Shoulder	0.043	0.000	0.001	0.999	0.046	0.000	0.000	1.000
Belly	0.032	0.001	0.012	0.987	0.034	0.000	0.003	0.997

[a] Lean of the ham, loin, belly, shoulder and tenderloin; [b] Fat of the ham, loin, belly and shoulder; [c] ham, loin, belly and shoulder

Table 2: Coefficient of model determination (CD) and standard deviation of the bias (SDBias) of the prediction approaches considering all of the genotypes together.

Estimated parameter (kg)	Individual equations approach		Global equation approach	
	Font-i-Furnols *et al*. (2015)		Carabús *et al*. (2015)	
	CD	SDBias	CD	SDBias
Lean[a]	1.00	0.37	1.01	0.48
Fat[b]	0.99	0.25	1.01	0.29
4 cuts[c]	1.01	0.66	0.98	0.62
Ham	1.00	0.37	1.01	0.38
Ham fat	0.97	0.15	1.02	0.16
Ham lean	1.05	0.31	1.02	0.33
Ham bone	1.05	0.03	1.01	0.02
Loin	1.02	0.27	1.01	0.25
Loin fat	0.99	0.19	1.03	0.20
Shoulder	1.02	0.27	1.01	0.19
Belly	1.04	0.26	1.02	0.26

[a] Lean of the ham, loin, belly, shoulder and tenderloin; [b] Fat of the ham, loin, belly and shoulder; [c] ham, loin, belly and shoulder

The individual equation approach (Font-i-Furnols *et al.,* 2015) presents almost all of the CD values as close to 1. Only the ham lean and bone were slightly underpredicted (5%), and, for the rest of the parameters, the over- or underprediction was less than 5%. Regarding the global equation approach (Carabús et al., 2015), it generally yields CD values close to one and always with a variation lower than 5%. This can be related with the fact that this approach was carried out considering all of the GEN together.

The comparison of the errors using individual equations within GEN is presented in Table 3. In general, both methodologies presented high ED, which means that the prediction is correct, and, as expected, equations from Font-i-Furnols et al. (2015) developed individually for each specific GEN showed higher levels of accuracy when comparing both predictions within GEN. Table 3 shows the estimated parameters and the distribution of the predicted errors by each approach within GEN. The individual equations approach of Font-i-Furnols et al. (2015), which developed one individual equation for each GEN, generally showed better results (lower MSPE and higher ED) than the global equation approach of Carabús et al. (2015), which developed a global equation for all of the GEN together and for pigs of a different genotype and different sexes. This makes sense because different equations for each GEN would allow a better adjustment within genotype than more general equations. However, as in the prediction of the fat, good results are obtained from both predictions. It is important to notice that the number and type of animals used to obtain these predictions were not the same in both cases. Individual equations within GEN were obtained from a reduced number of animals, which were the animals of each GEN that were CT scanned, slaughtered and dissected, while global equations had more than three times as many reference samples because there were the animals from the three GEN together plus some additional animals from another GEN and different sexes. Nevertheless, although the global approach (Carabús et al. 2015) yielded predictions more useful for a larger population than the individual ones (Font-i-Furnols et al., 2015), sometimes they are also less accurate.

One of the worst results from the global equation approach was found in the prediction of the total lean. When decomposing the error of the estimated lean for the individual equations approach within GEN, it can be observed that the MSPE is lower than 0.200 kg and that the ED is higher than 95%, but the same decomposition of the error by GEN for the global equation approach within GEN does show different results. The error for DU and PI presented a low ED and a high ECT. Figure 1a and Figure 1b present the visual decomposition of the error for the individual and global equations within GEN, respectively. Figure 1a shows no difference between the lines and no tendency in the biases. Figure 1b shows the higher ECT in the DU and PI lines. In this case, for PI pigs, there is an underestimation at all levels of the ham's lean, although it is higher at higher levels.

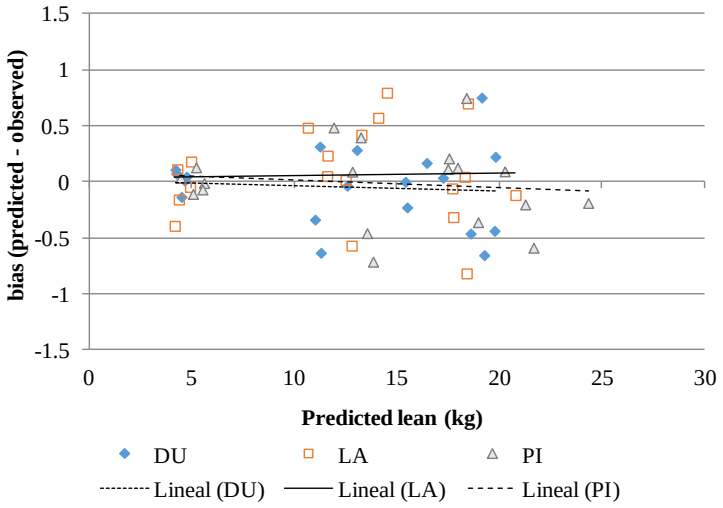
Table 3: Decomposition of the mean square prediction error (MSPE) considering the genotypes (DU=Duroc x (Landrace x Large White); LA= Landrace x Large White; PI = PI x (Landrace x Large White)) separately and together in error due to central tendency (ECT), error due to regression (ER) and error due to disturbances (ED) depending on the prediction approach.

Estimated parameter (kg)		Individual equations approach Font-i-Furnols *et al.*(2015)				Global equation approach Carabús *et al.* (2015)			
	GEN	MSPE	ECT	ER	ED	MSPE	ECT	ER	ED
Lean[a]	DU	0.125	0.018	0.001	0.981	0.173	0.296	0.132	0.572
	LA	0.181	0.020	0.009	0.971	0.224	0.087	0.002	0.911
	PI	0.132	0.002	0.004	0.994	0.313	0.428	0.034	0.538
Fat[b]	DU	0.078	0.024	0.028	0.948	0.089	0.026	0.048	0.926
	LA	0.051	0.004	0.012	0.984	0.082	0.008	0.027	0.966
	PI	0.071	0.010	0.046	0.945	0.087	0.064	0.011	0.925
4 cuts[c]	DU	0.122	0.005	0.003	0.992	0.052	0.009	0.020	0.972
	LA	0.886	0.002	0.004	0.993	0.111	0.004	0.009	0.987
	PI	0.366	0.013	0.011	0.975	1.099	0.237	0.094	0.669
Ham	DU	0.064	0.018	0.002	0.979	0.180	0.402	0.195	0.403
	LA	0.061	0.009	0.012	0.979	0.114	0.000	0.140	0.859
	PI	0.075	0.048	0.036	0.916	0.174	0.423	0.016	0.561
Ham fat	DU	0.014	0.000	0.001	0.999	0.021	0.053	0.029	0.918
	LA	0.011	0.0003	0.005	0.995	0.027	0.037	0.078	0.884
	PI	0.042	0.046	0.159	0.795	0.028	0.0001	0.038	0.962
Ham lean	DU	0.046	0.007	0.010	0.983	0.060	0.014	0.187	0.799
	LA	0.069	0.006	0.0003	0.994	0.088	0.125	0.011	0.864
	PI	0.180	0.041	0.022	0.937	0.190	0.094	0.006	0.900
Ham bone	DU	0.000	0.006	0.003	0.991	0.0004	0.058	0.003	0.940
	LA	0.001	0.016	0.036	0.948	0.001	0.006	0.046	0.948
	PI	0.001	0.003	0.006	0.991	0.001	0.103	0.023	0.874
Loin	DU	0.101	0.0002	0.001	0.999	0.088	0.011	0.064	0.925
	LA	0.077	0.00002	0.0065	0.993	0.063	0.102	0.003	0.895
	PI	0.056	0.001	0.001	0.998	0.045	0.056	0.086	0.858
Loin fat	DU	0.025	0.002	0.0002	0.998	0.056	0.002	0.055	0.943
	LA	0.023	0.000	0.012	0.988	0.020	0.029	0.022	0.949
	PI	0.069	0.037	0.133	0.830	0.054	0.023	0.140	0.837
Shoulder	DU	0.035	0.004	0.0002	0.996	0.024	0.065	0.004	0.931
	LA	0.152	0.000	0.000	1.000	0.045	0.054	0.0002	0.946
	PI	0.044	0.0003	0.0002	0.999	0.048	0.002	0.003	0.995
Belly	DU	0.041	0.0002	0.0001	1.000	0.044	3.10^{-5}	0.003	0.997
	LA	0.097	0.003	0.006	0.991	0.078	0.011	0.0001	0.989
	PI	0.076	0.000	0.000	1.000	0.088	0.009	0.001	0.990

[a] Lean of the ham, loin, belly, shoulder and tenderloin; [b] Fat of the ham, loin, belly and shoulder; [c] ham, loin, belly and shoulder

In DU pigs, there is an overestimation at higher lean content, also indicating the high ER. In the case of LA, the decomposition shows high ED and a slightly high ECT, which can be seen in the plot, because the regression line is slightly superior to the zero line (slight overestimation). A similar situation occurred with the weight of the ham. It presented a very low MSPE for the individual equations approach and a good distribution of the errors (Table 3 and Figure 2a). However, the decomposition of the errors for the global equation approach was worse, mainly for the DU and PI lines (Table 3 and Figure 2a). They presented low values for ED (<0.60), high values for ECT (>0.40) and DU and medium values for ER (>0.19). LA also presented an ER of 0.14. Thus, in this case, for PI pigs, there is an underestimation at all levels of the ham's lean (high ECT). In DU pigs, there is an overestimation only at higher lean content, indicating the high ECT and also the high ER. The high ER obtained for LA pigs can also be seen in the plot because there is an overestimation at lower lean content and an underestimation at higher lean content. In this case, the ECT is low because the positive and negative biases are compensated.

(a)



(b)

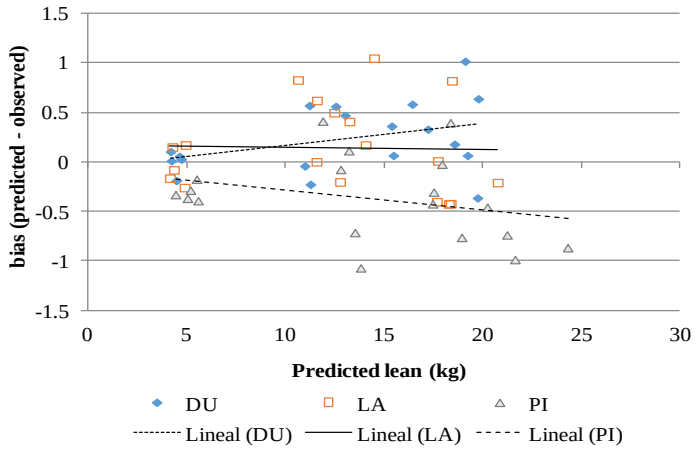
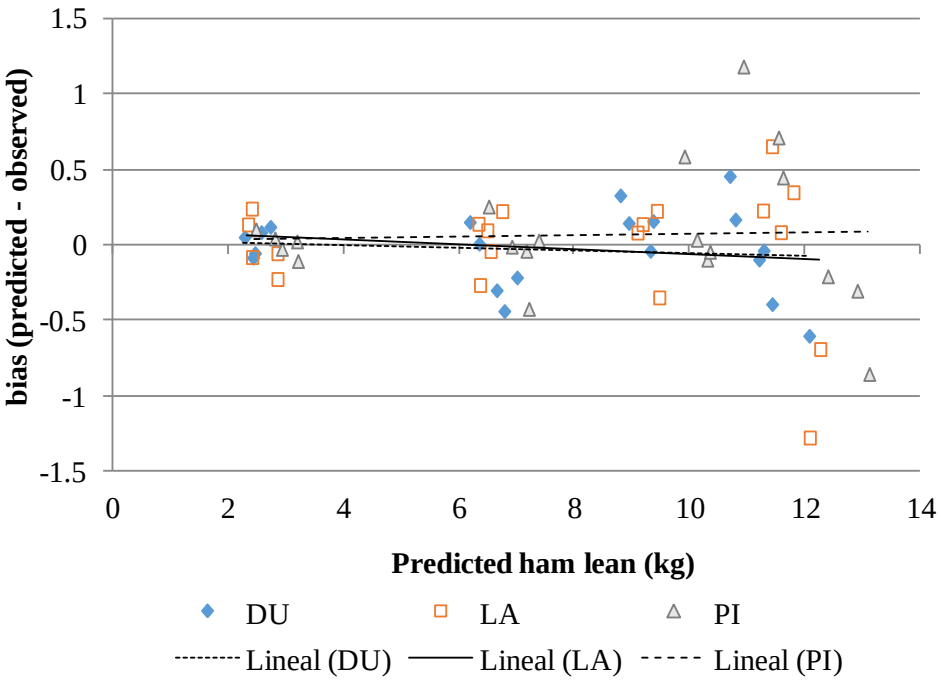


Figure 1: Residuals of the estimation of the lean obtained by (a) individual equations approach (Font-i-Furnols *et al.,* 2015) and (b) global equation approach (Carabús *et al.,* 2015).

(a)



(b)

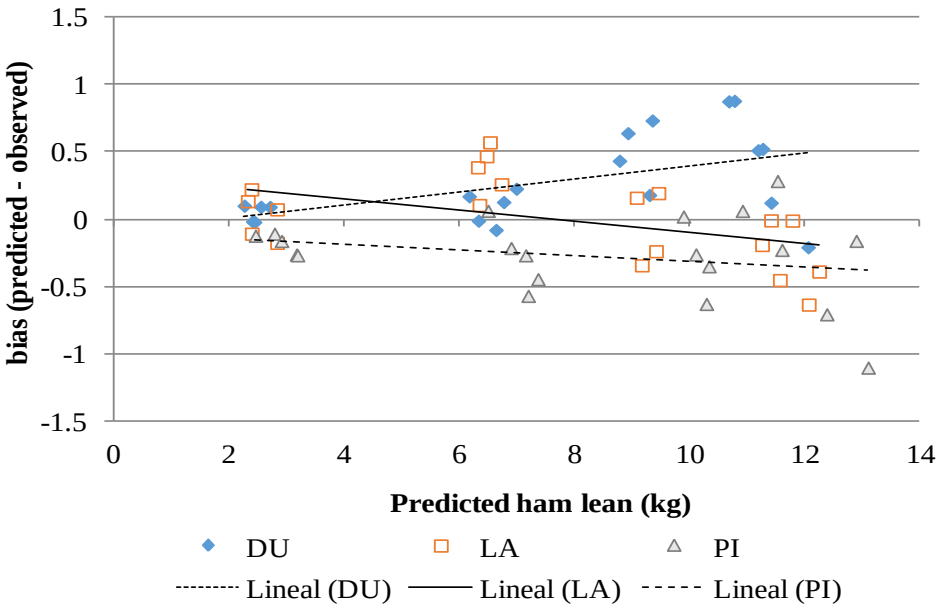


Figure 2: Residuals of the estimation of the lean of the ham obtained by (a) individual equations approach (Font-i-Furnols *et al.,* 2015) and (b) global equation approach (Carabús *et al.,* 2015).

The coefficient of model determination and the standard deviation of the bias for both approaches when the GEN were considered separately are presented in Table 4.

Table 4: Coefficient of model determination (CD) and standard deviation of the bias (SDBias) of the prediction approaches considering the genotypes (DU=Duroc x (Landrace x Large White); LA= Landrace x Large White; PI= Pietrain x (Landrace x Large White)) individually.

Estimated parameter (kg)		**Individual equations approach**		**Global equation approach**	
		Font-i-Furnols *et al*., (2015)		**Carabús *et al*., (2015)**	
	GEN	**CD**	**SDBias**	**CD**	**SDBias**
Lean[a]	DU	1.00	0.35	0.97	0.35
	LA	1.00	0.42	1.00	0.45
	PI	1.01	0.36	1.04	0.42
Fat[b]	DU	0.98	0.28	0.97	0.29
	LA	0.99	0.23	1.03	0.28
	PI	0.98	0.26	1.02	0.29
4 cuts[c]	DU	1.00	0.35	0.99	0.23
	LA	1.02	0.94	1.01	0.33
	PI	0.99	0.60	0.95	0.91
Ham	DU	1.01	0.26	0.91	0.32
	LA	1.02	0.41	1.08	0.32
	PI	0.97	0.43	1.05	0.31
Ham fat	DU	1.02	0.12	0.97	0.14
	LA	1.00	0.11	1.11	0.16
	PI	0.89	0.20	0.96	0.17
Ham lean	DU	1.03	0.21	0.92	0.24
	LA	1.01	0.26	1.06	0.28
	PI	1.09	0.42	1.07	0.42
Ham bone	DU	1.02	0.02	1.01	0.02
	LA	1.07	0.03	1.05	0.02
	PI	1.05	0.04	0.98	0.02
Loin	DU	1.02	0.32	1.06	0.29
	LA	1.03	0.28	1.00	0.24
	PI	1.01	0.24	0.96	0.21
Loin fat	DU	1.02	0.16	1.14	0.24
	LA	1.04	0.15	1.05	0.14
	PI	0.89	0.26	0.90	0.23
Shoulder	DU	1.01	0.19	1.00	0.15
	LA	1.04	0.39	1.01	0.21
	PI	1.01	0.21	1.02	0.22
Belly	DU	1.02	0.20	1.03	0.21
	LA	1.06	0.31	1.02	0.28
	PI	1.03	0.28	1.02	0.30

[a] Lean of the ham, loin, belly, shoulder and tenderloin; [b] Fat of the ham, loin, belly and shoulder; [c]Ham, loin, belly and shoulder

The coefficient of model determination and the standard deviation of the bias for both approaches when the GEN were considered separately are presented in Table 4. Although the lean of the four main cuts' estimation had lower ED values in the global equation approach than the individual equations approach, no differences in CD and in the standard deviation of the bias can be seen between the two approaches, with CD being lower than 5% for all of the GEN. Ham fat in the individual equations approaches a CD value of 0.89 for PI GEN, indicating an overprediction, while, in the global equation approach, the CD value of LA was 1.11, indicating an underprediction. In both cases, the error of disturbances was lower than in the other GEN. Loin fat estimation also presented some different CD values, from 1: 0.89 for PI in the individual equations approach and 1.14 and 0.90 for DU and PI, respectively, in the global equation approach. For PI in both approaches, the ED was lower than 85%.
Thus, except for certain parameters and GEN mentioned above, the CD generally reflects a small shift in the predicted and observed values, indicating the good model predictions.

3. Conclusions

Linear, nonlinear and volume measurements obtained from CT images at specific anatomical positions in live pigs are good predictors of carcass characteristics. There are different methodologies to obtain a prediction equation depending on the purpose, including prediction models that are useful only for a specific type of animal (e.g. the same genotype) or generalized for several types of animals (e.g., different genotypes and sexes). The comparison performed in the present work shows that both approaches for predicting carcass and cut compositions from CT images of growing live pigs are properly developed and useful. Errors are similar for the majority of the parameters, although the predictions are slightly better for some parameters if individual specific equations were used. However, the global equation permits generalization of the predictions to a larger number of animals; thus, it is preferable to use it when the population is mixed or when the parameter estimated does not need a high level of accuracy for a specific line. When this is needed, such as in the case of breeding companies, it is preferable to use individual equations specifically developed for that GEN. Nevertheless, when choosing individual equations, it is important to increase the size of the sample to have greater confidence in the results.

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Chapter 9

General discussion

“Life should not be a journey to the grave with the intention of arriving safely in a pretty and well preserved body, but rather to skid in broadside in a cloud of smoke, thoroughly used up, totally worn out, and loudly proclaiming "Wow! What a Ride!”

Hunter S. Thompson

Two experiments were performed in this Thesis. The first experiment took place between December 2011-June 2012 and included 90 gilts of different genotypes. The ones that were scanned at all the target body weights were raised individually, while the ones that were slaughtered and dissected after scanning were raised in group. The second experiment took place between December 2012-June 2013 and included 92 pigs of different sexual condition. Contrary to experiment 1, pigs that were scanned at all the target body weights were raised in group, while the ones that were slaughtered and dissected after scanning were raised individually. Although both experiments took place in the same seasons of the year, animals had de the same diet and they were raised in the same farm, experiments are not comparable.
Moreover, initially, the main goals were to study the evolution of tissues in genotypes and sexual conditions and their differences individually. And this is what is presented. The first step was to calibrate the device, to study the animals and to identify differences within a group (genotypes or sexual condition).

Phenotypic measurements

Chapter 5 contains the phenotypic measurement within genotypes. In general, DU and LA presented more subcutaneous fat in the loins, ham and shoulder than PI**.** In the loin area LA had more lateral fat than DU and DU presented more vertical fat than LA. It is surprising how fatty is the LA genotype, or maybe the observation should be how lean is the DU. Anyway, these results were not initially expected and there are some reasons that could explain them: first, feed characteristics. All the animals received the same diet, independently of the genotype. Probably, the DU line needed another type of diet to express its maximum potential and the same occurred for the LA line, known for its fast growth. And second, variability among DU crossbreds (Cilla *et al.,* 2006). In this case, they were 50% white Canadian Duroc, much leaner than other DU crossbreds. However, in all the cuts, as expected, PI presented the biggest area and perimeter, meaning that even using the same diet than other genotypes they still are the most conformated pig.

Chapter 7 presents differences between sexual conditions. CM followed (generally) by IM were the ones that presented the highest amount of subcutaneous vertical and lateral fat over the loin, ham and shoulder. IM followed the CM only after 70 kg, when the second vaccine started to show the effects. FE, still, presented the biggest loins and the biggest ham at 100 kg. Nevertheless, no differences for the area or perimeter of the ham and shoulder were found at other weights. Volumes of fat, lean and bones were also studied for different sexual conditions. Surprisingly, there were no differences of fat, lean and bones volume at early weights (30 kg), which suggest that although phenotypic differences exist at this weight (Chapter 5), tissues are not yet developed to express their potential. Situation changed at medium and heavier weights for the lean and fat, especially in the IM, which were similar to EM from 30 to 70 kg, similar to FE at 100 kg and to CM at 120 kg. This explains the timing of the immunocastration vaccine, whose effects are observed after the second vaccine in accordance with (Dunshea *et al*., 2001; Font-i-Furnols *et al*., 2012; Jaros *et al*., 2005).

Carcass and cuts composition

Chapter 5 presents the carcass and cuts composition of pigs of different genotypes. In general, PI was the leanest. It presented the leanest carcass, ham, loin and shoulder, which makes sense as PI is used to increase the amount of lean in the carcasses because generally it is a very lean breed (Gispert *et al*., 2007, Quiniou *et al.,* 1996). PI also presented the heaviest ham and shoulder, results that are in accordance with the area measurements, where PI showed to have the most conformated ham and shoulder. In the ham, this result was already seen at 30 kg, showing the genomic potential of this breed at younger weights. Contrary to PI, DU did not reach the results expected for the fat. No differences between genotypes were found for the amount of fat of the 4 cuts, and the only occasion were DU presented more fat than PI was in the belly cut, and the position was shared with LA, that was fatter than DU in all the cuts. As explained in the beginning of this Chapter, this could be due to the feed characteristics and/or DU variability within crossbreds.

Chapter 7 presents the carcass and cuts composition of pigs of different sexual conditions. In general, EM was the leanest. It presented the leanest carcass, and the leanest ham, sharing this first position with the FE. These results are in agreement with Gispert *et al*. (2010). EM and FE also presented the heaviest ham, however, in this case this is not in accordance with the area results, which did not present significant differences at 120 kg. Contrary to EM and as expected (Gispert *et al*., 2010), CM presented the fattest carcass. Even at 30 and 70 kg CM was as fat as FE, this changed at 100 kg, when CM was clearly the fattest pig from 100 kg to the end of the experiment. This indicates that fat tissue deposites later, thus, it has an allometic coefficient greater than one. Regarding the amount of fat at the final weight of 120 kg, FE and IM had the same behavior, being fatter than EM and less fat than CM. Similar results were found by Pauly *et al.* (2009) and Škrlep *et al.* (2010). So, the final deposition of the total fat is visible at 100 kg live weight, as well as the differences between sexes. The fat of the ham had a similar behavior between sexes, but not the same. At 100 kg, CM had fatter ham than FE and IM, and the three of them had fatter hams than EM, however, at 120 kg CM still showed fatter hams than FE but it was not significantly different than IM, being IM in between CM and FE. In pigs (Landrace x Duroc) x Pietrain crossbreds slaughtered between 108 and 120 kg, Gispert *et al.* (2010) found that the fat thickness over the *gluteus medius* was higher in CM than EM, being in between in FE and IM. This fat thickness was not different between CM, FE and IM in Duroc slaughtered between 135 and 142 kg. Most of the final differences seeing at 120 kg are already observed at 100 kg, and if there are changes, they are minor changes. Thus, valuable information for the final product can be known at 100 kg (3-4 weeks before the final weight) and if the results are not the expected ones there is still a chance to change the food or management to expect better results.

Allometric growth

The allometric growth of the tissues and cuts is presented in Chapter 5 (Exp. 1) and 7 (Exp. 2). It represents the growth rate of one tissue respects to another or, in this case, respects the body weight. In both experiments the growth of fat presented b-coefficients higher than one, meaning faster deposition rate of this tissue. Fisher *et al.* (2003) and Kouba and Bonneau (2009) also found allometric coefficients higher than one for fat, however, Kolstad (2001) found this coefficient higher than one only for inter/intramuscular fat. LA showed the fastest deposition of fat, while for the Exp. 2, IM and CM showed to be the fastest for this tissue.

The growth rate for the lean tissue with respect to the body weight presented few differences between experiments. In Chapter 5 (Exp. 1), the b-coefficient was lower than 1 (but very close to the unity – 0.97/0.95/0.93) and in Chapter 7 (Exp. 2) the same coefficient was slightly higher than 1 (1.00/1.07/1.02). Although the results are not exactely the same for both experiments, they indicate a very similar growth rate for the lean tissue with coefficient close to the unity in accordance with Fisher *et al.* (2003) and Wagner *et al.* (1999). Genotypes showed no differences for the lean of the 5 cuts, but FE and EM were clearly different than CM and IM, it makes sense, since these last two were the ones that deposited fast more rapidly.

The b-coefficient for the weight of the cuts (ham, loin, shoulder and belly) was also very similar between experiments. Ham and shoulder presented results close to the unity, meaning that their development is in parallel with body weight. The loin and the belly showed higher values, its growth rate is faster than the body weight. Again, the bones presented the same results in Chapter 5 and 7, a b-coefficient lower than 1, indicating its slow development in accordance with Fisher *et al.* (2003) and Wagner *et al.* (1999). Similar results for the lean, fat and bones were found when comparing the tissues with the cut weight (Chapter 5).

Estimation of the maturity body weight

As presented, the estimation of the maturity body weight (MBW) have been studied among different genotypes and sexual conditions. However, as far as the authors know, there are no studies of predicted maturity body weight in immunocastrated males. And although the MBW was not an objective of this work, the authors preferred to include it to add more knowledge about the immunocastration. That was the main reason to include this goal in this Thesis, to obtain more information about body changes in immunocastrated pigs. The use of the Gompertz equation is explained by its simplicity and the biological meaning attributed to some parameters (a = maturity body weight).

In the present work, the Gompertz curve fit the data very well from 0 to 150 days for all SEX, but seemed to overestimate live weights after that point, especially for IM. One reason could be the lack of observed weights above 120 kg. Real weights after 120 kg (170 days approximately) showed a low decrease of the slope and the very initial part of the asymptote for the EM, FE and CM, but this change was not visible for the IM. Thus, it was impossible to determine the mature weight from these data with any degree of confidence.

The predicted MBW for IM was also conditioned by the fact that this group of animals presented two clear behaviors, being similar to EM from birth to the second injection of the vaccine and more comparable to CM from that point to the final weight. (Dunshea *et al.,* 2001, Jaros *et al.,* 2005).

Prediction equations and their comparison

Chapter 4 presents a selection of different prediction equations for the Exp 1, obtained from CT predictors. Chapter 6 contains two types of prediction equations for the Exp 1 and Exp 2, the same equation for all the animals: one, obtained from CT predictors and the other, obtained from potential farming predictors. Finally, Chapter 8 compares equations from Chapter 4 and Chapter 6.

In Chapter 4 four types of prediction equations were evaluated: lineal, quadratic and allometric using tissue volumes as predictors and lineal using tissue volume plus additional measures (fat thicknesses, areas, etc.) as predictors. Allometric showed to be useful and in some traits it was the best choice for estimating tissue growth from tissues volumes obtained by CT. Even that, when combining the information provided by volumes with measurements (linear and non linear) the accuracy of some predictors increased, that is the reason why the best prediction equations (the ones that presented the lowest relative error of prediction were selected and used to predict carcass and cuts composition in Chapter 5, using one equation for each genotype. The majority of the equations selected were those that combined tissue volume and additional measurements as predictors in a linear way. This makes sense, since in carcass classification linear measurements of fat and muscle depth is well documented to be related with carcass characteristics (Font i Furnols and Gispert, 2009; Engel *et al*., 2012).

In Chapter 6, the majority of the prediction equations were linear, including as predictors volumes plus additional measurements (for the CT equations) and physical measurements for the potential on farm equations.

What differences equations obtained in Chapter 6 and Chapter 4 is that in Chapter 6, the same equations used to predict carcass and cuts composition for the genotypes were also used to predict the same parameters in pigs of different sexual conditions. Thus, they were more general equations. To do that, regression equations using predictors with no SEX or GEN effect were performed, then the mean squared error of prediction (MSEP) was decomposed into mean bias, slope bias and random error. The equation selected was the one that presented random error higher than 0.7.

With these two types of prediction equations presented in Chapter 4 and 6 to predict carcass composition from images of live pigs of different genotypes it was necessary to compare them and study which of them would be more useful for each specific occasion.

Chapter 8 contains this comparison. The criterion selected was the decomposition of the MSEP in: 1) error due to central tendency (ECT), 2) error due to regression (ER) and 3) error due to random effects (ED). At that time, prediction accuracy was studied individually (by each genotype) or globally (for all the genotypes together).

Both equations presented good results. As expected, the individual equations for each genotype presented better results than the global equations when comparing predictions by genotype. Contrary, the global equations were slightly better when predicting parameters without distinction of the genotype. Both equations are useful; however, the global equation permits to apply it for a bigger number of animals (without distinction of genotype or sexual condition), thus is preferable to use it when the population is mixed. Nevertheless, when a higher level of accuracy is need, such as the case of a breeding company, it is preferably to use individual equations developed for each genotype but, in this case, it is also recommended to use a big sample, in order to have high confidence in the results.

In the present Thesis, individual equations for different sexual conditions have not been developed but global equations presented in Chapter 6 have demonstrated to be strong enough.

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Chapter 10

Conclusions

“Buy the ticket, take the ride”

Hunter S. Thompson

This Thesis presented a step towards computed tomography image analysis, its applications and its results in farming pigs. The most important conclusions arising from the present work are summarized below:

1. Image analysis technologies have proved applications in the livestock field. Predictions show higher precision for CT and MRI devices than DXA, VIA and US. The election of the device depends on several aspects such as purposes, availability, need of precision and accuracy, cost, required labour and possibility to be used on farm.

2. There is a very good relationship between cross-sectional CT images obtained in live pigs. This information can be useful for breeding, optimizing management and, for example, in nutritional studies. Consequently, CT images can be used to predict, accurately, carcass and cuts composition from live pigs, being this information useful in breeding and nutritional studies among others.

3. Prediction equations of carcass and cuts composition derived from live pigs by using of on-farm measurements as predictors can be useful for genetic improvement, feeding programs and management for pigs of different genotypes and sexual conditions.

4. There are clear differences in the body composition between genotypes and sexes, particularly when pigs are close to the commercial weight but also at early weight. This reflects the real importance of genetic traits and sexual condition, which can be used to produce the desired product.

5. Although some differences in pigs from different genotypes or sexual conditions exist, in all the cases the fat growth rate, relative to the live weight and to the weight of the main pieces, was higher (allometric coefficient > 1) than the lean and the bone growth rates. This indicates that fat is the last tissue to be deposited in the body and, by controlling the slaughter weight (within genotype and sex), it is possible to control the fat deposition.

6. The growth rate for fat in carcass and cuts was faster in Landrace x Large White than in the other genotypes. Regarding sexual conditions, fat deposition was proportionately most rapid in immunocastrated and castrated males and least rapid in entire male and female, and lean deposition behaved inversely. Thus, although immunocastrated males behave as entire males until the second vaccine administration, immunocastrated and castrated males have a very similar performance regarding the speed of deposition of the fat.

7. Different crossbreeds are suitable for different markets. For the fresh meat market, where low fat product and great lean areas are required, Pietrain x (Landrace x Large White) and females would be the most adequate. Contrarily, for the cured ham porduction, that requires high level of

fat (subcutaneous and intramuscular), the Landrace x Large White and Duroc x (Landrace x Large White) crossbreed and castrated males would be the best candidates.

8. Prediction of body composition from images of live pigs can be obtained precisely using different types of equations. However, linear and allometric models using CT tissue volumes as predictors, or linear models using CT tissue volumes plus additional physical measurements at specific anatomical positions of the body, are more robust than quadratic models.

9. The global equation, obtained from and for animals of different genotypes and sexes, permits generalization of the predictions to a larger number of animals, thus it is preferable to use it when the population is mixed or when the parameter estimated does not need high level of accuracy for a specific line. When this is needed, such as in the case of breeding companies, it is preferable to use genotype specific prediction equations.

10. Computed tomography can be notably useful for the meat industry because the carcass quality parameters can be known at early weights of the live animals and models can be applied to know the carcass characteristics at slaughter. As a result, the use of this information can provide economic benefits for all of the stakeholders involved in the meat chain.

Chapter 10

Conclusiones
(in Spanish)

“Caminando, caminado voy buscando libertad, ojalá encuentre camino para seguir caminando”
Víctor Jara

Esta Tesis presenta avances importantes en el campo del análisis de imágenes de tomografía computerizada, su aplicación y los resultados obtenidos en cerdos de granja. Las conclusiones más importantes que se derivan del presente trabajo se resumen a continuación:

1. Las tecnologías de análisis de imágenes han demostrado ser aplicables para el estudio de los animales de granja. Las predictiones muestran niveles de precisión más altos para los equipos de CT y la MRI, seguidos por el DXA, VIA y US. No obstante, la elección de un dispositivo o el otro o, incluso de la tecnología, depende de muchos aspectos tales como el propósito u objetivo, la disponibilidad, el coste, la necesidad de precisión y la posibilidad de ser utilizado en granja.

2. Existe una relación muy buena entre las imágenes axiales obtenidas con CT en cerdos vivos y sus canales y cortes primarios. Consecuentemente, las imágenes de CT pueden ser utilizadas para predecir la composición de la canal y los cortes primarios de animales vivos, siendo esta información muy útil para estudios de genética e incluso de nutrición, entre otros.

3. Las ecuaciones de predicción de la composición de la canal y los cortes primarios de animales vivos, usando medidas obtenidas en granja como predictores, pueden ser útiles para la mejora genética, programas de alimentación y manejo de cerdos de distintas genéticas y sexos.

4. Existen diferencias claras en la composición del cuerpo de cerdos de distintas genéticas y sexos, particularmente cuando éstos están cerca del peso comercial, no obstante, estas diferencias también se observan a pesos tempranos. Ésto refleja la importancia real de los rasgos genéticos y del sexo, información que puede ser utilizada para obtener el producto deseado.

5. Aunque existen diferencias entre cerdos de distintas genéticas y sexos, en todos los casos, el ratio de deposición de la grasa relativo al peso vivo y al peso de los cortes primarios fue mayor (coeficiente alométrico > 1) que el ratio de deposición del magro y de los huesos. Ésto indica que la grasa es el último tejido que se deposita en el cuerpo, así pues, controlando el peso a sacrificio (dentro de genotipo y sexo), es posible controlar, al mismo tiempo, la deposición de grasa.

6. El ratio de deposición de la grasa para los cortes primarios fue más rápido en los Landrace x Large White que en las otras genéticas. Respecto a los sexos, la deposición de grasa fue proporcionalmente más rápida en los machos inmunocastrados y castrados y menos rápida en los machos enteros y en las hembras, mientras que en la deposición de magro ocurrió lo contrario. Entonces, aunque los machos inmunocastrados se comporten como los machos enteros hasta la segunda administración de la dosis de la vacuna, los machos inmunocastrados y los castrados tienen un crecimiento muy similar por lo que se refiere a la velocidad de deposición de magro y grasa.

7. Diferentes cruces genéticos son adecuados para diferentes mercados. Para la carne fresca, donde se requieren productos magros con piezas grandes y magras, los cerdos Pietrain x

(Landrace x Large White) y las hembras serian los más adecuados. Contrariamente, para la producción de jamón curado, que requiere un alto nivel de grasa (subcutánea e intramuscular), los cerdos Landrace x Large White y Duroc x (Landrace x Large White) y los machos castrados serían los mejores candidatos.

8. La predicción de la composición corporal a partir de imágenes de cerdos vivos se puede obtener de manera precisa utilizando distintos tipos de ecuaciones. No obstante, los modelos lineales y alométricos, utilizando volúmenes de tejidos obtenidos con CT como predictores, o los modelos lineales, utilizando volúmenes de tejido obtenidos con CT más medidas físicas obtenidas en puntos anatómicos específicos, son más robustos que los modelos cuadráticos.

9. La ecuación global, obtenida a partir y para animales de distintos genéticas y sexos, permite generalizar las predicciones para un mayor número de animales, así pues, es preferible utilizarla cuando la población es mixta o cuando el parámetro estimado no requiere un alto nivel de precisión. Cuando esta precisión es requerida, como es el caso de compañías genéticas, es preferible utilizar las ecuaciones individuales, específicamente desarrolladas para cada genotipo.

10. La tomografía computerizada puede ser de gran utilidad para la industria cárnica porque los parámetros de calidad de la canal se pueden conocer a en animales vivos a pesos tempranos y se pueden aplicar modelos fiables para conocer las características de la canal al sacrificio. Como resultado, la utilización de esta información puede aportar beneficios económicos para todos los actores involucadros en la cadena alimentaria.

Chapter 10

Conclusions
(in Catalan)

“Perquè hi haurà un dia que no podrem més i llavors ho podrem tot”
Vicent Andrés Estellés

Aquesta Tesi presenta avanços importants cap a l'anàlisi d'imatges de tomografia computeritzada, la seva aplicació i els resultats aplicats en porcs de granja. Les conclusions més rellevants que se'n deriven es resumeixen a continuació:

1. Les tecnologies d'anàlisi d'imatges han demostrat ser aplicables per animals de granja. Les prediccions mostren nivells de precisió més alts pels equips de CT i MRI, seguit pel DXA, VIA i US. No obstant, l'elecció d'un dispositiu o d'un altre o, fins i tot, de la tecnologia, dependrà de molts aspectes, tals com el propòsit o l'objectiu, la disponibilitat, el cost, la precisió requerida i la possibilitat de ser utilitzat en granja.

2. Existeix una relació molt bona entre les imatges de secció de CT obtingudes en porcs vius i les seves canals i talls primaris. Conseqüentment, les imatges de CT poden ser utilitzades per predir la composició de la canal i talls primaris d'animals vius, essent aquesta informació molt útil per estudis de genètica o, fins i tot, estudis de nutrició, entre altres.

3. Les equacions de predicció de la composició de la canal i talls primaris d'animals vius, utilitzant mesures obtingudes a granja com a predictors, poden ser útils per a la millora genètica, programes d'alimentació i maneig de porcs de diferents genètiques i sexes.

4. Existeixen diferències clares en la composició corporal de porcs de diferents genètiques i sexes, particularment, quan aquests animals estan a prop del pes comercial, no obstant, aquestes diferències també s'observen a pesos precoços. Això reflecteix la importància real de les característiques genètiques i del sexe; aquesta informació pot ser utilitzada per obtenir el producte desitjat.

5. Tot i que existeixen diferències entre porcs de diferents genètiques i sexes, en tots els casos, el rati de deposició del greix respecte al pes viu i al pes dels talls primaris va ser major (coeficient al·lomètric > 1) que el rati de deposició del magre i els ossos. Això indica que el greix és l'últim teixit que es diposita en el cos, així doncs, controlant el pes a sacrifici (dins genotip i sexe), és posible controlar, al mateix temps, la deposició de greix.

6. El rati de deposició del greix pels talls primaris va ser més ràpid en els Landrace x Large White que en les altres genètiques. Respecte als sexes, la deposició de greix va ser proporcionalment més ràpida en els mascles immunocastrats i castrats i menys ràpida en els mascles enters i en les femelles, mentre que en la deposició de magre va ocòrrer tot el contrari. Així doncs, encara que els mascles immunocastrats es comportin com a mascles enters fins a la segona administració de la dosis de la vacuna, els mascles immunocastrats i els mascles castrats tenen un creixement molt similar pel que es refereix a la velocitat de deposició de magre i greix.

7. Diferents creuaments genètics són adequats per a diferents mercats. Per a la carn fresca, on es busquen productes magres amb peces grans i magres, els porcs Pietrain x (Landrace x Large White) i les femelles serien els més adequats. Contrariament, per a la producció de pernil curat,

on es requereix un alt nivel de greix (subcutani i intramuscular), els porcs Landrace x Large White i Duroc x (Landrace x Large White) i els mascles castrats serien els millors candidats.

8. La predicció de la composició corporal a partir de les imatges de porcs vius es pot obtenir de manera precisa utilitzant diferents tipus d'equacions. No obstant, els models lineal i al·lomètric, utilitzant volums dels teixits obtingut amb CT com a predictors o, els models lineals, utilitzant volums dels teixit obtinguts amb CT més les mesures físiques obtingudes en punts anatòmics específics, són més robusts que els models quadràtics.

9. L'equació global, obtinguda a partir i per animals de diferents genètiques i sexes, permet generalitzar les prediccions per a un major nombre d'animals. Així doncs, és preferible utilizar-la quan la població és mixta o quan el paràmetre estimat no requereix un alt nivel de precisió. Quan aquesta precisió és requerida, com és el cas de les companyies genètiques, és preferible utilitzar equacions individuals, específicament desenvolupades per a cada genotip.

10. La tomografia computeritzada pot de ser gran utilitat per a la indústria càrnia perquè els paràmetres de qualitat de la canal es poden conèixer directament a partir d'animals vius a pesos baixos, i es poden aplicar models fiables per a conèixer les característiques de la canal al sacrifici. Com a resultat, la utilització d'aquesta informació pot aportar beneficis econòmics per a tots els actors involucrats en la cadena alimentària.

Annex 1

Dissemination paper

Included in Chapter 1 Part II

Aplicaciones de la tomografía computerizada en el campo de la producción y la tecnología de alimentos

En este trabajo los autores describen las diversas aplicaciones que la tomografía computerizada tiene en la producción agrícola y ganadera y en la tecnología alimentaria. Esta técnica no invasiva se puede utilizar tanto para la determinación de la composición de los alimentos, y de los animales vivos o sus canales, como para seguir la difusión de la sal durante el proceso de curado del jamón.

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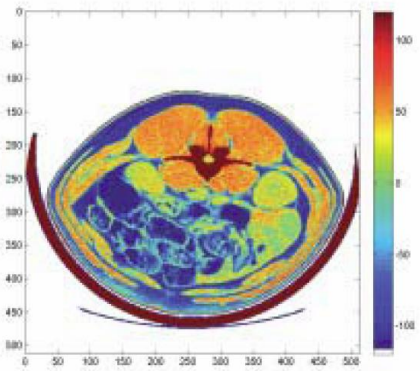
¿En qué consiste la tomografía computerizada?

Los rayos X son ondas electromagnéticas que pueden atravesar la materia, perdiendo en este proceso, parte de su energía inicial. La tomografía computerizada (TC) consiste en la obtención de imágenes digitales de secciones de un objeto, llamadas tomogramas, a partir de una serie de proyecciones producidas por los rayos X (Kalender, 2005; Seeram, 2009).

La aplicación de la TC en el campo de la producción y la tecnología de alimentos se basa en las diferentes atenuaciones que producen los distintos tejidos biológicos, dependiendo de su densidad, sobre los rayos X que los atraviesan. Por esta razón, en los tomogramas obtenidos se distinguen los diferentes tejidos y estructuras biológicas. Es de especial utilidad porque se trata de una tecnología no invasiva.

Innovación

Figura 1. Tomograma de la zona abdominal de un cerdo vivo



Aplicaciones de la tomografía computerizada

El equipo de TC es muy utilizado en medicina humana para el diagnóstico de diferentes tipos de enfermedades (Jongbloed *et al*., 2005). También se encontraron otras utilidades de la TC en agricultura (Elliot *et al*., 2010), forestales (Schmoldt *et al*., 1999), etc. Del mismo modo, esta técnica se ha aplicado en alimentación y se ha comprobado que puede ser una herramienta muy valiosa para la estimación de la composición de los alimentos. En este sentido, en el campo de la fruta, se han hecho estudios para determinar el contenido de agua de las manzanas (Tollner *et al*., 1992), para determinar cambios internos en el melocotón (Barcelon *et al*., 1997) o para determinar el grado de madurez del tomate (Brecht *et al*., 1991). También se han hecho estudios con animales y sus canales. En acuicultura se ha evaluado la forma del cuerpo del salmón y los contenidos de grasa del mismo (Einen *et al*., 1998); en avicultura se ha medido la producción de carne de pechuga en pollos Broiler (Remignon *et al*., 1997); en ovinocultura se ha estudiado la composición de corderos vivos (Toldi *et al*., 2007) y de sus canales (Johansen *et al*., 2007); en porcinocultura se ha medido la deposición y distribución de la grasa (Kolstad, 2001), la composición del cuerpo del cerdo en vivo (Luiting *et al*., 1995), y en canal (Font i Furnols *et al*., 2008). Así pues, la aplicación de TC en animales es de gran importancia para determinar la composición del cuerpo y, en términos económicos, re-

Figura 2. Media canal en el equipo de tomografía computerizada

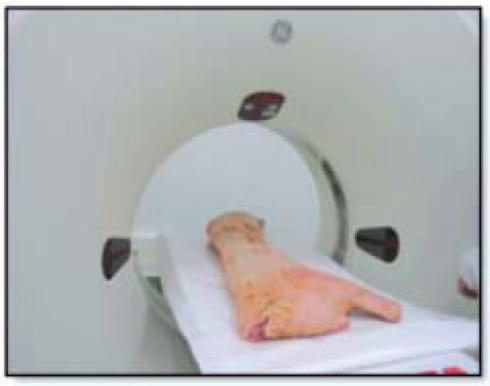
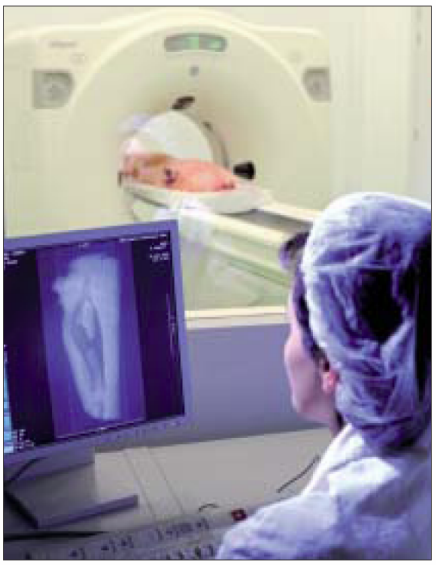


Figura 3. Media canal durante el proceso de escaneo



sulta importante la predicción que se puede hacer del porcentaje de magro de la carne (tanto vivo como en canal), sin necesidad de despiezarla ni disecarla. La TC también se ha usado para determinar la grasa intramuscular (Font i Furnols *et al*., 2009) y la composición en ácidos grasos de la carne (Prieto *et al*., 2010). También permite hacer un seguimiento de la difusión de la sal durante el proceso de curación de la carne así como cuantificar el contenido de sal y agua en distintos momentos del proceso de elaboración del jamón curado (Fulladosa *et al*., 2010; Santos-Garcés *et al*., 2010).

Evaluación de la composición corporal de animales vivos

Conocer la composición corporal en animales vivos y la evolución y deposición de las diferentes tejidos durante el crecimiento es vital cuando se quiere optimizar el producto final obtenido, ya sea a partir de la genética o de la alimentación. Está generalmente asumido que la variación en la composición corporal juega un rol importante en el crecimiento de los cerdos. Esta información, referente a la calidad del producto, debería potenciar la comunicación entre los diferentes eslabones de la cadena cárnica, desde los ganaderos al consumidor (Cross y Whittaker, 1992; Kirton y Purchas, 1996). Es bien conocido que a un peso similar, las diferentes genéticas tienen canales con características muy distintas (Gispert *et al*., 2007), que ya se aprecian a 30 kg de peso (Carabús *et al*., 2011), obteniendo una gran variedad de tipos de canales según sus espesores de grasa, áreas del lomo, proporción de jamón y contenido en magro, entre otras características. Una de las mejores maneras de estudiar la composición del cuerpo de los animales vivos es usando un equipo de TC ya que los diferentes tejidos tienen densidades diferentes, lo que permite que se puedan distinguir y cuantificar en las imágenes obtenidas (**figura 1**). Dichas imágenes se tratan con *software* adecuados, como el *VisualPork* (Boada *et al*., 2009), con técnicas estadísticas avanzadas como las regresiones por mínimos cuadrados parciales o PLS, o bien combinando ambas metodologías.

La evaluación en vivo de los animales con TC permite observar *in vivo* e *in situ* el efecto de una dieta determinada (cómo y cuándo se depositan los distintos tejidos), el efecto de las vacunas en el crecimiento y las características de calidad de la canal y de la carne. Además, se pueden obtener coeficientes alométricos de las diferentes características de composición de la canal de interés, ya sea según la genética del animal, el sexo, la alimentación, etc. Hasta la aplicación de estas nuevas tecnologías, era muy difícil conocer la evolución de la composición corporal en el tiempo en un mismo animal. La técnica que se utilizaba era tomar medidas en la zona del lomo mediante ecógrafos o si-

Figura 4. Tomograma donde se ha seleccionado el área del lomo y la grasa subcutanea

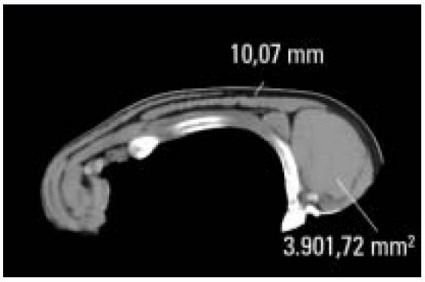
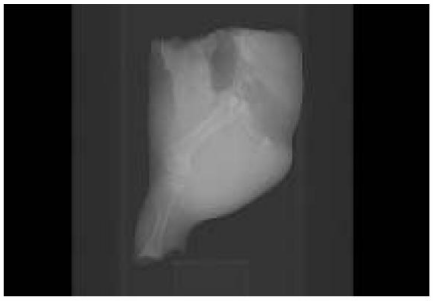


Figura 5. Jamón escaneado



milares, sin embargo, la TC permite un análisis integral del animal. Recientemente, en el IRTA, se ha empezado un proyecto para determinar el crecimiento alométrico de animales de diferentes líneas genéticas y sexos evaluándolos en vivo, con TC, en diferentes momentos de su crecimiento (INIA RTA 2010-00014-00-00).

Caracterización de la canal

El contenido en magro de la canal es muy importante para clasificar dicha canal. Por esta razón, se han hecho bastantes trabajos de investigación en los que se ha estudiado la predicción de este contenido (Font i Furnols *et al*., 2001; Gispert y Font i Furnols, 2003). Los mataderos estiman el contenido de magro con equipos basados en ultrasonidos (Autofom, Ultrafom y Ultrameater), reflectancia (Fat-o-Meat'er, Hennessy Grading Probe y Captador Grasa-Magro) y de visión (VCS2000 y Imagemeater) o medidas lineales en la línea media de la canal. Para obtener la mejor ecuación para estimar el porcentaje de magro, estos equipos se han de calibrar, lo que requiere llevar a cabo un trabajo extenso: el corte y disección usando el método simplificado de referencia (Walstra y Merkus, 1995) o la disección completa de, al menos, 120 canales representativas. El error de predicción de las ecuaciones

Figura 6. Estructura interna de varios alimentos

de estimación tiene que ser menor del 2,5% (Reglamento (CE) nº 1234/2008).

Jopson *et al*. (1995) así como Glasbey y Robinson (1999, 2002) sugirieron la utilización de la TC como método no destructivo alternativo a la disección en estudios donde esta práctica es requerida (**figura 2** y **3**). A partir de los datos del proyecto *EU EUPIGCLASS*, Dobrowolski *et al*. (2003) recomendaron la utilización de la TC como método de referencia para la estimación del porcentaje de magro y recientemente, esta técnica está permitida por la legislación (Reglamento (CE) nº 1234/2008). Las medidas tomadas con la TC tienen un error de predicción bajo (Judas *et al*., 2007; Font i Furnols *et al*. 2008), pero escanear la canal entera tiene un coste elevado. Una manera de reducir costes podría ser obtener algunas imágenes en puntos concretos de la canal (**figura 4**) o escanear sólo algunas piezas (**figura 5**) ya que esto permitiría reducir costes de imágenes adquiridas y, por tanto, costes totales (Teran *et al*., 2009).

Aplicaciones en el producto final

La TC también puede utilizarse como soporte en el diseño y desarrollo de nuevos procesos y productos, para la evaluación de la calidad del producto final sometido a distintos procesos o formulaciones y para el análisis de estructuras internas de alimentos. En la **figura 6** se muestra un ejemplo de las imágenes que se pueden obtener utilizando esta tecnología. Se pueden ver las estructuras internas de los alimentos de forma no invasiva; como por ejemplo la formación de ojos en el queso según el proceso al cual han sido sometidos, el grado de madurez de las frutas o la formación de la estructura del pan según la composición de este.

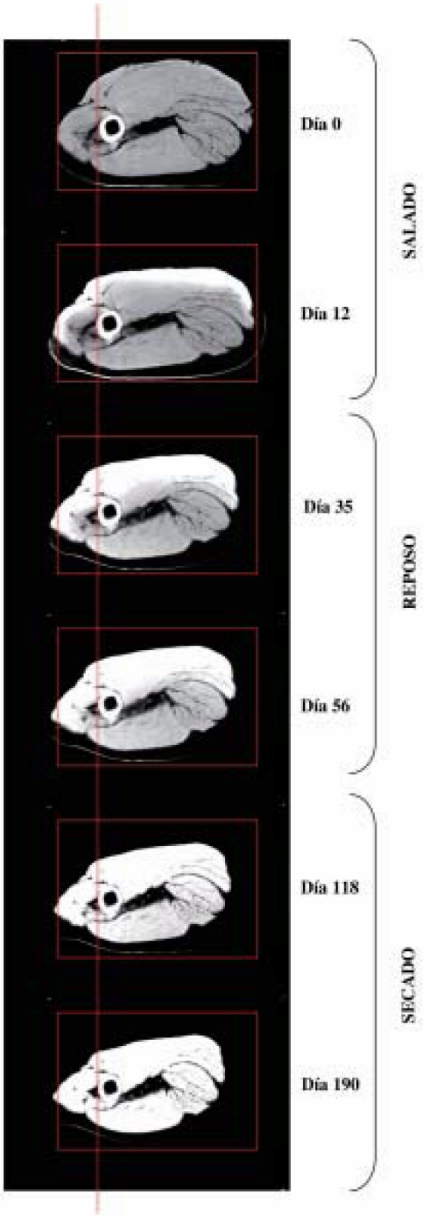
La tomografía computerizada también tiene un interés especial para el estudio de los procesos de salado y curado de carne. La elevada densidad de los iones de la sal, produce un marcado incremento de los valores de atenuación de la TC. Los iones Na^+ y Cl^- tienen más densidad que los componentes principales de la carne (C, H, N, O), lo cual permite distinguir la presencia de sal en ella. Por este motivo, esta tecnología no destructiva, permite el estudio de la difusión de sal y agua, así como su distribución en una misma pieza a lo largo de todo el proceso de elaboración (**figura 7**). Además, se han desarrollado modelos de predicción de sal y agua en jamón curado permitiendo determinar los contenidos de sal y agua de cualquier punto del jamón con un error del 0,3% y del 1,5%, respectivamente (Fulladosa *et al*., 2010; Santos-Garcés *et al*., 2010).

Figura 7. Imagen de un jamón fresco y un jamón salado donde se observa la difusión de la sal hacia el interior del producto

Por lo tanto, gracias a lo comentado anteriormente, la TC tiene un importante potencial como herramienta para la optimización de procesos alimentarios, especialmente para el estudio de los procesos de salado en jamón curado, permitiendo evaluar cualitativamente y cuantitativamente la difusión y distribución de sal y agua a lo largo de todo el proceso de elaboración (**figura 8**).

También se pueden obtener imágenes de la distribución de sal y agua en toda la sección (**figura 9**), lo cual da una información, además de no destructiva, complementaria y más específica que los tradicionales análisis fisicoquímicos. Al mismo tiempo se puede utilizar para el diseño de nuevos procesos de post-salado. En productos reducidos en sal, es necesario adaptar los procesos tradicionales en función del contenido de sal en las zonas más críticas del producto (**figura 9**). En este sentido, la TC ha sido utilizada por varias empresas para adaptar las condiciones de procesado en jamones con contenido de sal reducido, asegurando así su estabilidad microbiológica. La extensión de la etapa de post-salado a baja temperatura hasta alcanzar, en la zona interna más crítica, un contenido de sal idéntico al adquirido por el producto con un salado estándar, permite reducir la aparición de defectos en el producto final.

Figura 8. Secciones transversales de un mismo jamón curado durante el proceso de salado, reposo y secado adquiridas con tomografía computerizada



Asesoramiento e innovación

Esta tecnología está disponible en el IRTA para todas las empresas interesadas. A partir de la información obtenida, el IRTA ofrece asesoramiento e innovación a la industria alimentaria:

- Mejora de la productividad.
- Mejora de la calidad de productos elaborados.
- Diseño de nuevos procesos.
- Optimización de los procesos de elaboración.
- Estudio de los procesos de congelación/descongelación.
- Estudio de los gradientes de agua en distintos productos.
- Estudio de la formación de anomalías en el interior del producto.
- Estudio de las estructuras y texturas de todo tipo de alimentos, formación de ojos en quesos, etc.
- Estimación de los contenidos de grasa intramuscular y veteado en carne.
- Soporte al diseño de procesos para elaborar productos con un contenido de sal reducido.
- Evaluación y caracterización de canales y de sus piezas: contenido en magro, espesores, áreas, etc.
- Calibración de equipos para la clasificación de porcino.
- Evaluación del efecto de la genética o la dieta en la deposición de los diferentes tejidos a lo largo del crecimiento del animal.

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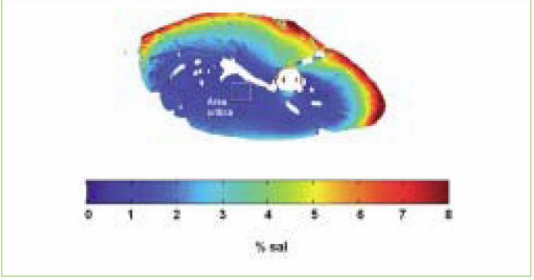
Figura 9. Imagen de distribución de sal en una sección de jamón curado



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La tomografía computerizada tiene un importante potencial como herramienta para estudiar los procesos de salado en jamón curado

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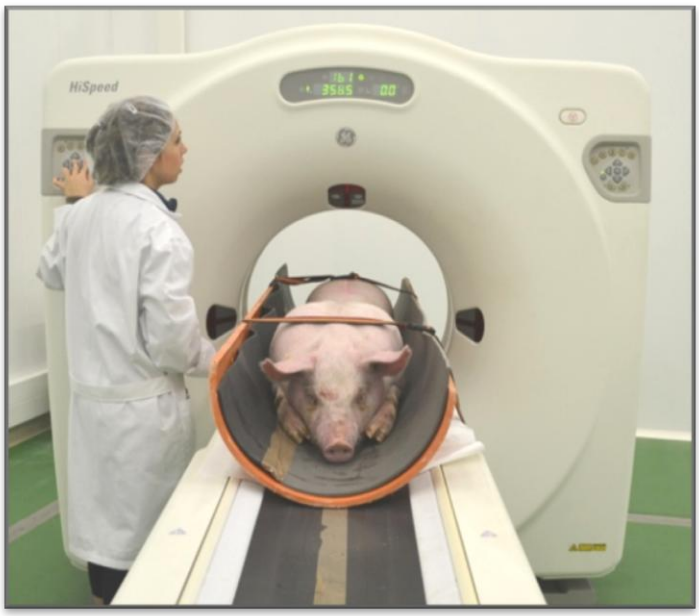
Some extras

Pictures about the process…

From the farm to the CT:

Sleeping and scanning:



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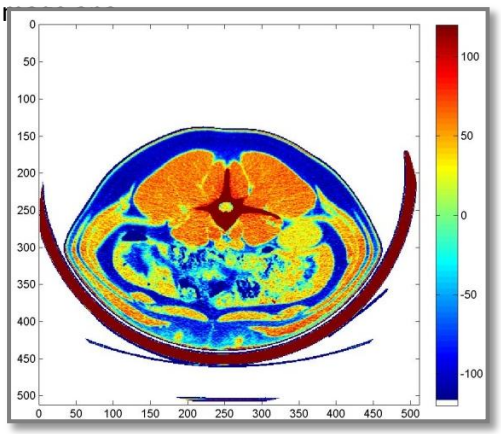

About the author…

Anna Carabús i Flores was born on February 12th 1985 in Cervià de Ter (Girona). After classical grammar school and a very short non-promising career in the ski world, she enrolled at the University of Girona in 2003 to study Agricultural Technical Engineering. In 2007, as part of the final university project, she founded a small company called *Pigallat,* that commercialises high quality meat from the farm to the consumer (it is still running). During her studies, and with the purpose of learning, she worked as a project and vet assistant in different companies of the region. In 2008, she enrolled at the University of Lleida to study Agricultural Engineering. During that period she obtained a grant to do research at the Colorado State University (USA).

In 2011 she obtained her MSc in Pig's Health and Production (carried out at the University of Lleida, University of Zaragoza, University Complutense of Madrid and Autonomous University of Barcelona). Afterwards, she started her Ph. D. Thesis at IRTA (Research Institution of Agrifood Technologies) in collaboration with the University of Zaragoza.

In 2014 she travelled to UCDavis in California (USA) where she conducted an important part of this Thesis. Currently, she is the Innovation Manager of the Agrifood Industry at IRTA, trying to be the bridge between "science" and "industry". Always keeping in mind that science must have a real application and that the primary sector and the industry should take advantage of this knowledge. In the spare-time, she runs the family farm and the very small company as mentioned above. She loves mountains, specially the Pyrenees, and most of the crazy outdoors sports. She is passionate for her work and the primary sector and totally in love with her family and best friends.

" (…) i en acabat, que cadascú es vesteixi com bonament li plagui, i via fora!
Que tot està per fer i tot és possible"

Miquel Martí i Pol